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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in the placenta and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S.provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY REFERENCE THEREOF

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file pto_PLACENTA.txt, created 24 January 2001, having 26,548,337 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-derived single exon nucleic acid probes expressed in human

placenta and single exon nucleic acid microarrays that include such probes.

Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger *et al.*, *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert *et al.*, *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins — known or suspected — about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick *et al.*, *Nature* 308(5955):153-8 (1984).

More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences — that is, those accessible through isolation of mRNA — are of greatest initial interest. This "expressed sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*, *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches — and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species — there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999), there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin *et al.*, *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher *et al.*, *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu *et al.*, *Genet. Eng.* 16:241-53 (1994); Uberbacher *et al.*, *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev *et al.*, *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev *et al.*,

Ismb 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*, *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. *Reviewed in* Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi *et al.*, *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single exon genes, *i.e.*, lack introns, Lopez *et al.*, *RNA* 5:1135-1137 (1999); Goffeau *et al.*, *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy. There is a need for methods and apparatus that permit analysis of placenta samples for the prediction and diagnosis of diseases caused by genetic defect, particularly those with polygenic etiology.

Summary of the Invention

The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,232 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable

substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 13,233 - 26,232, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,232.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,232 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a

nucleic acid expressed in the human placenta.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 13,233 - 26,232 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human placenta.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or

fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human placenta, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 26,232 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 13,233 - 26,232, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any

of SEQ ID NOS.: 1 -13,232 .

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 26,233 - 38,837.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 26,233 - 38,837, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the

term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7, preferably at least 10^8, more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display

of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color

hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad

outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly

include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigsii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic

assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational

substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, *e.g.*, syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the

sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been

described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to

report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can

be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,

where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For

the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In

particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs

predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not

exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, *e.g.*, Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis *et al.*, Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support

substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, http://cmgm.stanford.edu/pbrown/mguide/index.html), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays

typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid

probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived – either directly or indirectly – from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question,

R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention – that is, the one third of sequences that had previously been accessioned in EST or other expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from

genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the

probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of

human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn

from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i*.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound

noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* – that is, only about 4 - 5% – have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, *Reviewed in* Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis *et al.*, or purchased

commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, *etc.*, and can be provided in dry (*e.g.*, lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the

genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,

SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query – including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively

described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 – or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (*e.g.*, a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is

anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or

approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, *e.g.*, by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (*e.g.*, mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as

many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe

immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of

rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the

spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,232 of these ORFs in placenta.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in placenta is currently available for use in measuring the level of its ORF's expression in placenta.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been

interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Classically, such antenatal diagnosis was effected during second trimester by metaphase karyotyping of fetal cells that had shed spontaneously into amniotic fluid.

More recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy.

One technique in current clinical practice is chorionic villus sampling, which can be used to detect gene defects or polymorphisms in cells from the developing fetus, usually between 10 and 12 weeks of pregnancy. In chorionic villus sampling, a small sample of chorionic villi, which are tiny projections that make up part of the placenta, a fetal-derived tissue, is removed through the mother's cervix or the abdominal wall. Placental chromosomal DNA is then isolated from the chorionic villus cells and analyzed to detect a small number of known genetic defects. Such defects range from gross karyotypic changes, such as triploidy, to discrete point mutations known to cause diseases having significant morbidity or mortality.

Although only a few diseases are at present diagnosed by antenatal analysis of human placenta, a far higher number of human diseases and disorders have been catalogued in which dysfunction or misregulation of one or more genes contributes to the disease phenotype. At one end of the spectrum of genetic diseases are those, such as sickle cell trait, in which a single point mutation is responsible for the disease phenotype. At the other end of the spectrum lie disorders such as Down syndrome wherein the presence of a supernumerary chromosome manifests itself in variety of phenotypic defects that vary in severity

among affected individuals. For most, possibly all genetic diseases, the precise phenotypic manifestation and its severity is a function of a complex interaction between the definable genetic lesion and the action of many other genes and environmental factors.

Although the incidence of many genetic diseases is low, a sufficient number of such genetic diseases affect a sufficiently large population that they impact the national health economy. For example, cystic fibrosis, caused by mutations in a gene encoding a chloride ion channel and resulting in lung and other disorders, occurs at a rate of about 1 in 3000 births among Caucasians and costs over $1 billion annually for direct medical treatment in the U.S. alone. Furthermore, it is increasingly thought that for many diseases where no clear-cut genetic lesion appears responsible, possession by individuals of particular gene alleles naturally occurring within certain populations places such individuals at increased risk for developing those diseases. Examples include heart disease, neurogenerative disorders, diabetes, cancer and autoimmune disorders. For yet other diseases, especially cancer, the etiology is truly polygenic in that defects in multiple genes must cooincide in the same individual or even the same cell for the disease to develop and/or progress.

A large number of human genetic diseases and disorders are known, as are the gene or genes implicated in the etiology of the disease. Although in some cases single gene defects are known to be responsible for the etiology of a genetic disease, it is believed that for most or all such diseases, penetrance of the disease is affected by interaction with other genes. For other diseases or disorders, is believed that their mechanism is explained by the interaction of multiple genes, or by mutations or other defects in multiple genes. Such diseases and disorders may be detected in placenta.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for antenatal diagnosis of human genetic disorders. With each of the single exon probes described herein shown to be expressed at detectable levels in human placenta, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, antenatal diagnosis can be based upon the quantitative relatedness of a placental gene expression profile to one or more reference expression profiles known to be characteristic of a given disease, or to specific grades or stages thereof.

In one embodiment, the gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from placenta, typically through chorionic villus sampling, to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits presence and/or predisposition to disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation of exons known to be expressed in human placenta. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis *et al.* – each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the placenta has been demonstrated are useful for both measurement in the placenta and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and

for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski *et al.*, "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz *et al.*, "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss *et al.*, "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton *et al.*,"Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer *et al.*, "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," Proc. Natl. Acad. Sci. USA 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon *et al.*, "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou *et al.*, "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang *et al.*, "Identification of Genes Differentially Over-expressed in Lung Squamous Cell

Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney *et al.*, "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf *et al.*, "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi *et al.*, "*In vivo* Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements

from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in placenta. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are

to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, *etc.*, required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a

hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,233 - 26,232, respectively, for probe SEQ ID NOS. 1 - 13,232. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,233 - 26,232 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis *et al*. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high

stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have

sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^{3}H, ^{32}P, ^{33}P, ^{35}S, ^{125}I, ^{131}I; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is

obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human placenta.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis *et al.*

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human placenta. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group

consisting of SEQ ID NOS.: 1 - 13,232.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,232 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,233 - 26,232, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,232 can be used, or that portion thereof in SEQ ID NOS. 13,233 - 26,232 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis *et al.*

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (*e.g.*, HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA;

Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan *et al.* (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 13,233 - 26,232. Such amino acid sequences are set out in SEQ ID NOS: 26,233 - 38,837. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces

that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb

window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto,

CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear,

but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e^{-5} to 1 e^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were

then analyzed for protein similarities with the SwissProt database using BLASTX, Gish *et al.*, *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA$^+$ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution

containing 50% formamide, 5X SSC, 0.2 μg/μl poly(dA), 0.2 μg/μl human c_ot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all

tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal – where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) – 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data – that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (*i.e.*, degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective

tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present

in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain

Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca^{2+} binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates

				activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097

(1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi *et al.*, *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1□ (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai *et al.*, *Genomics*

49(2):283-89 (1998))(AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes *et al.*, *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH

	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ±0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION

identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in placenta tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,232 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 13,232 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,232 . The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,233 - 26,232, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the

signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more that a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human placenta and thus presents the subset of probes that was recognized to be

useful for measuring expression of their cognate genes in human placenta tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,233 - 26,232 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO:. of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (*i.e.*, highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (*i.e.*, lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The

peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (*e.g.*, those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (*i.e.*, 1×10^{-5}) and 1e-100 (*i.e.*, 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, *e.g.*, less than about 1e-100 — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely

exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,232) and probe exon (SEQ ID NOs.: 13,233 - 26,232, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Placenta

Table 4 (550 pages) presents expression, homology, and functional information for the genome-derived single exon

probes that are expressed significantly in human placenta.

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
463	13658	26695	5				
912	14087	27152	9.68				
1070	14236		3.01				
1330	14487	27555	10.9				
1645	14797	27882	1.92				
1666	14818	27901	4.94				
1764	14913	28008	1.03				
1788	14937	28030	1.67				
1794	14943	28036	8.53				
1939	15082	28183	1.57				
2034	15175	28285	2.66				
2234	15368	28497	3.39				
2353	15484	28616	2.53				
3255	16429	29447	3.75				
3537	16702	29713	1.48				
3604	16768	29783	10.5				
3651	16814		0.84				
3747	16908	29912	0.98				
4057	17213		0.94				
4314	17457	30445	1.55				
4377	17520	30500	6.88				
4396	17539	30519	0.87				
4396	17539	30520	0.87				
4457	17597		1.69				
4512	17651	30639	0.61				
4958	18088	31064	1.86				
5002	18131		0.6				
5157	18279	31244	5.14				
5168	18290	31255	1.24				
5371	18574	31442	1.76				
5371	18574	31443	1.76				
5538	18735		4.12				
5714	18907		7.26				
5796	18735		3.31				

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5858	19048	32354	4.22				
6146	25820	32668	1.61				
6174	19350	32696	1.92				
6546	19708		1.01				
6679	19838	33226	1.25				
6679	19838	33227	1.25				
7275	20358	33812	1.42				
7275	20358	33813	1.42				
7569	20641	34117	1.18				
7569	20641	34118	1.18				
8251	21333	34851	1.44				
8682	21762	35296	1.14				
9061	22140	35684	0.76				
9061	22140	35685	0.76				
9734	22799	36373	3.82				
9968	23007	36602	0.56				
10086	23124	36725	1.51				
10229	23264	36853	0.88				
10643	23677	37286	0.74				
10643	23677	37287	0.74				
10922	24005		2.32				
11280	24346		1.76				
11348	24410	38063	2.79				
11641	24721	38414	1.73				
11749	23935	37561	1.36				
11749	23935	37562	1.36				
11792	24782		2.09				
12057	25038	38746	1.56				
12623	25419		2.06				
12967	25628	31980	1.5				
6177	19353	32700	16.82	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8195	21277	34800	1.5	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9944	22983	36575	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9944	22983	36576	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7139	20274	33714	0.82	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7139	20274	33715	0.82	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10636	23670	37279	0.93	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
10636	23670	37280	0.93	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
2731	15849	28959	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2731	15849	28960	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2990	16156	29182	3.08	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8290	21372	34893	1.08	9.3E+00	AF130990.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9204	22282	35822	3.03	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
7625	20695	34171	0.6	9.2E+00	Q61767	SWISSPROT	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(5)-STEROID DEHYDROGENASE) (3-BETA-HYDROXY-5-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5411	18613	31586	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5411	18613	31587	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9630	22685		1	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6160	19336	32681	5.15	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6510	19675	33044	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6510	19675	33045	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
453	13649	26685	1.79	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9654	21097	34611	2.09	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11443	24504		1.96	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8345	21426		0.98	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7501	20576		1.85	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8556	21637	35174	1.42	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8556	21637	35175	1.42	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5921	19108	32421	3.6	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
8953	22032	35573	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8953	22032	35574	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3042	16218	29238	3.41	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
3042	16218	29239	3.41	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
7174	20307	33750	1.07	7.2E+00	BE179090.1	EST_HUMAN	RC0-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA
7299	20381	33838	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7299	20381	33839	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9798	22838		9.23	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11668	24745	38437	2.44	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
10187	23224	36818	2.76	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11528	24584	38261	1.52	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MSI3
8478	21559	35093	3.17	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10559	23594	37200	1.12	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10579	23614	37219	0.6	6.9E+00	P34226	SWISSPROT	SKT5 PROTEIN
8092	21174	34688	1.64	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'
8092	21174	34689	1.64	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'
9333	22409		1.62	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10413	23448	37053	3.6	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5398	18600		0.65	6.6E+00	Q99028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6675	19834	33223	0.86	6.6E+00	BF672121.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
9234	26226		0.55	6.6E+00	P51825	SWISSPROT	AF-4 PROTEIN (FEL PROTEIN)
10279	23314	36912	2.14	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10279	23314	36913	2.14	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10843	23876	37496	0.47	6.6E+00	H29330.1	EST_HUMAN	ym60f06.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52737 3'
11393	24454		1.48	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
9382	22457	36020	7	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10512	23547	37168	0.52	6.5E+00	BE866001.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960969 5'
9943	22982	36574	1.34	6.2E+00	AY010901.1	NT	Schizophyllum commune unknown mRNA
10787	23820	37444	0.7	6.2E+00	6754621	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
7181	20313	33756	1.6	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
10021	23059	36655	0.49	6.0E+00	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (6/7)
10732	23765	37373	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10732	23765	37374	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6650	19809	33197	7.14	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11933	24919		3.02	5.9E+00	BE958630.1	EST_HUMAN	601645279F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930451 5'
3613	16777		1.15	5.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7312	20394	33855	0.74	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7312	20394	33856	0.74	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7742	20803		1.34	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11289	24355	37996	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11289	24355	37997	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11765	23951	37581	2.52	5.6E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE
6381	19550	32906	0.74	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
9982	23021		0.56	5.5E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11018	24097		1.46	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11763	23949	37578	2.32	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7069	20122	33536	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7069	20122	33537	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7484	20559		1.04	5.4E+00	Q99435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8013	21063	34575	0.74	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8054	21137		1.62	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
8999	22078	35618	0.93	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8999	22078	35619	0.93	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
10242	23277	36870	1.45	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
10242	23277	36871	1.45	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4906	18036	31024	1.47	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6617	19777		0.7	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN CEH-20
8270	21352		3.39	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
9184	22262		0.72	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
11928	24914	38616	1.51	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
5580	18775		1.16	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-186-f09 HT0691 Homo sapiens cDNA.
10583	23618		0.96	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11470	24529		1.93	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
9162	22240	35784	0.94	5.1E+00	O16005	SWISSPROT	RHODOPSIN
10030	23068	36667	1.33	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6415	19584	32946	0.74	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10397	23432		0.7	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10645	23679	37289	2.89	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11569	24624	38304	7.24	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10437	23472		0.76	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4172	17322		12.39	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
8348	21429	34953	0.6	4.8E+00	BF367909.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8738	21817		4.92	4.8E+00	AW750067.1	EST_HUMAN	PM0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
300	13517	26550	3.04	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
301	13517	26550	1.85	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3347	16520	29534	1.02	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7962	21012	34522	0.59	4.6E+00	U67569.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9397	22471	36036	1.1	4.6E+00	BE646437.1	EST_HUMAN	7e86g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN. ;contains element PTR5 repetitive element ;
9397	22471	36037	1.1	4.6E+00	BE646437.1	EST_HUMAN	7e86g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN. ;contains element PTR5 repetitive element ;
10600	23635		0.63	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
7947	20997		0.7	4.5E+00	AF126177.1	NT	Issatchenkia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
11904	24892	38593	1.87	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
12058	25039	38747	1.53	4.5E+00	BF668841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3105	16281	29296	0.84	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
3105	16281	29297	0.84	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
6331	19502		1.58	4.4E+00	X13414.1	NT	Murine I gene for MHC class II(Ia) associated invariant chain
6245	19419		0.77	4.3E+00	AF059679.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7596	20686	34142	2.53	4.3E+00	Y13402.1	NT	Plasmodium falciparum R29R+var1 gene, exon 1
7792	20848	34341	0.68	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
11101	24174	37809	14.74	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5634	18828		4.1	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5711	18904	32199	1.07	4.2E+00	P51826	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
5880	19070		0.71	4.2E+00	O27830	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
6911	20226	33657	1.67	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6911	20226	33658	1.67	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9160	22238	35783	5.3	4.2E+00	AI809013.1	EST_HUMAN	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
10122	23160	36759	1.03	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWAIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10352	23387		0.47	4.2E+00	P40886	SWISSPROT	HEXOSE TRANSPORTER HXT8
7261	20344	33796	0.98	4.1E+00	BE253668.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7839	20894	34396	7.66	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7960	21010		0.64	4.1E+00	AB041523.1	NT	Patinopecten yessoensis mRNA for calcineurin A, complete cds
7963	21013	34523	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7963	21013	34524	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8101	21183	34703	2.88	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9740	22805	36381	0.61	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9873	22913	36498	2.25	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10370	23405		0.55	4.1E+00	AJ235273.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4
10514	23549		0.52	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
11124	24196		2.15	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1
11214	24283		12.25	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
3635	16799		0.72	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5575	20130	33546	0.93	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
5575	20130	33547	0.93	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7077	20130	33546	0.99	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7077	20130	33547	0.99	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7339	20419	33881	1	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9074	22153	35697	0.49	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
10148	23186	36783	0.65	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10368	23403	37014	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10464	23499	37111	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10464	23499	37112	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11762	23948	37577	1.59	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11843	24832	38524	2.98	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]

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11843	24832	38525	2.98	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
12133	25113	38817	1.34	4.0E+00	P35611	SWISSPROT	ERYTHROCYTE ADDUCIN ALPHA SUBUNIT
3591	16755	29770	5	3.9E+00	X64518.1	NT	N.tabacum chitinase gene 50 for class I chitinase C
4441	17581		0.87	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5775	18967	32270	2.92	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5775	18967	32271	2.92	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6772	19927	33322	0.93	3.9E+00	AF298209.1	NT	Dictyostelium discoideum non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6829	19982	33389	0.7	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7013	20149	33570	4.43	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7519	20592	34066	4.25	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8512	21593	35128	2.44	3.9E+00	X65865.1	NT	X.laevis mRNA for M4 muscarinic receptor
11674	23902	37524	2.77	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2693	15813		1.53	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6520	19685	33057	1.05	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
8627	21707	35244	1.12	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9999	23037		0.6	3.8E+00	AJ390961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
12120	25100		11.65	3.8E+00	9631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
4129	17282	30277	12.79	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7316	20398		0.83	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
9379	22454	36017	1.04	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11715	24755	38450	2.11	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11715	24755	38451	2.11	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
12260	25196		1.87	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
606	13795	26814	3.76	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
5369	18572	31440	0.78	3.6E+00	BF316316.1	EST_HUMAN	601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
8749	21828	35364	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8749	21828	35365	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8847	21926	35464	3.67	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome

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8847	21926	35465	3.67	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
9864	22904	36488	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
9864	22904	36489	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11093	24167		3.21	3.6E+00	M96795.1	NT	Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
3319	16492	29509	1.04	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
6123	19302		1	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6341	19511	32868	0.93	3.5E+00	R19745.1	EST_HUMAN	yg40c08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34940 5'
8681	21761		0.56	3.5E+00	P24557	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9232	22310	35851	0.99	3.5E+00	AA190998.1	EST_HUMAN	zp86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
9232	22310	35852	0.99	3.5E+00	AA190998.1	EST_HUMAN	zp86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
9694	22743	36313	1	3.5E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
10739	23772	37383	0.58	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1542	14694	27773	3.81	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
2644	15767	28882	1.07	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7518	20591	34065	2.33	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7880	20932	34437	0.76	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8876	21955		0.77	3.4E+00	U65406.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
9274	22350	35901	0.77	3.4E+00	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9312	22388	35939	0.54	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
10471	23506	37119	3.35	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11822	24811	38506	2.06	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6193	19369	32719	0.97	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6193	19369	32720	0.97	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8077	21159	34676	1.03	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10681	23715	37321	1.04	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10681	23715	37322	1.04	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
513	13707	26735	1.79	3.2E+00	X96422.1	NT	D.rerio zp-50 POU gene

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4136	13707	26735	0.78	3.2E+00	X96422.1	NT	D.rerio zp-50 POU gene
4850	17983	30971	0.95	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5686	18880	32170	1.16	3.2E+00	P54924	SWISSPROT	SQUALENE--HOPENE CYCLASE
5686	18880	32171	1.16	3.2E+00	P54924	SWISSPROT	SQUALENE--HOPENE CYCLASE
5719	18912	32207	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5719	18912	32208	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6436	19603	32966	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6436	19603	32967	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7781	20837	34330	0.86	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7952	21002	34513	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7952	21002	34514	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9230	22308		5.26	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9730	22795	36369	1.31	3.2E+00	M36383.1	NT	S.cerevisiae threonine deaminase (ILV1) gene, complete cds
10345	23380	36991	2.06	3.2E+00	AB016081.2	NT	Oryzias latipes OlGC6 gene for guanylyl cyclase C, complete cds
12219	25169		2.95	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5996	19181	32503	2.29	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7547	20619	34095	0.91	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
7904	20956		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
8279	21361	34880	0.51	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN--PROTEIN LIGASE HUL4
8801	21880	35417	5.14	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
8801	21880	35418	5.14	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
9459	22575		3.7	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9526	22591	36162	0.55	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10100	23138	36739	0.76	3.1E+00	7524759	NT	Chlorella vulgaris chloroplast, complete genome
10193	23230		0.56	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10543	23578	37187	4.09	3.1E+00	P49365	SWISSPROT	DEOXYHYPUSINE SYNTHASE (DHS)
11751	23937		2.45	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11771	24783		2.49	3.1E+00	S56660.1	NT	retinoic acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
13019	25670		1.17	3.1E+00	U77666.1	NT	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2899	16078	29095	0.95	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5454	18654	31633	1.29	3.0E+00	X53096.1	NT	S.aureus genes encoding Sau96I DNA methyltransferase and Sau96I restriction endonuclease
6686	19844	33234	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6686	19844	33235	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7306	20388		11.21	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7346	20426		0.7	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9108	22187		1.62	3.0E+00	X67838.1	NT	B.napus DNA for myrosinase
10501	23536	37146	0.56	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11259	24328	37967	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
11259	24328	37968	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
11885	24873	38570	1.37	3.0E+00	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2067	15208	28324	2.69	2.9E+00	AE002225.2	NT	Chlamydophila pneumoniae AR39, section 53 of 94 of the complete genome
7049	20102	33519	1.65	2.9E+00	Z36879.1	NT	F.pringlei gdcsPA gene for P-protein of the glycine cleavage system
7360	20439	33899	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7360	20439	33900	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7614	20684	34160	6.19	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8052	21135	34655	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8052	21135	34656	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8289	21371	34892	0.81	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4153059 5'
9438	22512		0.82	2.9E+00	AJ002153.2	NT	Seguinus oedipus gene for seminal vesicle secreted protein semenogelin I
1486	14639	27722	4.77	2.8E+00	AF186398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
1662	14814		3.14	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7460	20535	34010	5.05	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9813	22853		0.6	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10928	20535	34010	1.53	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
240	13462	26490	13.96	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
240	13462	26491	13.96	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA

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5669	18863	32148	1.41	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8339	21420		0.74	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHSB) gene including complete 5'UTR and complete cds
9168	22246		2.16	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9632	21075	34587	0.61	2.7E+00	AW088191.1	EST_HUMAN	xc88e12.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733 THYMOSIN BETA-4 (HUMAN);
10718	23751		1.94	2.7E+00	BE063527.1	EST_HUMAN	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
4796	17931	30917	5.51	2.6E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5665	18859	32143	2.04	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5665	18859	32144	2.04	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5947	19133		2.55	2.6E+00	Y17062.1	NT	Mycobacterium fortuitum furA II gene
7727	26220		1.16	2.6E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
7879	20931		11.25	2.6E+00	AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8249	21331	34847	1.17	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
8249	21331	34848	1.17	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
9858	22898	36481	2.85	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10563	23598		1.91	2.6E+00	9055193	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
11281	24347	37984	2.2	2.6E+00	AF143675.1	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
12917	26064		3.3	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1492	14645	27726	3.03	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1492	14645	27727	3.03	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5934	19120	32431	2.24	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5934	19120	32432	2.24	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6586	19120	32431	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6586	19120	32432	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6868	20020	33429	0.77	2.5E+00	D30052.1	NT	Vibrio cholerae ctxA gene and ctxB gene for cholera toxins, complete cds
7936	20986	34494	1.19	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
7985	21034	34547	0.62	2.5E+00	4502902	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9304	22380	35931	1.55	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
10057	23095	36697	0.71	2.5E+00	BE297758.1	EST_HUMAN	601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
11832	24821		1.39	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
12216	25167		1.85	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3078	16254	29276	0.89	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
5027	18156	31134	4.93	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA

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6134	19313	32652	4.09	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7538	20611	34085	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7538	20611	34086	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
8334	21416	34941	2.06	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8334	21416	34942	2.06	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8406	21487		2.8	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8852	21931		1.72	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
9028	22107	35648	8.99	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10244	23279	36874	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10244	23279	36875	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10313	23348	36954	2.31	2.4E+00	X92511.1	NT	H.sapiens CTGF gene and promoter region
10449	23484		7.28	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
10528	23563	37169	1.64	2.4E+00	BE326702.1	EST_HUMAN	hr63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10528	23563	37170	1.64	2.4E+00	BE326702.1	EST_HUMAN	hr63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10818	23851	37474	1.06	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11335	24398	38047	1.36	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFKD operon and downstream
11640	24720	38413	2.44	2.4E+00	AF158652.2	NT	Fregaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1282	14438	27507	9.98	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4237	17383		1.41	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
5957	19143		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7612	20682	34158	2.76	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7771	26221		2.37	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7958	21008	34518	1.28	2.3E+00	X60265.1	NT	M.mazei dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9310	22386	35938	0.52	2.3E+00	5835317	NT	Polypterus ornatipinnis mitochondrion, complete genome
9371	22446	36008	1.66	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
11041	24120	37753	2.72	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
12075	25056	38763	2.14	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12075	25056	38764	2.14	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12445	25315	32091	7.41	2.3E+00	BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
4126	17280	30276	1.06	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4432	17572	30553	4.12	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)

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4432	17572	30554	4.12	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5458	18658	31636	11.22	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5458	18658	31637	11.22	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5975	19160	32478	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5975	19160	32479	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6187	19363	32711	9.39	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6484	19651	33013	2.87	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6730	19886	33278	3.14	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7097	18524		3.4	2.2E+00	AA594574.1	EST_HUMAN	nl95b02.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7470	20545	34017	0.83	2.2E+00	AA137027.1	EST_HUMAN	zn97f04.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7783	20839	34332	11.91	2.2E+00	AA449012.1	EST_HUMAN	zx05g10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
7866	20920	34427	0.66	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8294	21376	34896	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8294	21376	34897	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9542	22607		12.49	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9768	25860		2.12	2.2E+00	Q04706	SWISSPROT	TRANSPOSON TY1 PROTEIN A
10259	23294	36890	1.12	2.2E+00	AI290373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10259	23294	36891	1.12	2.2E+00	AI290373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10301	23336	36941	3.04	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10673	23707	37315	2.6	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11726	23912	37536	3.3	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11915	24902	38605	6.04	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
583	16016	26795	13.2	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3678	16841		1.19	2.1E+00	AW449366.1	EST_HUMAN	UI-H-BI3-akl-e-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'

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6260	19434		0.97	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6947	20260	33698	3.51	2.1E+00	O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7169	20302	33745	0.77	2.1E+00	4503430	NT	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7191	20056	33466	5.88	2.1E+00	N28575.1	EST_HUMAN	yy08a10.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
8694	21774		2.43	2.1E+00	AU123630.1	EST_HUMAN	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1223	14383	27444	1.32	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1223	14383	27445	1.32	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1366	14520	27585	1.37	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Na+,K+-ATPase beta 1 subunit mRNA, complete cds
1606	14759		3.09	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2216	15350	28480	7.2	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2216	15350	28481	7.2	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4216	17365	30353	1.71	2.0E+00	AW664496.1	EST_HUMAN	hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
4216	17365	30354	1.71	2.0E+00	AW664496.1	EST_HUMAN	hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7722	20786		0.96	2.0E+00	P07566	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
8214	21296	34815	4	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8214	21296	34816	4	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8214	21296	34817	4	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
9122	22201	35743	3.04	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
12815	26022	31670	6.76	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5715	18908	32202	4.28	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
5715	18908	32203	4.28	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
6225	19400	32750	1.2	1.9E+00	BE969695.1	EST_HUMAN	601679636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6792	19947		0.92	1.9E+00	AW845689.1	EST_HUMAN	MR0-CT0063-071099-002-g02 CT0063 Homo sapiens cDNA
6888	20040		1.91	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8653	21733	35272	2.21	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8653	21733	35273	2.21	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8859	21938		3.32	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
9095	22174		1.86	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9830	22870	36452	0.63	1.9E+00	AA669125.1	EST_HUMAN	ab94a04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element;contains element L1 L1 repetitive element ;
10790	23823	37447	0.67	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3162	16337	29346	1.69	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3190	16365	29370	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3190	16365	29371	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5988	19173		1.63	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6230	19405	32755	2.02	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6528	19692		1.28	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
6879	20031	33441	1.15	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7204	20069	33479	1.22	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7411	20489		0.8	1.8E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--(GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8308	21390	34913	0.98	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8308	21390	34914	0.98	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9055	22134	35679	2.28	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9376	22451	36013	0.78	1.8E+00	R31042.1	EST_HUMAN	yh72c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9462	22519	36081	0.82	1.8E+00	AW880004.1	EST_HUMAN	QV0-OT0030-070300-148-e03 OT0030 Homo sapiens cDNA
9996	23034	36626	0.47	1.8E+00	P06828	SWISSPROT	FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2; FUSION GLYCOPROTEIN F1]
10054	23092	36694	0.94	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10490	23525		4.71	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10777	23810		0.75	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12575	25994		4.97	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtil alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12667	25444		6.01	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
13005	25887	31854	1.45	1.8E+00	BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
1132	14297	27352	1.68	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2345	15476	28609	4.9	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2445	16573	28702	1.49	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4581	17718	30701	0.98	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5730	18923	32216	1.73	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5730	18923	32217	1.73	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
6141	19319	32661	3.02	1.7E+00	Q9TTR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
6682	19840	33230	0.67	1.7E+00	P35816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)
7367	20446	33908	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7367	20446	33909	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8038	21121	34641	1.1	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8222	21304	34825	1.08	1.7E+00	6765715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA
8252	21334	34852	0.61	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214669 5'
8739	21818	35352	0.75	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8828	21907		1.63	1.7E+00	BF306000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8901	21980	35519	0.66	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
8901	21980	35520	0.66	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9014	22093	35633	1.03	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9350	25859	35981	2.44	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9350	25859	35982	2.44	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9806	22846		1	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10375	23410		0.54	1.7E+00	AW953681.1	EST_HUMAN	EST365751 MAGE resequences, MAGC Homo sapiens cDNA
10857	23890	37509	0.47	1.7E+00	BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890464 5'
10857	23890	37510	0.47	1.7E+00	BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890464 5'
11896	24884	38582	1.67	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
12523	25356	32066	1.94	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.t1 MSR1 repetitive element ;
2090	15230	28352	19.53	1.6E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2101	15241	28362	4.14	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2107	15246	28367	1.26	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
2357	15488		0.97	1.6E+00	X98373.1	NT	B.napus gene encoding endo-polygalacturonase
3026	16202	29225	1.22	1.6E+00	W58426.1	EST_HUMAN	zd25f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3857	17017		1.06	1.6E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4142	17294		6.05	1.6E+00	BF570077.1	EST_HUMAN	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4472	17612	30590	1.25	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4472	17612	30591	1.25	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5184	18306	31270	0.59	1.6E+00	AF127897.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
5194	18316	31284	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5194	18316	31285	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5948	19134	32447	2.38	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6035	19218	32540	0.78	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgasel) gene, promoter region
6599	19759	33147	0.91	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6849	20002	33411	1.05	1.6E+00	AW294881.1	EST_HUMAN	UI-H-BI2-ahr-b-04-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7394	20472	33938	2.37	1.6E+00	BE697267.1	EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
8219	21301		1.3	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8574	21655	35196	3.3	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9101	22180	35724	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9101	22180	35725	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9272	22348	35898	0.49	1.6E+00	BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9659	25857	34615	1.05	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-I
9659	25857	34616	1.05	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-I
9786	22826		0.7	1.6E+00	AF043466.1	NT	Thermoanaerobacter ethanolicus D-xylose-binding protein (xylF) gene, complete cds
9935	22974	36566	1.49	1.6E+00	T41290.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
10388	23423	37029	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
10388	23423	37030	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
10552	23587	37195	0.52	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
11010	24089	37726	1.77	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE) ; CAPSID ASSEMBLY PROTEIN]
11082	19218	32540	4.8	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgasel) gene, promoter region
12006	24991	38695	3.68	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
33	13271	26275	2.95	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
241	13463	26492	2.44	1.5E+00	AE002201.2	NT	Chlamydophila pneumoniae AR39, section 32 of 94 of the complete genome
636	13821		1.81	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2481	15608	28732	1.56	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2584	15709	28828	2.02	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

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3208	15608	28732	1.75	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3462	16629	29649	0.77	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5846	19036	32342	0.71	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1. ;
5846	19036	32343	0.71	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1. ;
6536	19699	33072	2.43	1.5E+00	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
7278	20361		1.68	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7311	20393	33853	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7311	20393	33854	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7500	20575	34048	0.61	1.5E+00	AA889259.1	EST_HUMAN	ak26f10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7768	20826	34317	0.77	1.5E+00	AI003254.1	EST_HUMAN	an07b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8313	21395	34920	0.9	1.5E+00	BE887446.1	EST_HUMAN	601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8367	21448	34971	0.5	1.5E+00	AB040887.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8846	21926	35463	1.09	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
9218	22296		0.48	1.5E+00	AB038516.1	NT	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9334	22410	35963	0.51	1.5E+00	BF217818.1	EST_HUMAN	601882662F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9684	22733	36303	0.85	1.5E+00	R81928.1	EST_HUMAN	yj03h01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9835	22875	36459	1.6	1.5E+00	AW375697.1	EST_HUMAN	QV3-CT0192-261099-008-d09 CT0192 Homo sapiens cDNA
10064	23102	36705	6.49	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
10258	23293		1.85	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183865 5'
10399	23434	37040	2.26	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10399	23434	37041	2.26	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11684	24683	38373	3.4	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P243 3'
11834	24823		7.68	1.5E+00	X07380.1	NT	Maize mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
11929	24915	38617	1.39	1.5E+00	AI400798.1	EST_HUMAN	tg94d09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
11929	24915	38618	1.39	1.5E+00	AI400798.1	EST_HUMAN	tg94d09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12515	26095	31662	1.61	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12765	25508		3.92	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
12888	25589		2.17	1.5E+00	6978492	NT	Rattus norvegicus 5 - Lipoxygenase (Alox5), mRNA
13220	25794	31888	1.31	1.5E+00	BF223935.1	EST_HUMAN	7q82b06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
30	13268	26271	2.27	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
30	13268	26272	2.27	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

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2351	15482		0.97	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2411	15541		9.39	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2734	15851	28964	1.7	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2833	15947	29055	3.22	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2833	15947	29056	3.22	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3414	16583		0.79	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4370	17513	30493	1.13	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4370	17513	30494	1.13	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4708	17843		1.51	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5317	18434		0.94	1.4E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5488	18687	31705	1.73	1.4E+00	AW054976.1	EST_HUMAN	wt45g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5645	18839		6.04	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6409	19578	32939	3.07	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6424	26214		3.93	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6542	19705	33078	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6542	19705	33079	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6961	20189	33614	0.8	1.4E+00	AW893057.1	EST_HUMAN	CM3-NN0006-300300-132-b12 NN0006 Homo sapiens cDNA
7438	20515	33988	1.99	1.4E+00	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7454	20531	34005	1.14	1.4E+00	AW467760.1	EST_HUMAN	he23f05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element;
7514	20588	34062	0.7	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7514	20588	34063	0.7	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8530	21611		0.72	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8994	22073		5.4	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
9295	22371	35920	1.65	1.4E+00	R20459.1	EST_HUMAN	yg33f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5'
9398	22472	36038	3.83	1.4E+00	BE064667.1	EST_HUMAN	RC1-BT0313-301299-012-f05 BT0313 Homo sapiens cDNA
9432	22506	36072	0.65	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10412	23447	37052	0.88	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10457	23492	37102	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10457	23492	37103	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10744	23777	37390	0.96	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose bisphosphate carboxylase, partial cds
10744	23777	37391	0.96	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose bisphosphate carboxylase, partial cds
10852	23885	37504	1.15	1.4E+00	Q07283	SWISSPROT	TRICHOHYALIN
11499	24557	38232	4.52	1.4E+00	AB006682.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11691	24689	38379	3.46	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11691	24689	38380	3.46	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11711	24751	38444	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11711	24751	38445	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12359	26012		2.01	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12785	26204		2.99	1.4E+00	11545836	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen se70-2 (SE70-2), mRNA
584	13775		1.96	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydromethyl-trisporate dehydrogenase
925	14100	27164	2.79	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1153	14317		23.81	1.3E+00	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
1325	14482	27549	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1325	14482	27550	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1387	14542		0.98	1.3E+00	U61730.2	NT	Coix lacryma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1641	14793		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2316	15448		2.38	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2615	15739		1.81	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
3005	16180	29201	0.86	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
3686	16849	29857	1.14	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5631	18825	31900	1	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5827	19017	32322	0.58	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6142	19320	32662	7.56	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
6142	19320	32663	7.56	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
6547	19709	33085	1.14	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6890	20042		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6928	20243		0.58	1.3E+00	P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
6978	20206	33634	1.04	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7092	20186	33610	1.16	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'
7249	20332	33779	0.96	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7616	20686	34162	0.78	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8494	21575	35112	1.78	1.3E+00	AJ009912.1	NT	Sus scrofa pip gene
8642	21722	35259	2.28	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
8758	21837	35378	1.05	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8907	21986		1.87	1.3E+00	9910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8990	22069	35609	0.89	1.3E+00	AI927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9347	22423	35976	0.51	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:183076 3'
9347	22423	35977	0.51	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:183076 3'
9715	22780		5.02	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9724	22789	36359	2.47	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9724	22789	36360	2.47	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9823	22863	36444	1.21	1.3E+00	AF059250.1	NT	Homo sapiens lipoxygenase (ALOX12B) mRNA, complete cds
9847	22887		0.47	1.3E+00	AW024390.1	EST_HUMAN	wv03f03.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2628477 3' similar to gb:M31522 TRANSCRIPTION FACTOR ITF-1 (HUMAN);
9871	22911	36496	1.65	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9952	22991	36584	1.21	1.3E+00	AI927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
10031	23069	36668	0.68	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
10031	23069	36669	0.68	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
10070	23108	36711	3.93	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
10130	23168		0.57	1.3E+00	AI559944.1	EST_HUMAN	tq77a12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
10353	23388	36996	0.5	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10353	23388	36997	0.5	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10418	23453	37059	1.68	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10435	23470	37076	1.59	1.3E+00	M29953.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10811	23844		0.99	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10838	23871	37493	0.47	1.3E+00	AI990846.1	EST_HUMAN	ws32e10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN Q16881 THIOREDOXIN REDUCTASE ;
10851	23884		0.53	1.3E+00	8923637	NT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10854	23887	37506	0.46	1.3E+00	7949159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10854	23887	37507	0.46	1.3E+00	7949159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10861	23894	37515	0.45	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:183076 3'
10861	23894	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:183076 3'
10932	24014		4.05	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11145	24217	37844	2.4	1.3E+00	P25299	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
11169	24240	37872	1.77	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
11619	24670		1.43	1.3E+00	AW274791.1	EST_HUMAN	xp09e03.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739868 3'
11831	24820	38511	2.73	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11923	24909	38610	2.28	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.9kB fragment
11994	24979		1.35	1.3E+00	L31891.1	NT	Arabidopsis thaliana 3-ketoacyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12504	25347		3.81	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12698	25465	32022	2.76	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158452 5'
12707	25899		1.98	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12822	25549		1.53	1.3E+00	AF187035.1	NT	Sturnira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
13200	25783		1.34	1.3E+00	U38978.1	NT	Naphthalenesulfonate-degrading bacterium BN6 2,3-dihydroxybiphenyl dioxygenase (bphCII) gene, complete cds
13231	25981		1.63	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
667	13853	26881	8.73	1.2E+00	AA676246.1	EST_HUMAN	zi22d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
846	14024	27082	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
846	14024	27083	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
846	14024	27084	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
901	14076		1.21	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1187	14349	27407	7.6	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1232	14391	27453	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1232	14391	27454	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2066	15207	28323	1.02	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3179	16354	29359	1.06	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3234	16408	29421	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3234	16408	29422	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3358	16530		3.57	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3437	16605	29525	0.61	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3804	16964	29967	9.16	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4094	17249	30254	1.87	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA

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4413	16605	29625	1.06	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4594	17731		1.91	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4645	17781	30763	0.94	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4682	17817	30805	2.03	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4712	17847		6.6	1.2E+00	Y09200.1	NT	T.pinnatum chloroplast rbcL gene, partial
5554	18751	31788	1.13	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5672	18866	32152	2.34	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5917	19105		0.65	1.2E+00	X81879.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
5995	19180	32502	0.77	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6280	19454	32802	2.45	1.2E+00	X74885.1	NT	D.hydei ay1 repeat cluster DNA, fragment D
6342	19512	32869	3.81	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6420	19589	32953	1.28	1.2E+00	X89084.1	NT	C.glutamicum pta gene and ackA gene
6420	19589	32954	1.28	1.2E+00	X89084.1	NT	C.glutamicum pta gene and ackA gene
6463	19630	32991	36.06	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
6566	19728	33105	0.73	1.2E+00	N33295.1	EST_HUMAN	yy39b12.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273599 3' similar to gb|M87935|HUMAALU472 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:J04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6630	19790	33178	0.62	1.2E+00	P17671	SWISSPROT	ECDYSONE-INDUCIBLE PROTEIN E75-A
6634	19793	33182	1.94	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7055	20106	33524	1.72	1.2E+00	AB029010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7067	20120	33534	2.81	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7180	20312	33755	0.68	1.2E+00	AA187810.1	EST_HUMAN	zq38f05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632001 5' similar to gb:D10522 Human mRNA for 80K-L protein, complete cds. (HUMAN);
7403	20481		0.71	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
7542	25847	34092	1.85	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cdA Homo sapiens cDNA clone cdAAFH03 5'
7828	20883	34385	2.91	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
7997	21047	34560	0.6	1.2E+00	BE787646.1	EST_HUMAN	601481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
8767	21846	35387	3.19	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
8863	21942	35477	0.82	1.2E+00	P38427	SWISSPROT	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
9077	22156		0.7	1.2E+00	7706271	NT	Homo sapiens CGI-30 protein (LOC51611), mRNA
9226	22304	35847	1.81	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
9440	22514	36078	0.51	1.2E+00	H48599.1	EST_HUMAN	yq80a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202066 5'

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9598	22653	36224	3.79	1.2E+00	Z32850.1	NT	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9805	22845	36423	2.13	1.2E+00	D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
10135	23173	36771	3.6	1.2E+00	X56832.1	NT	H.sapiens ENO3 gene for muscle specific enolase
10532	23567		0.82	1.2E+00	AB009666.1	NT	Homo sapiens klotho gene, exon 1
11432	24493	38158	1.69	1.2E+00	M38686.1	NT	Mus musculus Id gene, exon 1
11627	24707	38400	1.51	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
11666	24743		7.69	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11744	23930	37556	3.13	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12101	25081	38788	1.68	1.2E+00	M10408.1	NT	Maize mitochondrial F-0-ATPase proteolipid (subunit 9) gene
12471	25984	31768	17.76	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12491	25339		1.74	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
13218	25793		2.66	1.2E+00	AA077909.1	EST_HUMAN	7H11A06 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H11A06
476	13671	26703	1.11	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1802	14951	28045	1.23	1.1E+00	AW995393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1948	15091	28192	1.21	1.1E+00	AW575889.1	EST_HUMAN	UI-HF-BR0p-ajk-f-02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
2017	15157		2.74	1.1E+00	AF137273.1	NT	Gallus gallus alpha 1 (V) collagen mRNA, complete cds
3409	16579	29594	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3409	16579	29595	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3575	16740	29757	1.02	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3670	16833	29844	0.99	1.1E+00	AI808360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3812	16972	29974	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3812	16972	29975	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3920	17079		0.92	1.1E+00	X85374.1	NT	H.parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4054	17210	30220	1.03	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA.
4130	17283	30278	0.72	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Psmb7), mRNA
4331	17474		6.82	1.1E+00	5835331	NT	R.unicornis complete mitochondrial genome
5107	18235	31204	3.45	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
5180	18302	31265	2.06	1.1E+00	X78425.1	NT	E.faecalis pbp5 gene
5422	18623	31599	1.49	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5731	18924	32218	14.33	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
5750	18942	32243	1.32	1.1E+00	AI138582.1	EST_HUMAN	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6217	19392	32740	0.9	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6404	19573	32935	0.59	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6537	19700	33073	0.72	1.1E+00	R06037.1	EST_HUMAN	ye89e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124924 5'
6856	20009	33419	0.78	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7447	20524	33997	0.58	1.1E+00	X55981.1	NT	Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
7632	20701	34179	0.67	1.1E+00	BF683714.1	EST_HUMAN	602139978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301322 5'
7659	20726	34201	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7659	20726	34202	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7680	20745	34226	8.35	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7754	25853	34305	1.04	1.1E+00	11967980	NT	Mus musculus silent mating type information regulation 2, (S.cerevistae, homolog)-like (Slr2l), mRNA
8325	21407	34934	3.2	1.1E+00	BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8416	21497	35029	0.91	1.1E+00	AI478339.1	EST_HUMAN	tm39h11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
8935	22014	35554	0.86	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COXI-like gene
9015	22094	35634	0.87	1.1E+00	S80750.1	NT	VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
9126	22205	35748	0.53	1.1E+00	AI079946.1	EST_HUMAN	oz34f05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9637	21080		0.75	1.1E+00	BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9828	22868	36450	0.51	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9883	22923		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9974	23013	36607	1.03	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10038	23078	36676	1.85	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
10141	23179	36777	4.09	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10202	23239	36829	20.74	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10719	23752	37358	1.21	1.1E+00	P73789	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10831	23864	37486	0.56	1.1E+00	AI878921.1	EST_HUMAN	au51c11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518292 5' similar to gb:D10522 Human mRNA for 80K-L protein, complete cds. (HUMAN);
10886	23970	37600	1.97	1.1E+00	11067364	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
10947	24029		3.14	1.1E+00	AF068942.1	NT	Klebsormidium flultans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11343	24406	38055	3.72	1.1E+00	L16877.1	NT	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
11361	18489		2.74	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11366	24427	38083	2.93	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11368	24427	38084	2.93	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11637	24717	38409	3.99	1.1E+00	AI809699.1	EST_HUMAN	wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11870	24858	38552	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
11870	24858	38553	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12441	25312		1.82	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12547	25371	32070	3.56	1.1E+00	AF216696.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
12689	25980		1.86	1.1E+00	AF234169.1	NT	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
101	13337		1.84	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
116	13347	26374	2.1	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threoine kinase, complete cds
431	13626		-2.78	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
590	13781	26800	1.44	1.0E+00	AJ251660.1	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
694	13877	26910	7.14	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
696	13879		2.29	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1417	16037		1.35	1.0E+00	X80416.1	NT	V.carteri Algal-CAM mRNA
1795	14944	28037	1.33	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2554	15679	28803	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2554	15679	28804	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2621	15744		0.95	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204 ;contains element MER22 MER22 repetitive element ;
2940	16117	29129	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2940	16117	29130	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3032	16208		0.96	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME I
3269	16443	29463	1.16	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204 ;contains element MER22 MER22 repetitive element ;
3459	16626		0.73	1.0E+00	AF222761.1	NT	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6
3688	13337		0.75	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3772	16933	29939	1.61	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase

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4180	17330	30322	1.12	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4390	17533		0.72	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5396	18598	31668	2.3	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5971	19157	32472	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5971	19157	32473	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6077	19259	32588	1.74	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6
6241	19415	32763	4.85	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6248	19422	32768	1.67	1.0E+00	AW452782.1	EST_HUMAN	UI-H-BI3-abx-d-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6618	19778	33167	2.04	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6671	19830	33219	0.83	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 though 5
6767	19923		1.07	1.0E+00	P46506	SWISSPROT	SRB-11 PROTEIN
6795	19950	33349	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6795	19950	33350	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6916	20231	33664	1.27	1.0E+00	Y11204.1	NT	V.carteri gene encoding volvoxopsin
7288	20371	33826	1.15	1.0E+00	S52770.1	NT	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7647	20716		9.68	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7889	20941	34447	1.51	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7903	20955	34462	6.02	1.0E+00	AA775191.1	EST_HUMAN	ac79b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3'
8019	21070		0.72	1.0E+00	BF679213.1	EST_HUMAN	602163792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8148	21230	34749	1.65	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8148	21230	34750	1.65	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8335	18496		1.48	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8545	21626	35163	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
8545	21626	35164	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]

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8672	21762		1.07	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8708	21788	35321	0.64	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8708	21788	35322	0.54	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8735	25858		1.82	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA
8776	21855	35397	1.15	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8922	22001	35540	1.8	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), Isolate SF33,
9471	22528	36091	1.95	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9682	22731	36301	1.62	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9682	22731	36302	1.62	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9810	22850	36429	1.81	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9815	22855	36434	1.32	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds
9815	22855	36435	1.32	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds
10318	23353	36961	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10318	23353	36962	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10408	23443	37050	0.69	1.0E+00	AI077920.1	EST_HUMAN	oy15d07.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10633	23568	37175	3.99	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAWC04 5'
10694	23727	37333	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10694	23727	37334	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10728	23761	37368	1.22	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11216	24285	37924	1.37	1.0E+00	S90825.1	NT	PBR1=proline-rich protein {intron 3} [human, Genomic, 898 nt]
11342	24405	38064	1.46	1.0E+00	AA701494.1	EST_HUMAN	zi63b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element;contains element MER38 repetitive element ;
11825	24814		1.62	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
12329	25238		5.49	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12676	25451		2.67	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAGE resequences, MAGN Homo sapiens cDNA
3693	16855		1.04	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5752	18944	32246	8.8	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

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5990	19175	32498	0.83	9.9E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9461	22518		1.68	9.9E-01	U65667.1	NT	Lycopersicon esculentum putative Mi1 copy 1 nematode-resistance gene
9755	22693		2.14	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
536	13729	26753	1.17	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2370	15501		1.26	9.8E-01	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
2862	15976		1.29	9.8E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3903	17062	30061	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3903	17062	30062	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7349	20429	33890	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7349	20429	33891	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7823	20876	34378	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
7823	20878	34379	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8916	21995	35534	0.94	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10653	23687		1.02	9.8E-01	AA825565.1	EST_HUMAN	od55d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11242	24311	37948	1.84	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11242	24311	37949	1.84	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12554	25377		2.43	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7309	20391	33851	2.73	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8701	21781	35314	1.9	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8707	21787	35320	1.54	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
9039	22118	35661	0.73	9.7E-01	BE799822.1	EST_HUMAN	601592165F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945904 5'
11444	24505		3.56	9.7E-01	BF511209.1	EST_HUMAN	UI-H-BI4-aci-e-07-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
13208	25789		3.17	9.7E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4558	17696	30675	0.74	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4558	17696	30676	0.74	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4580	17717	30700	1.28	9.6E-01	AW799674.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5872	19062	32369	3.51	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
5872	19062	32370	3.51	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
6886	20038	33447	0.6	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7512	20586	34059	0.63	9.6E-01	AF197881.1	NT	Helix lucorum presenilin (PS) mRNA, complete cds
8586	21667		1.52	9.6E-01	X95275.1	NT	P.falciparum complete gene map of plastid-like DNA (IR-A)
9052	22131	35675	0.92	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
11346	24408	38060	1.42	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11808	24798	38496	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11808	24798	38497	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
12225	25174		1.31	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12915	26061	31656	1.68	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2545	15670	28794	1.61	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3882	17041	30038	2.1	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3882	17041	30039	2.1	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
9202	22280	35819	0.71	9.5E-01	AI190162.1	EST_HUMAN	qd57d07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9306	22382	35933	1.04	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-b02 CT0295 Homo sapiens cDNA
11520	24576	38254	1.56	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11737	23923	37548	1.57	9.5E-01	AW293799.1	EST_HUMAN	UI-H-BI2-ahp-f-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3271	16445		5.72	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3289	16463		2.17	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9066	22145	35692	0.79	9.4E-01	M90724.1	NT	Human Fc-gamma-receptorIIA (FCGR2A) gene, exon 4
12496	25343		1.86	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5'
12914	25975		1.4	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1769	14918		1.24	9.3E-01	AF242382.1	NT	Homo sapiens phytanoyl-CoA hydroxylase (PHYH) gene, exon 5
2699	15818	28934	3.62	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4146	17298	30289	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4146	17298	30290	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5709	18902	32197	1.6	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5795	18986	32289	3.48	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7486	20561		1.08	9.3E-01	AF270648.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8257	21339	34856	1.99	9.3E-01	AA847040.1	EST_HUMAN	oe09b03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
9013	22092		1.1	9.3E-01	AF061981.1	NT	Xenopus laevis CCCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9137	22216	35760	0.89	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13039	25683	31961	2.09	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA
13049	25688		1.22	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpL34 mRNA, complete cds
3311	16484	29505	3.92	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
4999	18128		0.61	9.2E-01	BF129973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5835	19025		1.58	9.2E-01	7105410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6109	19289	32624	4.97	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
6770	19925	33320	0.65	9.2E-01	M64703.1	NT	N.crassa valyl-tRNA synthetase (cyt-20/un-3) gene
9860	22900	36484	0.98	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9949	22988	36582	1.31	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10472	23507	37120	3.6	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10627	23661	37269	1.64	9.2E-01	BF593251.1	EST_HUMAN	7o58e06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;
10883	23967	37596	1.76	9.2E-01	BE563811.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
12022	25006	38707	1.5	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1654	14807	27892	1.52	9.1E-01	T96675.1	EST_HUMAN	ye52f01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element;
2193	15328		1.49	9.1E-01	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3275	16449	29468	1.28	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3275	16449	29469	1.28	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6296	19469	32824	1.54	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6635	19794	33183	3.25	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7750	20810	34300	17.46	9.1E-01	AA806623.1	EST_HUMAN	ob71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
7916	20967	34473	2.81	9.1E-01	U72995.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10379	23414	37023	0.6	9.1E-01	P38432	SWISSPROT	P80-COILIN
12595	26054		19.67	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3277	16451	29472	0.8	9.0E-01	7661625	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
3439	16607		0.73	9.0E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4219	17368	30357	0.68	9.0E-01	8922310	NT	Homo sapiens hypothetical protein FLJ10251 (FLJ10251), mRNA
4498	17638	30620	1.43	9.0E-01	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
5127	18252	31218	13.05	9.0E-01	AF017729.1	NT	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds
7551	20623	34100	0.82	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7579	20651		1.42	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9549	22614	36183	0.68	9.0E-01	AF086761.1	NT	Danio rerio semaphorin Z1a mRNA, complete cds
10035	23073	36673	0.48	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
12113	25093	38797	1.41	9.0E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
5814	19004	32309	2.5	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6378	19547		1.28	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-DF DNA
6590	25827	33134	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
6590	25827	33135	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
8621	21701	35237	0.92	8.9E-01	AF259667.1	NT	Olithona nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
12080	25060	38766	2.72	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12423	25300		4.02	8.9E-01	AE002186.2	NT	Chlamydophila pneumoniae AR39, section 21 of 94 of the complete genome
4664	17799	30786	2.11	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5489	18688	31706	0.66	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
7701	20766	34250	0.59	8.8E-01	M81182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10436	23471	37077	1.07	8.8E-01	7656978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEB), mRNA
11337	24400	38049	2.23	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12092	25072	38779	7.56	8.8E-01	AA808055.1	EST_HUMAN	oc38h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
12240	26158		2.13	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
477	13672	26704	2	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2475	15602	28727	0.98	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2938	16115	29127	5.32	8.7E-01	AA595863.1	EST_HUMAN	nn05f11.s1 NCI_CGAP_Pr4.1 Homo sapiens cDNA clone IMAGE:1076877
5120	18246		4.12	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put>
8229	21311	34831	0.66	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
9130	22209	35752	0.66	8.7E-01	AI239456.1	EST_HUMAN	qh36e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9130	22209	35753	0.66	8.7E-01	AI239456.1	EST_HUMAN	qh36e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9939	22978	36569	2.07	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
10511	23546	37156	1.08	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10511	23546	37157	1.08	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
11070	24145	37782	5.87	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
12034	25017	38720	3.32	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12034	25017	38721	3.32	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12652	25940		2.8	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'
487	13681		2.39	8.6E-01	X17012.1	NT	Rat IGFII gene for insulin-like growth factor II
881	14057	27123	3.14	8.6E-01	W69089.1	EST_HUMAN	zd44e03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2344	15475	28608	1.31	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3710	16871	29875	0.85	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3901	17060	30059	1.31	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
6019	19202	32521	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6019	19202	32522	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6508	25825	33042	0.7	8.6E-01	S76772.1	NT	polyprotein [Coxsackie B4 virus CB4, host=mice, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
6848	20001	33409	1.96	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6848	20001	33410	1.96	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7696	20761		0.64	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
8112	21194		1.82	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8232	21314	34834	0.56	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9887	22927		0.54	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12856	25883		2.11	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2509	15635		1.46	8.5E-01	AJ011624.1	NT	Arabidopsis thaliana (ecotype Columbia) spl2 gene, exons 1-5
6866	20018	33427	1.1	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7694	20759	34243	2.36	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8180	21262	34784	0.57	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8613	21693	35230	0.92	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8613	21693	35231	0.92	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8702	21782	35315	0.68	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10558	23593	37198	1.49	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10558	23593	37199	1.49	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12577	26056		5.29	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1), mRNA
12585	25394		6.39	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4873	18006	30989	0.68	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5611	25808	31871	2.75	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5611	25808	31872	2.75	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7991	21041	34553	0.57	8.4E-01	AF051142.1	NT	Mamestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
10163	23200		3.42	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
760	13941	26986	2.17	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3164	16339	29347	3.45	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3912	17071	30069	0.69	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4120	17274	30273	3.17	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5383	18585	31454	2.32	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9870	22910		4	8.3E-01	AI791952.1	EST_HUMAN	nn01f12.y5 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR repetitive element ;
10316	23351	36958	1.32	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10423	23458	37063	3.9	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10911	23994	37627	2.18	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10930	24012		1.65	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11584	24637	38317	9.95	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2111	15249	28369	2.72	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2156	15292		1.32	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2744	15861		0.95	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
4009	17166	30174	0.68	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4247	17393	30381	0.7	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL062w
4247	17393	30382	0.7	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL062w
5217	18338	31311	1.19	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6781	19936	33332	0.59	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrate-1 protein
6781	19936	33333	0.59	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrate-1 protein
6913	20228	33661	0.76	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SCIII25 protein
7037	20173	33595	3.19	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7419	25844	33966	4.48	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8639	21719	35256	0.55	8.2E-01	BE263145.1	EST_HUMAN	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10231	23266	36856	0.81	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
10264	23299	36897	1.51	8.2E-01	AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10428	23463	37070	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10428	23463	37071	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10596	23631	37239	3.78	8.2E-01	Q9JI70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10596	23631	37240	3.78	8.2E-01	Q9JI70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11942	24928	38631	4.72	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
12030	25013	38715	6.12	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12035	25018	38722	3.97	8.2E-01	H87398.1	EST_HUMAN	yw14d02.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252195 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
12607	25406	32046	3.01	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2817	15931		1.38	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3547	16712	29723	2.77	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
3547	16712	29724	2.77	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
4730	17865	30847	0.63	8.1E-01	4506290	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2) mRNA
5825	19015	32321	0.63	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R)
6445	19612	32975	0.89	8.1E-01	U16790.1	NT	Mus musculus putative collagen alpha-2 (XI) chain (COL11A2) gene, partial cds
6759	19915	33309	2.17	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
6759	19915	33310	2.17	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7681	20746	34227	0.7	8.1E-01	O47477	SWISSPROT	CYTOCHROME B
8095	21177	34693	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8095	21177	34694	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8808	21887	35428	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8808	21887	35429	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8969	22048	35591	1.14	8.1E-01	AW242647.1	EST_HUMAN	xn01h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW:LYAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN. ;contains MER22.b1 PTR5 repetitive element ;
10330	23365	36974	0.58	8.1E-01	P06425	SWISSPROT	PROBABLE E4 PROTEIN
10623	23657	37267	0.62	8.1E-01	N84541.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to EST(CLONE C-0PE11)
10759	23802		0.54	8.1E-01	AE001226.1	NT	Treponema pallidum section 42 of 87 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11772	24764	38459	2.62	8.1E-01	BE938558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11772	24764	38460	2.62	8.1E-01	BE938558.1	EST_HUMAN	RC0-TN0080-220800-025-d10.TN0080 Homo sapiens cDNA
12303	25221	32102	2.22	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
181	13404		2.62	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pta gene for phosphate actyltransferase allele 15
299	13516	26549	10.2	8.0E-01	AJ132772.1	NT	Bos taurus futb and rtlf genes
2093	15233		1.95	8.0E-01	BF530962.1	EST_HUMAN	602072473F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215091 5'
3146	16322	29334	1.32	8.0E-01	AF127897.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3387	16557	29572	1.29	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
4655	17791	30775	6.77	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5096	18224	31196	1	8.0E-01	7657352	NT	Mus musculus myosin IXb (Myo9b), mRNA
8179	21261		2.66	8.0E-01	AW901489.1	EST_HUMAN	RC0-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
8722	21802	35338	1.21	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
10635	23669		0.48	8.0E-01	BE833329.1	EST_HUMAN	QV3-OT0065-280600-250-c09 OT0065 Homo sapiens cDNA
10827	23860	37483	0.48	8.0E-01	AB045597.1	NT	Gallus gallus PPAR gamma mRNA for peroxisome proliferator-activated receptor, complete cds
11198	24267	37902	1.43	8.0E-01	Q92793	SWISSPROT	CREB-BINDING PROTEIN
466	13661	26697	0.75	7.9E-01	D11476.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
733	13915		0.92	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1635	14787		28.32	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1887	14839		1.06	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2337	15468	28603	9.03	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2338	15469	28604	4.11	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3605	16769	29784	3.57	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4416	17557		0.87	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4734	17869	30852	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4734	17869	30853	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5210	18331		0.68	7.9E-01	6753753	NT	Mus musculus enabled homolog (Drosophila) (Enah), mRNA
5235	18357	31325	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5236	18357	31326	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5283	18402		0.66	7.9E-01	AF139718.1	NT	Chrysomya bezziana peritrophin-48 precursor, gene, complete cds
6475	19642	33003	0.68	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8300	21382	34903	2.66	7.9E-01	X90996.1	NT	P.sativum GR gene
9747	22811	36390	3.24	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
10255	23290	36887	5.43	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10298	23331	36934	1.17	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10729	23762	37369	0.78	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10845	23878	37498	0.61	7.9E-01	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11256	24325		1.75	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11487	24546	38218	1.94	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
899	14074		1.49	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2349	15480	28612	6.99	7.8E-01	AW959567.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4823	17956	30942	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5149	18271		0.89	7.8E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6194	19370	32721	2.26	7.8E-01	AF116856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
6348	19518	32876	2.28	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6591	19751	33136	0.84	7.8E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8688	21768	35299	1.13	7.8E-01	BF108927.1	EST_HUMAN	7l54d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
9434	22508	36074	1.53	7.8E-01	Y10159.1	NT	D.discoideum racGAP gene
9533	22598	36170	0.56	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
10329	23364		1.28	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12571	26033		1.92	7.8E-01	L29260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS6) gene, complete cds
146	13371	26403	5.78	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
744	13925		1.72	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-li>
2776	15892	29003	1.34	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3438	16606		0.89	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA
3689	16851	29859	3.86	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4516	17655	30643	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4516	17655	30644	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18872	32159	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5678	18872	32160	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6076	19258	32587	1.41	7.7E-01	R08600.1	EST_HUMAN	yf24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
10049	23087	36689	0.68	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12452	25317		7.14	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome

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6224	19399	32748	5.26	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6224	19399	32749	5.26	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6647	19806	33193	0.66	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6990	18509	31501	0.74	7.6E-01	AI253399.1	EST_HUMAN	aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6990	18509	31526	0.74	7.6E-01	AI253399.1	EST_HUMAN	aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7196	20061	33472	0.84	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8255	21337	34855	1.54	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8318	21400	34924	2.38	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8318	21400	34925	2.38	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8520	21601	35137	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8520	21601	35138	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9167	22245	35789	1.33	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbitol inducible, type a (Cyp2b9), mRNA
9479	22536	36100	5.24	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9479	22536	36101	5.24	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11639	24719	38411	2.29	7.6E-01	X86347.1	NT	H.aspersa mRNA for neurofilament NF70
11639	24719	38412	2.29	7.6E-01	X86347.1	NT	H.aspersa mRNA for neurofilament NF70
12010	24995		2.78	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	25157		8.21	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
526	13719		1.31	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
597	13787	26807	1.08	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7690	20755	34240	0.8	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12521	25354		5.2	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
1154	14318	27372	1.61	7.4E-01	AI598146.1	EST_HUMAN	tn14b09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element;contains element MIR repetitive element ;
2419	15548	28676	0.97	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3820	16980	29983	0.97	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds

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4010	17167	30175	0.71	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rstR-a (rstR-a) and Calcutta-rstR-b (rstR-b) genes, complete cds
4429	17569	30551	8.12	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8027	21110	34628	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8027	21110	34629	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8834	21913	35451	1.01	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154340 5'
8910	21989		1.45	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9298	22374	35925	6.86	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9357	22432	35990	1.24	7.4E-01	AA187986.1	EST_HUMAN	zp67h01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPQ_MOUSE P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10613	23647	37256	0.7	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
12170	25133		3.69	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1nh), mRNA
12287	25213		1.7	7.4E-01	AI472641.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4083	17238		0.73	7.3E-01	AP000062.1	NT	Aeropyrum pernix genomic DNA, section 5/7
4738	17873	30856	0.8	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4822	17955	30941	2.38	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
6741	19897	33287	5.5	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6741	19897	33288	5.5	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7243	25841	33771	0.93	7.3E-01	AJ011418.1	NT	Lycopersicon esculentum mRNA for ubiquitin activating enzyme
7617	20687	34163	0.69	7.3E-01	Z14133.1	NT	D.melanogaster Chc mRNA for clathrin heavy chain
7718	20782	34268	7.25	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
7718	20782	34269	7.25	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
11714	24754	38448	3.29	7.3E-01	AA678019.1	EST_HUMAN	zi25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
11714	24754	38449	3.29	7.3E-01	AA678019.1	EST_HUMAN	zi25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
854	14031		1.86	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2012	15152	28257	3.43	7.2E-01	X79140.1	NT	N.tabacum NeIF-4A13 mRNA
2532	15657	28781	1.96	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3135	16311	29323	1.27	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3541	16705	29717	2.36	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-1 allele, complete cds
3702	16863	29866	1.35	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
3975	17132	30136	1.57	7.2E-01	BF338350.1	EST_HUMAN	602035589F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4173	17323		0.73	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4892	18022	31007	2.68	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5225	18347	31317	1.07	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
5225	18347	31318	1.07	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
5308	18425	31395	0.65	7.2E-01	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7362	20441	33903	0.59	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8648	21728	35265	1.31	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9163	22241		0.54	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10548	23583	37192	2.25	7.2E-01	BF670061.1	EST_HUMAN	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
10977	24056	37690	3.26	7.2E-01	U82623.1	NT	Rattus norvegicus cytocentrin mRNA, complete cds
12530	18491	31530	1.51	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds
12737	25488		4.37	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
12784	26075		1.46	7.2E-01	Y10168.1	NT	B.thuringiensis PK1 & cap genes, putative
710	13892	26928	11.37	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3130	16306	28320	16.1	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4324	17467	30453	3.07	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4324	17467	30454	3.07	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
6069	19251	32579	1.73	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6069	19251	32580	1.73	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
7088	20182	33606	6.48	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pr) gene, complete cds
8934	22013	35552	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA
8934	22013	35553	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA
10059	23097	36700	1.6	7.1E-01	BE904406.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10621	23655	37265	1.1	7.1E-01	M12961.1	NT	Human T-cell receptor germline gamma-chain J2 gene
12505	25955		2.64	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1257	14415	27479	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1257	14415	27480	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2521	15647	28770	1.29	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;

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2521	15647	28771	1.29	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5169	18291		2.32	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6073	19255		0.89	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8573	21654		6.52	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9517	22582	36150	0.58	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds
9517	22582	36151	0.58	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds
11382	24443	38102	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'
11382	24443	38103	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'
13133	25997	31772	1.47	7.0E-01	9630464	NT	Bacteriophage N15 virion, complete genome
992	14164	27224	6.3	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
992	14164	27225	6.3	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1338	14495	27565	2.91	6.9E-01	AA593530.1	EST_HUMAN	nn28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3291	16465	29484	1.71	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3531	16696	29707	15.79	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
5311	18428	31398	97.22	6.9E-01	BE782751.1	EST_HUMAN	601465594F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868943 5'
5902	19091	32405	0.82	6.9E-01	AB035662.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord actin, complete cds
6112	19292	32627	0.85	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6500	19666	33029	1.12	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7979	21028	34542	0.58	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
8168	21250	34769	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8168	21250	34770	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9372	22447		0.66	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9896	22936	36520	0.56	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9896	22936	36521	0.56	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10619	23653	37263	0.78	6.9E-01	BF242367.1	EST_HUMAN	601880580F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109419 5'
11536	24592	38268	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11536	24592	38269	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12146	25949		3.77	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)

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979	14152	27212	1.94	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2739	15856		1.41	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2890	14798	27883	1.43	6.8E-01	AA854475.1	EST_HUMAN	aj75a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411_rna1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4694	17829	30815	1.32	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
4980	18109	31085	0.62	6.8E-01	4758521	NT	Homo sapiens hevin (HEVIN) mRNA
9838	22878	36460	1.06	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10567	23602		5.72	6.8E-01	AA687936.1	EST_HUMAN	nv13e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546_rna1 Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
11344	24407	38056	2.4	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11344	24407	38057	2.4	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11376	24437	38096	1.91	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11376	24437	38097	1.91	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11579	24633	38312	1.57	6.8E-01	AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
11906	24893	38594	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11906	24893	38595	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
309	13525	26559	30.38	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
349	13560	26588	25.24	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1961	15104		1.14	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds
2214	15348	28477	1.98	6.7E-01	AA451864.1	EST_HUMAN	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2235	16058	28498	5.15	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3060	16236	29256	5.81	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4575	17712	30696	0.62	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
5626	18820	31894	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5626	18820	31895	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds

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6083	19265	32594	0.79	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6453	19620	32983	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6453	19620	32984	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6754	19910	33304	0.59	6.7E-01	BE966241.2	EST_HUMAN	601650177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6754	19910	33305	0.59	6.7E-01	BE966241.2	EST_HUMAN	601650177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7468	20543		3.97	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7495	20570	34042	0.94	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10348	23383		1.01	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
11196	24265	37900	2.06	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11746	23932	37558	2.75	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
11959	24944	38649	2.48	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2570	15695	28819	0.97	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIL2) mRNA, partial cds
2765	15880	28989	1.13	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3578	16743	29760	1.16	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3748	16909	29913	4.58	6.6E-01	Y07669.1	NT	C.albicans random DNA marker, 282bp
4225	17373		2.48	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6462	19629	32990	3.82	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7272	20355	33808	0.62	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7272	20355	33809	0.62	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7862	20916	34421	3.7	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'
8764	21843	35384	0.58	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9865	22905		2.34	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10207	23243		0.51	6.6E-01	AU118198.1	EST_HUMAN	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
640	13825	26848	2.02	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
640	13825	26849	2.02	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3519	16685	29696	5.5	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4148	17300	30292	1.73	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4397	17540	30521	7.71	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5174	18296	31258	2.88	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds

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5559	25807	31795	1.86	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4)
6865	20017	33426	1.3	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7760	20819	34309	0.74	6.5E-01	X04769.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7846	20901	34404	0.99	6.5E-01	AI799882.1	EST_HUMAN	wc46a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321642 3'
10042	23080		0.86	6.5E-01	T78904.1	EST_HUMAN	yd21b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847 3'
10542	23577	37186	2.53	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10869	23954	37583	2.55	6.5E-01	H87583.1	EST_HUMAN	yw17f06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252515 5'
10925	24008	37643	2.98	6.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
11030	24109		3.38	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11899	24887	38586	5.43	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12566	25386		8.69	6.5E-01	BE465050.1	EST_HUMAN	hv74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12840	25889		3.83	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
262	13481	26513	8.59	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3545	16710	29721	4.42	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3964	17122	30125	1.46	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4614	17751	30731	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
4614	17751	30732	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
8812	21891	35432	1.58	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
10221	23257		0.5	6.4E-01	11418320	NT	Homo sapiens hypothetical protein FLJ10140 (FLJ10140), mRNA
10294	23329	36933	7.31	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10309	23344	36949	1.31	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
12693	25461		19.53	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSCGC09 5'
447	13643	26682	3.76	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
548	13741	26765	1.85	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2230	15364	28493	3.29	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2646	15769	28884	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2646	15769	28885	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3081	16257		0.93	6.3E-01	Y17275.1	NT	Lycopersicon esculentum p69a gene, complete CDS
6189	19365	32713	0.84	6.3E-01	BE093906.1	EST_HUMAN	PM0-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6733	19889	33281	1.01	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6733	19889	33282	1.01	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8718	21798		3.44	6.3E-01	BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
9087	22166	35712	0.79	6.3E-01	S62927.1	NT	glycoprotein IIIa {Alu 1 and 3 fusion junction} [human, Genomic Mutant, 300 nt]
9421	22495	36062	0.65	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5'
9620	22675	36245	3.14	6.3E-01	9627521	NT	Variola virus, complete genome
9620	22675	36246	3.14	6.3E-01	9627521	NT	Variola virus, complete genome
10142	23180		0.68	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10641	23675	37285	1.59	6.3E-01	Z73003.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR218w
10747	23780	37393	1	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10781	23814		0.48	6.3E-01	AW795395.1	EST_HUMAN	PM0-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
11315	24379	38024	1.78	6.3E-01	AA877715.1	EST_HUMAN	nr09h06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:O02916 O02916 HLARK. ;
11620	24671	38359	6.18	6.3E-01	AI804160.1	EST_HUMAN	CM-BT043-090299-046 BT043 Homo sapiens cDNA
11709	24749	38442	1.55	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11888	24876	38573	2.12	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12086	25066	38772	1.47	6.3E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12262	26130	31546	15.92	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12358	25257		1.6	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12582	26029		4.27	6.3E-01	X83528.1	NT	C.limicola pscD gene
5991	19176	32497	2.15	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7664	20731		3.59	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7715	25852	34266	1.16	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8497	21578	35114	4.67	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
9057	22136	35681	0.7	6.2E-01	AF034411.1	NT	Lycopersicon esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinate dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9648	21091	34606	1.47	6.2E-01	BE562687.1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
9710	22759		2.56	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
10283	23318	36919	6.83	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10426	23461	37067	0.63	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10426	23461	37068	0.63	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10756	23789	37405	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10756	23789	37406	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2468	15595		6.27	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5653	18847	32129	1.33	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CeMyoD (hlh-1) alternatively spliced genes, complete cds
7009	20145	33564	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7009	20145	33565	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7160	20293	33736	0.67	6.1E-01	AW105653.1	EST_HUMAN	xd50h03.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7254	20337	33787	0.69	6.1E-01	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8428	21509	35041	3.47	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8995	22074	35612	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA
8995	22074	35613	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA
9615	22670	36239	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9615	22670	36240	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10047	23085	36686	1.05	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
10252	23287	36883	0.92	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10833	23866	37489	0.47	6.1E-01	AF025993.1	NT	Sus scrofa neural cell adhesion molecule (NCAM) gene, 3' UTR and microsatellite repeat region
12033	25016	38718	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12033	25016	38719	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
13062	25695		1.16	6.1E-01	X95287.1	NT	M.mazei orfA, orfB, and orfC of archaeal ABC-transporter system
507	13701	26730	1.79	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
575	13767		4.74	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1393	14547	27623	1.83	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3917	17076	30073	0.87	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4305	17448		1.26	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5395	18597	31567	1.96	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5555	18753	31791	2.5	6.0E-01	AW139713.1	EST_HUMAN	UI-H-BI1-aeb-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6669	19828	33216	2.74	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6800	19955	33355	0.66	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)

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6955	20268	33705	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
6955	20268	33706	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7509	20583	34056	6.49	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8315	21397	34922	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8315	21397	34923	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10028	23066	36664	1.57	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10480	23515		1.04	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
10594	23629		0.61	6.0E-01	BE837779.1	EST_HUMAN	RC2-FN0094-190700-017-d08 FN0094 Homo sapiens cDNA
11312	24376	38021	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11312	24376	38022	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11846	24835	38529	2.74	6.0E-01	AI420623.1	EST_HUMAN	tf08f07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095621 3'
12663	25440	32052	2.08	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12781	25523		1.46	6.0E-01	AA706087.1	EST_HUMAN	zj93g05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12953	25956		1.44	6.0E-01	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12998	25993	31766	5.46	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
13032	25880		8.12	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1025	14195	27254	1.09	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3343	16516	29530	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3343	16516	29531	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3916	17075	30072	0.62	5.9E-01	U74341.1	NT	Pterodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
4337	17480		3.95	5.9E-01	AF162756.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
5289	18407	31374	0.66	5.9E-01	AF026566.1	NT	Ovis aries SRY gene promoter region
6594	19754	33140	1.95	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7416	20494	33962	3.08	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7556	20628		0.63	5.9E-01	X68801.1	NT	G.gallus gene for skeletal alpha-actinin, exon EF2
8188	21270	34795	0.48	5.9E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
8839	21918	35456	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9743	22807	36385	1.01	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K/UW31/Cx major outer membrane protein (omp1) gene, complete cds
10117	23155		0.64	5.9E-01	P06463	SWISSPROT	E6 PROTEIN
10391	23426	37033	1.28	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)

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10908	23991	37624	2.24	5.9E-01	Q9X0I3	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10916	23999	37632	1.71	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11203	24272	37908	2.76	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
11469	24528	38201	1.98	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds
12302	25220	32101	1.78	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12549	25372		1.92	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
12799	25533		4.82	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1958	15101	28201	1.26	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
4092	17247	30252	1.11	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56.Homo sapiens cDNA clone IMAGE:4076131 5'
4637	17773	30753	3.59	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4917	18047		2.22	5.8E-01	AF110846.1	NT	Megasella scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5490	18689		1.02	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5648	18842	32123	0.81	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6313	19485	32840	1.69	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-500E06 5'
6442	19609	32972	0.58	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
6952	20265		2.37	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8071	21153		2.87	5.8E-01	H41571.1	EST_HUMAN	yn91b03.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8278	21360	34878	0.66	5.8E-01	AI280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8278	21360	34879	0.66	5.8E-01	AI280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21466	34991	2.71	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8385	21466	34992	2.71	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
9092	22171	35716	10.4	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9172	22250	35793	1.23	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
9173	22251	35794	0.57	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
9795	22835		0.79	5.8E-01	BF031606.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11237	24306	37943	7.26	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11291	24357		3.35	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11407	24468		1.44	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3108	16284		0.73	5.7E-01	6755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3295	16469	29488	1.46	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3593	16757		2.84	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6485	19652	33014	4.41	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'

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6850	20008	33412	0.92	5.7E-01	AA194201.1	EST_HUMAN	zr38c06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665674 5'
7000	18519	31512	1.15	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7941	20991	34501	1.88	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8157	21239		0.55	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts
10004	23042	36634	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10004	23042	36635	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10803	23836	37461	0.91	5.7E-01	BF540962.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
12255	25192		1.29	5.7E-01	BE715051.1	EST_HUMAN	MR3-HT0736-180700-003-a02 HT0736 Homo sapiens cDNA
13025	25675		1.31	5.7E-01	BE959722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839763 3'
3449	16617	29635	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3449	16617	29636	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3989	17146	30152	0.59	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4354	17497	30476	0.77	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
9003	22082	35625	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5'
9003	22082	35626	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5'
9575	22717	36285	1.13	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	25123		7.84	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
12272	25204	38362	1.39	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element ;
12661	17146	30152	2.38	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12690	25460		2.56	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13167	25758		3.64	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1238	14397	27459	6.04	5.5E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2766	15881	28990	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2766	15881	28991	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2985	16161	29178	1.17	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3134	16310		1.57	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3306	16480	29501	2.93	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3783	16944	29951	1.34	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
5249	18370		1	5.5E-01	AF063866.1	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
5269	18388	31356	1.01	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7405	20483	33950	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, comple>
7405	20483	33951	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, comple>
7439	20516		0.74	5.5E-01	AB015596.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8676	21756	35291	0.47	5.5E-01	BE163243.1	EST_HUMAN	QV3-HT0458-170200-090-b05 HT0458 Homo sapiens cDNA
9969	23008		0.56	5.5E-01	U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10588	23623	37230	0.83	5.5E-01	T05047.1	EST_HUMAN	EST02935 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCQ35
11406	24467	38132	1.64	5.5E-01	BF129507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
147	13372	26404	8.11	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
147	13372	26405	8.11	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
598	13788	26808	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes
598	13788	26809	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes
1300	14456	27522	2.21	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2173	15308		2.8	5.4E-01	AE002247.2	NT	Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome
2329	15461	28594	2.82	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
5774	18966	32269	0.83	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6320	19492	32850	0.93	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7170	20303	33746	0.77	5.4E-01	BE966592.2	EST_HUMAN	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7490	20565	34035	1.96	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7490	20565	34036	1.96	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7492	20567	34039	1.47	5.4E-01	Q04428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
10195	23232		2.69	5.4E-01	BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
11334	24397	38046	2.68	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11920	24906	38607	2.76	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11920	24906	38608	2.76	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12039	19492	32850	1.3	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
12217	25168		2.41	5.4E-01	AI858398.1	EST_HUMAN	wi37g04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
529	13722	26748	2.12	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
2843	15957	29065	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2843	15957	29066	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3315	16488	29506	3.8	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4327	17470		1.2	5.3E-01	U39687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5574	18770	31813	1.55	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5574	18770	31814	1.55	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5671	18865	32150	0.95	5.3E-01	AA193672.1	EST_HUMAN	zr42g09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5671	18865	32151	0.95	5.3E-01	AA193672.1	EST_HUMAN	zr42g09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5762	18954	32257	2.32	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5762	18954	32258	2.32	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9105	22184		1.59	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast product
9156	22234	35779	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element ;
9156	22234	35780	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element ;
10416	23451	37056	0.65	5.3E-01	AI954210.1	EST_HUMAN	wx94b02.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11857	24845	38542	5.63	5.3E-01	BE566291.1	EST_HUMAN	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
12145	25958		1.73	5.3E-01	AA916053.1	EST_HUMAN	og30e05.s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
839	14017	27072	20.65	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1190	14352	27410	7.57	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1218	14379	27438	3.05	5.2E-01	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1935	15078		3.88	5.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2213	15347	28476	2.85	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3189	16364	29369	2.1	5.2E-01	U65942.1	NT	Chlamydophila abortus strain S25/3 POMP91A and POMP90A precursor, genes, complete cds
3309	16483		1.05	5.2E-01	D73443.1	NT	Azotobacter vinelandii icd gene for isocitrate dehydrogenase, complete cds
3491	16658		1.61	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3530	16695	29706	2.01	5.2E-01	AA984165.1	EST_HUMAN	am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3722	16883		0.77	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3724	16885	29891	0.87	5.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
4729	17864	30846	0.61	5.2E-01	6752947	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
5770	18962	32263	0.92	5.2E-01	AA284261.1	EST_HUMAN	zc44d09.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
9932	25862	36562	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9932	25862	36563	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10136	23174	36772	0.49	5.2E-01	AA194518.1	EST_HUMAN	zq05b09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5'
10233	23268	36858	1.32	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13128	25736		4.83	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
632	13817	26841	2.5	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
665	13851	26878	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene
665	13851	26879	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene
1684	14836		1.02	5.1E-01	X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
4188	17338	30331	3.87	5.1E-01	AI858495.1	EST_HUMAN	wl39b12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427263 3'
4303	17446	30432	2.89	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5179	18301		0.6	5.1E-01	BE091796.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6352	19522	32879	1	5.1E-01	BE541068.1	EST_HUMAN	601063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6406	19575		0.9	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAUF07 5'
7057	20110	33526	1.35	5.1E-01	R80873.1	EST_HUMAN	yl94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8770	21849	35389	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8770	21849	35390	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9886	22926	36510	4.65	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9889	22929	36513	3.95	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
10363	23398	37009	0.99	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12368	25874		3.49	5.1E-01	BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12634	25427		1.31	5.1E-01	BF439982.1	EST_HUMAN	nac51f10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element ;
2203	15338	28464	1.65	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2203	15338	28465	1.65	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2211	15345	28472	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28473	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2231	15365		1.56	5.0E-01	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3842	17001	30004	0.85	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3934	17093	30091	0.93	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3977	17134	30137	2.67	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6782	19937		0.82	5.0E-01	BF576199.1	EST_HUMAN	602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'
7842	20897	34398	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7842	20897	34399	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8727	21807		1.63	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8870	21949	35484	0.66	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9657	21100	34613	2.13	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136832 5'
9824	22864	36445	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22864	36446	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10602	23637		1.23	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
12307	25225		3.64	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13093	25713		2.25	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13109	25724		4.71	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
812	13991	27045	1.83	4.9E-01	BF571462.1	EST_HUMAN	602076849F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1692	14844	27928	1.08	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1955	15098	28198	1.34	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5522	18719	31735	1.17	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6161	19337	32682	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6161	19337	32683	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7610	20680	34156	1.61	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7882	20934	34439	0.86	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7882	20934	34440	0.86	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9190	22268		1.96	4.9E-01	BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
9389	22464	36028	0.96	4.9E-01	AW339905.1	EST_HUMAN	hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:O95714 O95714 HERC2. ;
9496	26228		2.2	4.9E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10524	23559	37166	1.05	4.9E-01	AF053980.1	NT	Mus musculus adenylyl cyclase 1 (Adcy1) cDNA, partial cds
12197	25154		2.61	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
13085	26174		4.94	4.9E-01	AA613562.1	EST_HUMAN	nq22e11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
13094	25714	31939	1.69	4.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
13181	25768		1.27	4.9E-01	11431438	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
4452	17592		0.59	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5624	18818	31892	9.66	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6817	19970	33378	0.69	4.8E-01	U92882.1	NT	Mus musculus slow skeletal muscle troponin T (Tnnt1) gene, complete cds
6827	19980		4.18	4.8E-01	AA659878.1	EST_HUMAN	nu85f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7469	20544		1.83	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
7845	20900	34403	1.06	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7938	20988	34497	3.59	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7938	20988	34498	3.59	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8089	21171	34686	1.81	4.8E-01	AI820744.1	EST_HUMAN	yj77f10.y5 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element ;
9446	22562		1.05	4.8E-01	BE155148.1	EST_HUMAN	PM1-HT0350-201299-004-b04 HT0350 Homo sapiens cDNA
10212	23248		0.55	4.8E-01	BF568633.1	EST_HUMAN	602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
10966	24047		1.9	4.8E-01	X83502.1	NT	S.cerevisiae ORFs from chromosome X
12279	25208		1.56	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12509	25918		5.78	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
3142	16318		0.59	4.7E-01	AF192387.1	NT	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
6644	19803	33190	8.07	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7186	20051	33461	0.84	4.7E-01	AI204374.1	EST_HUMAN	qf72e09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8049	21132	34652	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8049	21132	34653	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9276	22352	35904	0.61	4.7E-01	6981501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11084	24158		4.37	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
11340	24403	38052	1.94	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
11658	24737	38428	1.45	4.7E-01	AW889448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12401	25281		1.84	4.7E-01	BE887763.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12529	25361		1.25	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'
3837	16997	29999	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3837	16997	30000	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5535	18732	31747	0.93	4.6E-01	BF313693.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5535	18732	31748	0.93	4.6E-01	BF313693.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5588	18783	31828	3.52	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5588	18783	31829	3.52	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5663	18857	32140	1.84	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5677	18871	32157	3.62	4.6E-01	AI247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN. ;
5677	18871	32158	3.62	4.6E-01	AI247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN. ;
5685	18879	32169	1.44	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5763	18955		0.85	4.6E-01	AF212124.1	NT	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5850	19040		0.9	4.6E-01	BE817247.1	EST_HUMAN	PM0-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6386	19555	32914	0.82	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6906	20221	33649	2.39	4.6E-01	U62332.1	NT	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6906	20221	33650	2.39	4.6E-01	U62332.1	NT	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7379	25843	33920	0.66	4.6E-01	L07320.1	NT	Murine cytomegalovirus e1 protein gene, complete cds
7906	20958	34484	0.78	4.6E-01	AA493577.1	EST_HUMAN	nh04h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element;contains element L1 repetitive element ;
8515	21596	35131	14.55	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
8946	22025	35565	0.54	4.6E-01	AA932237.1	EST_HUMAN	co76b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8946	22025	35566	0.54	4.6E-01	AA932237.1	EST_HUMAN	oc76b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9501	22557	36120	0.93	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9501	22557	36121	0.93	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9866	22906	36490	0.52	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9866	22906	36491	0.52	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10181	23218	36809	1.15	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10181	23218	36810	1.15	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11238	24307		2.31	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
11248	24317	37956	5.06	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11248	24317	37957	5.06	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11760	23946	37573	4.3	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11760	23946	37574	4.3	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
1960	15103	28203	1.15	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1960	15103	28204	1.15	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2933	16110	29124	4.83	4.5E-01	AA677086.1	EST_HUMAN	zj55d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3380	16552	29565	0.66	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3380	16552	29566	0.66	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3393	16563	29578	4.46	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3465	16632	29651	1.51	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4139	17291		1.18	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN
4186	17336	30329	1.02	4.5E-01	AI708908.1	EST_HUMAN	as96e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4292	18478		4.71	4.5E-01	AW873495.1	EST_HUMAN	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5058	18186	31161	1.18	4.5E-01	BE963445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5666	18860	32145	1.57	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
6740	19896		1.38	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
7571	20643	34120	0.91	4.5E-01	M37036.1	NT	Rat nucleolar proteins B23.1 and B23.2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7785	20841	34333	2.39	4.5E-01	AI858849.1	EST_HUMAN	wl32e02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923 SWI/SNF COMPLEX 170 KDA SUBUNIT. ;
8502	21583		1.11	4.5E-01	M32661.1	NT	D.melanogaster Shaw2 protein mRNA, complete cds
8598	21679	35217	2.87	4.5E-01	AI648596.1	EST_HUMAN	tz56g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
8756	21835	35376	0.85	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8981	22060		2.36	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
9200	22278	35817	0.86	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10145	23183		0.96	4.5E-01	9630816	NT	Bombyx mori nuclear polyhedrosis virus, complete genome
10713	23746	37352	25.59	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
10713	23746	37353	25.59	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
11104	24176	37812	2.52	4.5E-01	AW591271.1	EST_HUMAN	xo14h01.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1] ;
11225	24294	37935	2.16	4.5E-01	11430799	NT	Homo sapiens cadherin 3, P-cadherin (placental) (CDH3), mRNA
11530	24586		1.3	4.5E-01	AV719382.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'
12164	26162		5.58	4.5E-01	BE871461.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12895	25592		1.2	4.5E-01	BF337531.1	EST_HUMAN	602035275F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183290 5'
12970	25630		12.42	4.5E-01	11422099	NT	*Homo sapiens* testis-specific kinase 2 (TESK2), mRNA
2094	15234		1.11	4.4E-01	6680503	NT	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2462	15589	28715	4.16	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3390	16560	29575	1.54	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3390	16560	29576	1.54	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3395	16565	29580	2.12	4.4E-01	BF056726.1	EST_HUMAN	7j91d02.y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4349	17492		1.35	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5536	18733	31749	1.31	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5536	18733	31750	1.31	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5805	18995	32300	1.58	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5823	19013	32319	1.81	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
6074	19256	32584	1.12	4.4E-01	AI198413.1	EST_HUMAN	qi62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1851125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6074	19256	32585	1.12	4.4E-01	AI198413.1	EST_HUMAN	qi62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN ;
6370	19539	32899	1.67	4.4E-01	AW080795.1	EST_HUMAN	xc27e08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O95154 AFLATOXIN B1-ALDEHYDE REDUCTASE. ;
6458	19625		1.05	4.4E-01	AA776132.1	EST_HUMAN	ae85d11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN);
7557	20629	34104	1.14	4.4E-01	AE000571.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
8024	21107		12.3	4.4E-01	Z11679.1	NT	S.tuberosum mRNA for induced stolon tip protein (partial)
8962	22041	35584	1.11	4.4E-01	AA056427.1	EST_HUMAN	zl69a03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509836 3'
9352	22427	35985	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9385	22460	36023	0.62	4.4E-01	AW612578.1	EST_HUMAN	hh05c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9490	22547	36110	1.13	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
10167	23204	36798	1.95	4.4E-01	AI268650.1	EST_HUMAN	qo39f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
10168	23205		2.09	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10302	23337	36942	4.94	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10585	23620	37226	1.76	4.4E-01	S76404.1	NT	beta -HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10585	23620	37227	1.76	4.4E-01	S76404.1	NT	beta -HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10829	23862	37485	0.46	4.4E-01	P02716	SWISSPROT	ACETYLCHOLINE RECEPTOR PROTEIN, DELTA CHAIN PRECURSOR
11522	24578	38256	1.64	4.4E-01	6691408	NT	Terebratulina retusa mitochondrion, complete genome
12435	25308	32087	4.23	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12447	26084		13.47	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
13051	25689		1.41	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
424	13619	26659	2.42	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
424	13619	26660	2.42	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1633	14785	27871	1.11	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2935	16112		1.34	4.3E-01	AW935269.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3127	16303	29316	0.95	4.3E-01	AW999477.1	EST_HUMAN	MR0-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4526	13619	26659	1.27	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4526	13619	26660	1.27	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5071	18199		1.04	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5220	18342		0.94	4.3E-01	9635250	NT	Xestia c-nigrum granulovirus, complete genome
5480	18679	31693	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5480	18679	31694	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6009	19194	32512	1.31	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
6027	19210	32530	1.99	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSC186) gene, partial cds
6847	20000	33408	3.1	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica ifnG gene
6925	20240	33675	0.67	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7005	20141		0.77	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7586	20658		1.28	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158296 5'
8622	21702		3.15	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-I (flaC-flaI) genes, complete cds
9455	22571	36137	1.02	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9928	22968	36556	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
9928	22968	36557	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
10433	23468	37075	0.99	4.3E-01	AW170559.1	EST_HUMAN	xn63e05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to TR:O00189 O00189 MU-ADAPTIN-RELATED PROTEIN 2. ;
11172	20240	33675	2.27	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
13162	25754		1.56	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1389	16036	27619	1.17	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
2002	15143		1.02	4.2E-01	AA761653.1	EST_HUMAN	nz24a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3697	16858	29862	4.1	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3727	16888	29892	1.09	4.2E-01	AI280338.1	EST_HUMAN	qi94b01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3803	16477		0.73	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
3984	17141	30146	0.74	4.2E-01	AW835527.1	EST_HUMAN	QV0-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA
4819	17952	30937	2.57	4.2E-01	AA534093.1	EST_HUMAN	nj69h01.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4903	18033	31022	3.8	4.2E-01	R13467.1	EST_HUMAN	yf77e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28278 5'
5832	19023	32330	1.42	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5901	19090	32404	1.63	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6334	19505	32863	0.99	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7090	20184	33608	8.72	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7090	20184	33609	8.72	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7151	25839	33727	3.21	4.2E-01	S82504.1	NT	Brca1=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7242	20328	33770	6.61	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7745	20805	34294	0.81	4.2E-01	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8182	21264	34786	4.01	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
8182	21264	34787	4.01	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8401	21482	35010	0.72	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9511	22576	36141	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9511	22576	36142	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
10175	23212		0.81	4.2E-01	AA705007.1	EST_HUMAN	zj95f01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462649 3'
10714	23747	37354	1.44	4.2E-01	AW863666.1	EST_HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
11298	24364	38005	1.43	4.2E-01	AB023489.1	NT	Oryzias latipes OlGC7 mRNA for membrane guanylyl cyclase, complete cds
11679	24678	38368	1.87	4.2E-01	BE966485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
1118	14283	27338	2.11	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210199-142 BT091 Homo sapiens cDNA
1127	14292	27347	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1127	14292	27348	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1640	14792	27877	1.77	4.1E-01	AI905949.1	EST_HUMAN	PM-BT103-270499-684 BT103 Homo sapiens cDNA
2775	15890	29001	1.46	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
3006	16181	29202	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3006	16181	29203	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3375	16547	29561	0.66	4.1E-01	AA906344.1	EST_HUMAN	oj94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3871	17030	30028	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
3871	17030	30029	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
4389	17532	30513	3.78	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoA, isoB, isoC, isoD, isoE and isoF genes
4422	17563		0.99	4.1E-01	AA909257.1	EST_HUMAN	om33d02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4789	17924	30912	1.36	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
6111	19291	32626	4.84	4.1E-01	BF681393.1	EST_HUMAN	602156590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6857	20010	33420	0.65	4.1E-01	U02298.1	NT	Mus musculus NIH 3T3 chemokine rantes (Scya5) gene, complete cds
7590	20661	34137	2.48	4.1E-01	U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
8225	21307	34827	1.36	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
9292	22368	35918	1.51	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA
9765	22762		0.75	4.1E-01	AF160597.1	NT	Voalavo gymnocaudus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10470	23505		1.56	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
10622	23656	37266	1.15	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLCBVD12 3'
10725	23758	37365	0.68	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10725	23758	37366	0.68	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10806	23839		1.14	4.1E-01	BF349382.1	EST_HUMAN	CM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11078	24153	37790	40.17	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
11675	23903	37525	1.88	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HBK1)
12810	26139		2.33	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
13153	26169		1.24	4.1E-01	AJ131016.1	NT	Homo sapiens SCL gene locus
1064	14229	27286	1.49	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1370	14525	27599	1.21	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1514	14667		5.48	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2061	16053	28316	1.08	4.0E-01	Z96933.1	NT	Ascobolus immersus masc2 gene
2061	16053	28317	1.08	4.0E-01	Z96933.1	NT	Ascobolus immersus masc2 gene
2866	13369	26402	1.11	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 componen n-recognin (Ubr1), mRNA
3033	16209	29231	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3033	16209	29232	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3786	16947	29955	1.87	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae YIIC (yIIC), YIID (yIID), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3932	17091	30088	3.21	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30089	3.21	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4938	18068		8.59	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6031	19214	32535	1.07	4.0E-01	AW970610.1	EST_HUMAN	EST382691 MAGE resequences, MAGK Homo sapiens cDNA
6568	19730	33108	0.62	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPROTEIN (P130) [CONTAINS: COAT PROTEIN C ; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
8113	21195	34714	0.51	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
8201	21283	34806	0.73	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
9208	22286	35827	1.11	4.0E-01	AA323289.1	EST_HUMAN	EST26066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11869	24857		1.67	4.0E-01	BF030262.1	EST_HUMAN	601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
12021	25005		2.38	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12453	25978		2.5	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
13027	26116		1.38	4.0E-01	Z49301.1	NT	S.cerevisiae chromosome X reading frame ORF YJL026w
13168	26036		1.21	4.0E-01	BF432020.1	EST_HUMAN	nab84e05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' similar to SW:NTCR_BOVIN O18875 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1 ;
13222	25907		1.26	4.0E-01	Z49301.1	NT	S.cerevisiae chromosome X reading frame ORF YJL026w
1409	14563	27638	1.84	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2707	15825	28940	3.34	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2770	15885	28994	5.03	3.9E-01	X82032.1	NT	H.sapiens B-myb gene

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2770	15885	28995	5.03	3.9E-01	X82032.1	NT	H.sapiens B-myb gene
3166	16341	29349	4.24	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egl, syrB2, cya3 genes and orf3
4190	17340	30333	1.48	3.9E-01	BF592611.1	EST_HUMAN	7i61d01.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
5106	18234	31203	1.47	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
6055	19237	32562	4.58	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6410	19579	32940	0.64	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8140	21222	34740	0.99	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
9062	22141	35686	0.83	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170899-004-b08 CT0105 Homo sapiens cDNA
9071	22150		0.82	3.9E-01	BF348634.1	EST_HUMAN	602019944F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155322 5'
9435	22509	36075	1.73	3.9E-01	AW195888.1	EST_HUMAN	xn86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O94821 O94821 KIAA0713 PROTEIN ;
9745	22809	36387	1.59	3.9E-01	AI937337.1	EST_HUMAN	wp76a02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX5_HUMAN P48382 BINDING REGULATORY FACTOR. ;
10082	23120	36722	2.88	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
10150	23188		0.58	3.9E-01	11465620	NT	Porphyra purpurea mitochondrion, complete genome
10369	23404	37015	0.92	3.9E-01	D86722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10562	23597	37203	0.61	3.9E-01	BF361856.1	EST_HUMAN	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
10562	23597	37204	0.61	3.9E-01	BF361856.1	EST_HUMAN	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
10836	23869		0.47	3.9E-01	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11059	24135		1.37	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBQC11 5'
12049	25030	38736	1.89	3.9E-01	AV702623.1	EST_HUMAN	AV702623 ADB Homo sapiens cDNA clone ADBDBE06 5'
12221	26055		4.03	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12916	25603		1.75	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
164	13389		7.58	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
518	13711		6.1	3.8E-01	AB029291.1	NT	Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
1919	15062		1.36	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2637	15760	28874	1.84	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds
2697	16069	28931	5.2	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3066	16242		0.71	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3113	16289	29305	1.91	3.8E-01	AF043383.1	NT	Pleuronectes americanus aminopeptidase N (ampN) gene, partial cds
3572	16737	29752	8.7	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3628	16792		1.09	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3643	16792		0.97	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3852	17012	30012	1.07	3.8E-01	BE154080.1	EST_HUMAN	PM0-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4027	17183	30192	0.65	3.8E-01	6754095	NT	Mus musculus general transcription factor II I (Gtf2i), mRNA
5727	18920	32214	1.11	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6469	19636		0.63	3.8E-01	S46825.1	NT	prion protein [mink, Genomic, 2446 nt]
6761	19917	33312	5.74	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
6899	20214	33644	4.39	3.8E-01	AI374601.1	EST_HUMAN	ta54f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
7079	20132	33549	1.38	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7685	20750		4.27	3.8E-01	X61597.1	NT	M.musculus gene for kallikrein-binding protein
8493	21574	35111	0.54	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8754	21833	35373	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8826	21905	35444	1.08	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9017	22096	35636	1.29	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9761	22699		4.35	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element;contains PTR5 repetitive element ;
11034	24113		1.38	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11699	24696	38388	1.57	3.8E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
11824	24813		2.87	3.8E-01	BE719219.1	EST_HUMAN	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11992	24977	38681	2.5	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11992	24977	38682	2.5	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12436	25309		2.61	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12569	26082		2	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12695	25463		1.71	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-e05 ET0063 Homo sapiens cDNA
13105	25720		1.48	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
13188	25772	31933	1.78	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2551	15676	28799	12.91	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3549	16714	29726	10.67	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3974	17131	30135	1.09	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4344	17487	30470	9.09	3.7E-01	AI218707.1	EST_HUMAN	ok39c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4440	17580	30559	1.31	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4509	17648	30636	2.91	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5280	18399	31368	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5280	18399	31369	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5883	19072	32380	1.27	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6071	19253	32582	1.25	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6639	19798	33187	0.7	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6660	19819		0.8	3.7E-01	L10353.1	NT	Mus saxicola haptoglobin mRNA, complete cds
7293	20375	33832	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7965	21015	34527	0.69	3.7E-01	T66802.1	EST_HUMAN	ya50a07.r3 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66324 5'
8524	21605	35143	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8524	21605	35144	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8560	21641	35180	0.68	3.7E-01	AA902912.1	EST_HUMAN	ok43b11.s1 NCI_CGAP_Lei2 Homo sapiens cDNA clone IMAGE:1516701 3'
9402	22476		1.34	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10373	23408		0.5	3.7E-01	K00691.1	NT	mouse ig germline alpha membrane exons region
10414	23449	37054	4.21	3.7E-01	AI336411.1	EST_HUMAN	qt46b07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
10783	23816	37437	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
10783	23816	37438	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
11097	24170	37805	1.8	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11285	24351	37989	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11285	24351	37990	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11754	23940	37566	2.73	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12004	24989		1.42	3.7E-01	AA973540.1	EST_HUMAN	oo46d03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698 TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12066	25047		3.5	3.7E-01	6677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12137	25654		1.17	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12314	25229		3.94	3.7E-01	AJ243525.1	NT	Chlamydophila psittaci partial omp1 gene for outer membrane protein 1
12410	25289		1.82	3.7E-01	D86976.1	NT	Human mRNA for KIAA0223 gene, partial cds
12821	25548		2.94	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
12902	25597	31971	6.99	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
271	13489	26520	0.77	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1020	14191		9.07	3.6E-01	U89241.1	NT	Human mibp gene, partial cds
1342	14498	27570	3.97	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1342	14498	27571	3.97	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1966	15109	28209	6.55	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1966	15109	28210	6.55	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2007	15147	28253	5.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2113	15251		1.15	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2343	15474		2.33	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2463	15590		2.8	3.6E-01	X76725.1	NT	P.irregulare (P3804) gene for actin
2556	15681	28806	2.66	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2694	15814	28929	1.69	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2964	18475		8.47	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3558	16723	29738	1.98	3.6E-01	X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3558	16723	29739	1.98	3.6E-01	X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
4528	17665	30652	1.2	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4863	17998	30981	0.69	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
5123	18249	31215	3.18	3.6E-01	AW339393.1	EST_HUMAN	he02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5209	18330	31302	0.92	3.6E-01	BE067699.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5498	18697	31713	0.64	3.6E-01	AJ006565.1	NT	Homo sapiens lipe gene intron 5
6211	19386	32735	0.96	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6607	19787	33155	1.63	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
7298	20380		3.85	3.6E-01	R94090.1	EST_HUMAN	yt74a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'
7435	20512	33985	1.52	3.6E-01	AW027174.1	EST_HUMAN	wt72c10.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117 O15117 FYN BINDING PROTEIN. [1] ;
8419	21500	35032	0.75	3.6E-01	P98167	SWISSPROT	SCO-SPONDIN
8474	21555	35087	16.45	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
9179	22257	35799	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9179	22257	35800	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9203	22281	35820	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9203	22281	35821	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9393	22468	36032	1.23	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9599	22654	36225	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9599	22654	36226	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9669	22631		0.58	3.6E-01	X62825.1	NT	C.perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
10067	23105	36708	16.64	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
11187	24256	37891	2.42	3.6E-01	BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
11370	24431	38088	3.27	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11729	23915	37540	4.44	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12173	26205		3.16	3.6E-01	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
12261	25197		7.87	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12420	25297		3.63	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12828	25552		1.98	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
13130	26141		1.4	3.6E-01	AW190229.1	EST_HUMAN	xl60e11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
13146	25745		1.38	3.6E-01	Z54173.1	NT	Pyrococcus sp. pol gene
214	13437	26467	3.71	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
695	13878	26911	1.03	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
743	13924	26965	1.53	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
743	13924	26966	1.53	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
801	13981	27033	4.66	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1670	14822	27905	1.28	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2671	16068	28908	1.34	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
3795	16956		0.73	3.5E-01	BF214381.1	EST_HUMAN	601845470F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4076680 5'
4378	17521	30501	2.62	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5048	18176	31153	4.34	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5323	13349	26376	0.6	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
5449	18649	31627	1.1	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5449	18649	31628	1.1	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5667	18861	32146	1.29	3.5E-01	D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6367	19537		1	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6538	19701	33074	0.79	3.5E-01	AA431833.1	EST_HUMAN	zw79f03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066935 G1066935 F10F2.1 ;
6580	19742	33124	0.69	3.5E-01	U37150.1	NT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6803	19958	33358	0.9	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7201	20066		3.38	3.5E-01	X98505.1	NT	S.scrofa mRNA for CD31 protein (PECAM-1)
7713	20778	34264	0.59	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
7713	20778	34265	0.59	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
8262	21344		2.12	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8265	21347	34862	0.82	3.5E-01	BF358871.1	EST_HUMAN	RC4-ET0024-260600-014-d07 ET0024 Homo sapiens cDNA
8662	21742		0.77	3.5E-01	AF051561.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9127	22206	35749	1.17	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receceptor 1 (TNK1), mRNA
9937	22976	36567	1.75	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
10090	23128	36731	4.78	3.5E-01	Z26825.1	NT	X.laevis gene for albumin including HP1 enhancer
10172	23209	36802	1.12	3.5E-01	BE174794.1	EST_HUMAN	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10972	24052	37685	2.62	3.5E-01	X61084.1	NT	C.griseus rhodopsin gene for opsin protein
11274	24342	37981	1.97	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11274	24342	37982	1.97	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11810	24800	38499	1.33	3.5E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11892	24880	38577	1.44	3.5E-01	N77597.1	EST_HUMAN	yz90h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280375 5'
11980	24965	38667	1.53	3.5E-01	L05145.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12271	26209		1.51	3.5E-01	AF297468.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
12344	26249		6.66	3.5E-01	X64565.1	NT	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12507	25348		2.91	3.5E-01	AE001774.1	NT	Thermotoga maritima section 86 of 136 of the complete genome
12710	25472		1.5	3.5E-01	AE001691.1	NT	Thermotoga maritima section 3 of 136 of the complete genome
13196	26026	31673	3.16	3.5E-01	H80814.1	EST_HUMAN	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
13196	26026	31674	3.16	3.5E-01	H80814.1	EST_HUMAN	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
725	13907		1.78	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
998	14169	27230	8.2	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene
1000	14171	27232	2.06	3.4E-01	AW380120.1	EST_HUMAN	QV3-HT0261-241199-019-g10 HT0261 Homo sapiens cDNA
1357	14512	27585	2.35	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2474	15601	28726	2.54	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3065	16241	29261	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3065	16241	29262	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3218	16392	29403	1.09	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3230	16404	29416	6.1	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3424	16593	29608	0.78	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3620	16784	29800	4.47	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3890	17049		1.89	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15 Q9UJ15 DJ18C9.1 ;
4163	17313		1.48	3.4E-01	AA584196.1	EST_HUMAN	no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4767	17902	30884	1.79	3.4E-01	BE069912.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5066	18194		4.3	3.4E-01	AI240973.1	EST_HUMAN	qj95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
5802	18992	32295	2.64	3.4E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5932	19118		4.92	3.4E-01	AA085313.1	EST_HUMAN	zn12d11.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:547221 3'
6130	19309		2.17	3.4E-01	L02971.1	NT	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6154	19330	32676	0.96	3.4E-01	BE748912.1	EST_HUMAN	601571811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838826 3'
6234	19409	32757	1.8	3.4E-01	AW204505.1	EST_HUMAN	UI-H-BI1-ael-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6384	19534	32893	1.71	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6882	20034		1.39	3.4E-01	N95225.1	EST_HUMAN	zb53e12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7086	20180	33604	1.07	3.4E-01	AI468082.1	EST_HUMAN	tm63g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
7205	20070	33480	0.6	3.4E-01	BF678702.1	EST_HUMAN	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
8090	21172		0.48	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8432	21513	35044	0.68	3.4E-01	Y14930.1	NT	Homo sapiens TCRAV28 gene, allele A4, partial
8684	21764		1.38	3.4E-01	AA337063.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
8760	21839	35380	0.71	3.4E-01	L04690.1	NT	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9053	22132	35676	1.87	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
9413	22487	36051	4.12	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9413	22487	36052	4.12	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9621	22676		0.57	3.4E-01	AB017510.1	NT	Ephydatia fluviatilis mRNA for PLC-gammaS, complete cds
9645	21088	34602	4.68	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9645	21088	34603	4.68	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9897	22937	36522	0.86	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scof-1) mRNA, complete cds
10093	23131	36735	2.44	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10695	23728		0.73	3.4E-01	AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11267	24336		3.26	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11307	24372	38014	2.1	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11350	24412	38066	1.86	3.4E-01	AF045981.1	NT	Rutilus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11561	24616	38295	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11561	24616	38296	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11791	24781	38478	1.68	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glcerin/MUC18, complete cds
11817	24806	38502	3.23	3.4E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12078	25058	38765	1.59	3.4E-01	BF061948.1	EST_HUMAN	7k69d12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480646 3'
12110	25090	38793	1.65	3.4E-01	Q27546	SWISSPROT	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (IU-NUCLEOSIDE HYDROLASE) (PURINE NUCLEOSIDASE)
12150	25120		2.03	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12264	25198		1.55	3.4E-01	Z21621.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
12367	25912		1.16	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
12489	25338		10.71	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
12517	25944		2.38	3.4E-01	BE218652.1	EST_HUMAN	hv42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.t3 PTR5 repetitive element ;
12579	26052		1.79	3.4E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12700	25466	32023	1.36	3.4E-01	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
12954	26160		1.96	3.4E-01	AJ288948.1	NT	Clostridium cellulolyticum partial spoIVB gene and spo0A gene, strain ATCC 35319
13055	25691		2.26	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
15	13253	26253	6.72	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
108	13253	26253	3.19	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
461	13656	26694	1.41	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
650	13836	26863	1.97	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1227	14387	27450	2.57	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1335	14492	27562	3.39	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1636	14788	27873	1.26	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dtgn5), mRNA
1674	14826		1.43	3.3E-01	6754477	NT	Mus musculus kappa B and Rss recognition component (Krc), mRNA
1777	14926		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week I Homo sapiens cDNA 5' end
2477	15604		6.23	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
3014	16190	29215	1.61	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3080	16256		1.09	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3121	16297	29311	0.78	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3584	16749	29766	1.04	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3911	17070	30068	2.72	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3921	17080	30076	0.82	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4072	17228	30235	1.19	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4108	17262	30262	1.81	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4487	17627		2.37	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4812	17945		1.91	3.3E-01	AI539114.1	EST_HUMAN	tp78b12.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4843	17976	30966	1.02	3.3E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
4960	18089	31065	1.14	3.3E-01	D64003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
5439	18639	31617	2.55	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5439	18639	31618	2.55	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5907	19096	32411	0.68	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6067	19249	32576	1.37	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6067	19249	32577	1.37	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6162	19338	32684	1.29	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6932	20247	33680	0.59	3.3E-01	AB034233.1	NT	Flexibacter litoralis gyrB gene for DNA gyrase B subunit, partial cds
6932	20247	33681	0.59	3.3E-01	AB034233.1	NT	Flexibacter litoralis gyrB gene for DNA gyrase B subunit, partial cds
7029	20165	33586	4.63	3.3E-01	AI628131.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;
7029	20165	33587	4.63	3.3E-01	AI628131.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;
7961	21011	34521	1.9	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT

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8759	21839	35379	23.1	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8926	22005	35544	0.73	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9314	22390	35941	0.83	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 1 (MAPK/ERK KINASE KINASE 1) (MEK KINASE 1) (MEKK 1)
9578	22720	36289	1.16	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9578	22720	36290	1.16	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9711	22760	36330	2.9	3.3E-01	N69866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9752	22690	36260	2.81	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10196	23233		2.08	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10865	23897	37520	0.74	3.3E-01	AE000631.1	NT	Helicobacter pylori 26695 section 109 of 134 of the complete genome
10960	24041	37675	3.35	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10960	24041	37676	3.35	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11279	24345		2.1	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213585 5'
11507	24565	38242	9.35	3.3E-01	BE219351.1	EST_HUMAN	hv51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11626	24706	38399	3.7	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
12018	25002		2.8	3.3E-01	AA806621.1	EST_HUMAN	ob71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
12036	13253	26253	2.33	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
12250	25190	38357	1.85	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
13044	25686		22.03	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-344000 nt. position (2/7)
469	13664		2.5	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
736	13918		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1188	14350	27408	23.03	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1311	14467	27535	1.48	3.2E-01	Z50202.1	NT	P.vulgaris arc5-1 gene
1421	14575	27648	6.74	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1663	14815		1	3.2E-01	AF209730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1815	14964	28057	1.3	3.2E-01	Z36041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1825	14974	28069	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGE resequences, MAGD Homo sapiens cDNA
1825	14974	28070	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGE resequences, MAGD Homo sapiens cDNA
1891	15035	28142	1.25	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2227	15361	28490	3.22	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2606	15729		2.83	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pknox1), mRNA
2774	15889	29000	1.23	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3698	16857		0.76	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4061	17217		0.93	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4514	17653	30641	1.37	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4621	17758	30740	1.35	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME I PRECURSOR
4860	17993		6.99	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
5386	18588	31560	2.93	3.2E-01	BE173964.1	EST_HUMAN	CM0-HT0569-060300-269-f10 HT0569 Homo sapiens cDNA
6078	19260	32589	1.08	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6433	19601	32965	0.73	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6729	19885	33277	0.65	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FHTA Homo sapiens cDNA clone FHTAABH01 5'
6872	20024		1.17	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8040	21123	34643	0.52	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8365	21446	34969	1.5	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8461	21542	35072	0.67	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12Wox1
8562	21643	35182	15.01	3.2E-01	X02508.1	NT	H.sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8565	21646	35187	14.52	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8656	21736		1.24	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8698	21778	36310	0.69	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8698	21778	35311	0.69	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8771	21850	35391	1.14	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8871	21950	35485	0.86	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8871	21950	35486	0.86	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9267	22344	35895	0.67	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9278	22354		2.54	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9351	22426	35983	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9351	22426	35984	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10198	23235	36824	4.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10402	23437	37044	0.62	3.2E-01	BE326230.1	EST_HUMAN	hv99f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10518	23553		3.94	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10905	23988	37620	3.05	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDZ21
12289	26083		3.11	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12861	25572		3.26	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12969	25891		2.2	3.2E-01	AF157625.1	NT	Bos taurus inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
13018	25669		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
13089	26129	31545	1.24	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2736	15853	28967	3.39	3.1E-01	R18051.1	EST_HUMAN	ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2762	16001	28985	3.77	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2762	16001	28986	3.77	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2920	16098		1.28	3.1E-01	AW629036.1	EST_HUMAN	hl46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3242	16416		3.51	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
4016	17173	30181	0.94	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5077	18205	31177	0.7	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5595	18790	31838	9.24	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5717	18910	32205	0.7	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN HI1236
5718	18911	32206	0.75	3.1E-01	Z74883.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141w
5729	18922		0.83	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5892	19080	32390	2.65	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6595	19755	33141	1.3	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6663	19822	33209	0.96	3.1E-01	AI264458.1	EST_HUMAN	qi39d01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874689 3'
6821	19974	33382	0.79	3.1E-01	X71887.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6905	20220		0.69	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-281099-005-h05 CT0222 Homo sapiens cDNA
7109	25801	31491	2.32	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7856	20911	34416	0.7	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8849	21928	35467	0.84	3.1E-01	R45318.1	EST_HUMAN	yg46f01.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3'
10106	23144	36742	0.68	3.1E-01	6679322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10272	23307	36903	1.04	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10272	23307	36904	1.04	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10334	23369	36979	1.68	3.1E-01	AI244001.1	EST_HUMAN	qj61e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10510	23545		0.98	3.1E-01	T55325.1	EST_HUMAN	yb47h08.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:M91036_rna2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11076	24151	37789	1.84	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11474	24533	38203	1.62	3.1E-01	AW074910.1	EST_HUMAN	xa62g09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2571424 3'
11827	24816	38507	2.08	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11828	24817	38508	1.67	3.1E-01	R55735.1	EST_HUMAN	yg89b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:40722 5' similar to contains Alu repetitive element;
12123	25103		1.3	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12418	25296		1.22	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12455	25319		1.73	3.1E-01	AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12613	25412		3.73	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
13028	25677		3.82	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
13068	26123		1.22	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrpl-pending), mRNA
74	15979	26336	1.65	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkce), mRNA
264	13483	26515	11.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
1251	14410	27472	2.35	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1537	14690	27769	5.77	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
1838	14984	28084	1.2	3.0E-01	X99082.1	NT	A.immersus putative gene encoding integrase, Mars2 (RP)
3069	16245		0.8	3.0E-01	AB008677.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3283	16457		1.33	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyguluronate lyase, complete cds
3968	17125	30129	1.58	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4082	17237	30243	1.16	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
4636	17772	30752	1.79	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5258	16649	29665	2.33	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
5467	18667	31646	5.1	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5548	18745	31780	0.64	3.0E-01	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5552	18749	31785	1	3.0E-01	AF229247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds
5621	18815	31883	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5621	18815	31884	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5658	18852	32135	3.87	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6970	20198	33624	2.82	3.0E-01	D16313.1	NT	Mouse cytokeratin 15 gene, complete cds
6999	18518	31511	0.76	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7065	20118	33532	1.15	3.0E-01	AF229247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7270	20353	33806	0.96	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7481	20566	34028	4.3	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7670	20736	34214	1.51	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
8111	21193	34713	1.34	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8568	21649		3.1	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clecsf9), mRNA
8658	21738	35279	0.48	3.0E-01	Z70200.1	NT	H.sapiens gene for U5 snRNP-specific 200kD protein
8671	21751	35288	1.23	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
9029	22108	35649	0.69	3.0E-01	AF141676.1	NT	Streptomyces sulfonofaciens isopenicillin N synthase (pcbC) gene, partial cds
9072	22151		0.82	3.0E-01	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9419	22493	36059	1.09	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9773	22813	36391	0.64	3.0E-01	P76389	SWISSPROT	HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9927	22967		0.46	3.0E-01	D90904.1	NT	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448
10173	23210	36803	0.84	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10346	23381	36992	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10346	23381	36993	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10606	23640	37248	0.6	3.0E-01	AW118111.1	EST_HUMAN	xe03d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10608	23642	37250	2.51	3.0E-01	AB030231.1	NT	Aspergillus oryzae bipA gene for ER chaperone BiP, complete cds
10629	23663	37271	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10629	23663	37272	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
12067	25048	38755	2.16	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12067	25048	38756	2.16	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12470	25324		1.3	3.0E-01	P54660	SWISSPROT	PONTICULIN PRECURSOR
12731	26062		1.88	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
13061	26121		4.49	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1771	14920		0.94	2.9E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1930	15073	28176	0.94	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2080	15220	28340	2.36	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2322	15454	28585	1.01	2.9E-01	AF222718.1	NT	Chrysodidymus synuroideus mitochondrion, complete genome
3253	16427	29445	0.96	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3323	16496	29513	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3323	16496	29514	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
4003	17160	30166	1.12	2.9E-01	AI610836.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN);contains element L1 repetitive element ;
4045	17201	30212	0.61	2.9E-01	AI769472.1	EST_HUMAN	wj14d10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:C34F6.7 CE15676 ;
4183	17333	30325	0.61	2.9E-01	AB016426.1	NT	Cavia porcellus mRNA for glutathione s-transferase, complete cds
4195	17345		0.79	2.9E-01	AW002902.1	EST_HUMAN	wr02f10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480395 3'
4608	17745	30724	0.98	2.9E-01	AA284468.1	EST_HUMAN	zs57d12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4805	17940		0.73	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4957	18087	31063	0.59	2.9E-01	AB019029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5222	18344		0.99	2.9E-01	AI670899.1	EST_HUMAN	wa06f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.t2 L1 repetitive element ;
5320	18087	31063	0.65	2.9E-01	AB019029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5372	18575		1.59	2.9E-01	R37485.1	EST_HUMAN	yf77e12.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:28291 3'
5511	20137	33555	0.98	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine sythetase 2 mRNA, complete cds
5884	19073	32381	5.27	2.9E-01	X56098.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5884	19073	32382	5.27	2.9E-01	X56098.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5897	19085	32397	5.53	2.9E-01	6679662	NT	Mus musculus Eph receptor A8 (Epha8), mRNA
6181	19357	32705	1.55	2.9E-01	AA418145.1	EST_HUMAN	zv97b12.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6411	19580	32941	1.07	2.9E-01	AI797128.1	EST_HUMAN	we27c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.t1 L1 repetitive element ;
6455	19622	32986	2.22	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
7001	20137	33555	0.71	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine sythetase 2 mRNA, complete cds
7126	18552	31466	1.4	2.9E-01	AF142329.1	NT	Mus musculus Fliih protein (Fliih) gene, complete cds; and Ligih protein (Ligih) gene, partial cds
7245	20328	33773	3.11	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
7310	20392	33852	1.54	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
8104	21186	34705	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8104	21186	34706	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8343	21424	34949	0.64	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8343	21424	34950	0.64	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8356	21437		0.75	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
8534	21615		0.53	2.9E-01	AF197456.1	NT	Buchnera aphidicola plasmid pLeu isolate MI 2-isopropylmaltate synthase (leuA) gene, partial cds; 3-Isopropylmaltate dehydrogenase (leuB) gene, complete cds; and isopropylmaltate dehydratase subunit (leuC) gene, partial cds
8794	21873	35412	0.82	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9125	22204	35747	1.09	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds
9233	22311	35853	0.81	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9447	22563	36125	0.96	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9447	22563	36126	0.96	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10405	23440	37047	0.46	2.9E-01	AW294100.1	EST_HUMAN	UI-H-BI2-ahg-b-02-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726714 3'
10405	23440	37048	0.46	2.9E-01	AW294100.1	EST_HUMAN	UI-H-BI2-ahg-b-02-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726714 3'
11133	24205	37830	1.94	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11433	24494	38159	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11433	24494	38160	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11881	24869	38566	2.71	2.9E-01	AA935373.1	EST_HUMAN	ny35h02.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.t2 LTR8 repetitive element ;
11886	24874	38571	3.12	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
11900	24888	38587	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11900	24888	38588	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12677	25452	32017	1.85	2.9E-01	AW005671.1	EST_HUMAN	wz88f05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER29 repetitive element ;
12774	25516		1.89	2.9E-01	V00202.1	NT	D. melanogaster: part of the 44D cuticle gene cluster encoding cuticle gene I
12777	25519	32001	2.23	2.9E-01	AF092453.1	NT	Homo sapiens TNF-a-inducible RNA binding protein (TIRP) gene, complete cds
13125	25734	31944	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13125	25734	31945	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13204	25785	31919	1.4	2.9E-01	AF200418.1	NT	Callinectes sapidus cadmium-inducible metallothionein CdMT-I mRNA, complete cds
582	13774		2.04	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
587	13778		1.96	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1107	14272	27331	3.34	2.8E-01	AF168050.1	NT	Guira guira oocyte maturation factor Mos (c-mos) gene, partial cds
1306	14462	27529	2.19	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1306	14462	27530	2.19	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1319	14475	27541	1.2	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1766	14915	28011	1.87	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
2069	15210	28326	1.49	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586I2321_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586I2321
2200	15335	28462	1.51	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2542	15667	28791	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2542	15667	28792	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2612	15736		2.95	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2730	15848	28958	1.16	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
3035	16211		1.37	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
3036	16212	29234	2.52	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3036	16212	29235	2.52	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3466	16633	29652	1.05	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
4103	17257	30257	1.67	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4240	17386		0.6	2.8E-01	AE004460.1	NT	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4315	17458		2.17	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
4582	17719	30702	2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4944	18074	31049	0.92	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4950	18080	31056	4.95	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4984	18113	31090	1.52	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
5006	18135	31109	3.66	2.8E-01	AI272669.1	EST_HUMAN	ql59c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element;contains element LTR5 repetitive element ;
5318	18473	31404	0.61	2.8E-01	X60797.1	NT	Mouse Kv3.3 gene for potassium channel protein, exon 2
5426	26804	31602	23.61	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5723	18916	32211	2.57	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5938	19124		0.93	2.8E-01	AW992583.1	EST_HUMAN	CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6042	19225	32548	0.66	2.8E-01	AA765296.1	EST_HUMAN	oa01d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK506-BINDING PROTEIN (HUMAN);
6059	19241		0.64	2.8E-01	AA404576.1	EST_HUMAN	zt41f01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6305	26212		0.67	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6347	19517	32874	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6347	19517	32875	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6870	20022	33432	7.84	2.8E-01	BF511215.1	EST_HUMAN	UI-H-BI4-aoi-f-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

WO 01/57272 PCT/US01/00663

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7145	20280	33721	0.64	2.8E-01	U65300.1	NT	Orthogeomys heterodus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7599	20669		1.14	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds
8284	21366	34884	1.31	2.8E-01	AI346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8284	21366	34885	1.31	2.8E-01	AI346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8404	21485	35014	2.31	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8712	21792	35328	0.6	2.8E-01	AA911629.1	EST_HUMAN	of02h05.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8789	21868		7.72	2.8E-01	BF347847.1	EST_HUMAN	602022987F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158525 5'
9666	22628	36199	1.14	2.8E-01	U17251.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
9912	22952		1.16	2.8E-01	L13654.1	NT	Lycopersicon esculentum peroxidase (TPX1) mRNA, complete cds
10092	23130	36733	0.98	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10092	23130	36734	0.98	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10152	23189	36786	0.46	2.8E-01	AE001310.1	NT	Chlamydia trachomatis section 37 of 87 of the complete genome
10156	23193	36789	0.7	2.8E-01	AF294393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10265	23300	36898	3.8	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10519	23554		1.1	2.8E-01	9626154	NT	Fujinami sarcoma virus, complete genome
10561	23596	37202	0.5	2.8E-01	BE959727.2	EST_HUMAN	601854822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839765 3'
10982	24061	37695	1.88	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10982	24061	37696	1.88	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11011	24090	37727	3.01	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
11119	24191	37823	1.53	2.8E-01	AF051662.1	NT	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11556	24611		3.58	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
11851	24840	38533	1.55	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
11851	24840	38534	1.55	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
12715	25475		12.79	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12846	25562	31987	7.61	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
12875	25582	31996	1.29	2.8E-01	BE900116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
13052	26066		1.59	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA

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489	13683	26717	4.34	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
628	13813	26835	13.64	2.7E-01	AA450061.1	EST_HUMAN	zx39b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1290	14446	27512	2.04	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1650	14803		1.63	2.7E-01	X79815.1	NT	G.lamblia SR2 gene
1768	14917	28012	3.16	2.7E-01	W58067.1	EST_HUMAN	zd22h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1817	14966	28059	1.46	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2204	16057		3.1	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2250	15383	28510	0.94	2.7E-01	AI372772.1	EST_HUMAN	EST175679 Infant brain, Bento Soares Homo sapiens cDNA clone UHIBO1R 5' end
2250	15383	28511	0.94	2.7E-01	AI372772.1	EST_HUMAN	EST175679 Infant brain, Bento Soares Homo sapiens cDNA clone UHIBO1R 5' end
2440	15568	28695	7.07	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial
2526	15651	28775	4.36	2.7E-01	AI310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element ;
3049	15225		0.99	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3361	16533	29547	0.66	2.7E-01	8393620	NT	Rattus norvegicus Insulin receptor (Insr), mRNA
4118	17272	30271	1.94	2.7E-01	AI928015.1	EST_HUMAN	wo92e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4133	17286	30281	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4133	17286	30282	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4140	17292	30286	2.39	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5153	18275		4.46	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5381	18583	31452	1.98	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4)
5607	18802		1.31	2.7E-01	AB033171.1	NT	Astreopora myriophthalma mitochondrial cytb gene for cytochrome b, partial cds
6472	19639	32998	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6472	19639	32999	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6745	19901	33293	1.05	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6745	19901	33294	1.05	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6918	20233	33667	1.74	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7197	20062		0.77	2.7E-01	AI540070.1	EST_HUMAN	td08h08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2075103 3'
7511	20585	34058	0.92	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7734	20795	34283	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7734	20795	34284	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7865	20919	34425	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7865	20919	34426	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7917	20968	34474	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
7917	20968	34475	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
7976	21026	34540	0.66	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8048	21131	34651	0.66	2.7E-01	AA013147.1	EST_HUMAN	ze35b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element;
8330	21412	34938	0.56	2.7E-01	AW868503.1	EST_HUMAN	MR1-SN0062-100500-002-d09 SN0062 Homo sapiens cDNA
8380	21461	34984	0.69	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:23511 3'
8486	21567	35104	0.83	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8959	22038	35580	1.4	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9534	22599	36171	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)
9534	22599	36172	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)
9537	22602		2.66	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
10005	23043	36636	0.8	2.7E-01	D89660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11,12, 13, 14, 15, 16, 17 and complete cds
10286	23321	36923	0.9	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10323	23358	36968	2.06	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATca) mRNA, complete cds
10455	23490	37099	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10455	23490	37100	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10749	23782		0.51	2.7E-01	AB011679.1	NT	Rattus norvegicus mRNA for class I beta-tubulin, complete cds
10765	23798	37418	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
10765	23798	37419	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
11050	24127	37761	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11050	24127	37762	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11061	24137	37772	2.58	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12816	25942		1.49	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
13034	26681		2.75	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
482	16013	26710	2.8	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2

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493	13688		1.94	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1424	14578	27651	1.77	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1468	14622	27705	1.09	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1945	15088	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1946	15088	28189	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
2159	15295		10.39	2.6E-01	AW733152.1	EST_HUMAN	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2220	15354	28485	1.13	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2611	15735		11.66	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
3161	16336		1.11	2.6E-01	AW974531.1	EST_HUMAN	EST386635 MAGE resequences, MAGM Homo sapiens cDNA
3671	16834	29845	0.84	2.6E-01	M22342.1	NT	Bacteriphage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3733	16894	29899	1.67	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4215	17364	30352	0.79	2.6E-01	AW959510.1	EST_HUMAN	EST371580 MAGE resequences, MAGF Homo sapiens cDNA
4270	17415	30404	16.93	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4476	17616	30597	1.71	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4617	17754	30735	0.69	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4617	17754	30736	0.69	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4670	17805	30794	1.14	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4770	17905	30887	2.25	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds
4837	17970	30958	1.15	2.6E-01	AF142703.1	NT	Ophrestia radicosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5086	18214	31187	3.63	2.6E-01	H04858.1	EST_HUMAN	yj51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5155	18277		0.61	2.6E-01	AA884625.1	EST_HUMAN	am33b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5457	18657		1.29	2.6E-01	AB035972.1	NT	Paramecium caudatum gene for PAP, complete cds
5565	18762	31802	0.67	2.6E-01	M96060.1	NT	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAx genes, complete cds
5689	18883		0.84	2.6E-01	AI862398.1	EST_HUMAN	td16a03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element ;
5895	19083	32394	0.64	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g>

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6196	26211		2.57	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6330	19501	32859	1.96	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
6330	19501	32860	1.96	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
6552	19714	33090	0.98	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
6807	19961	33364	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
6807	19961	33365	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7183	20315	33758	1.04	2.6E-01	AI914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7549	20621	34098	0.7	2.6E-01	BE148961.1	EST_HUMAN	CM0-HT0245-031199-085-f04 HT0245 Homo sapiens cDNA
7587	25848		0.96	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
7626	20698		0.78	2.6E-01	AA196149.1	EST_HUMAN	zp92e01.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
7918	20969	34476	1.73	2.6E-01	R10365.1	EST_HUMAN	yi37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8033	21116	34634	1.18	2.6E-01	R02411.1	EST_HUMAN	ye82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
8088	21170	34685	1.3	2.6E-01	BE144331.1	EST_HUMAN	MR0-HT0166-181199-003-d12 HT0166 Homo sapiens cDNA
8529	21610	35148	2.97	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150396 5'
8605	21686	35223	1.74	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8892	21971	35506	4.06	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8892	21971	35507	4.06	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9667	22629	36200	0.92	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9940	22979		0.5	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	23110	36713	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
10072	23110	36714	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
10393	23428		0.63	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10727	23760		1.09	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10840	23873		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11815	24804		31.14	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12468	26070		4.14	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12535	25365	32069	3.86	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12922	25607		2.04	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threoine kinase, complete cds
13007	25663		1.78	2.6E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
13057	25692		2.36	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
13098	15735		1.43	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
13107	25722		2.04	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
13150	25748		2.4	2.6E-01	U30729.1	NT	Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds
251	13472	26503	1.87	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
252	13472	26503	1.7	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
265	13484		2.51	2.5E-01	M26501.1	NT	Starfish (P.ochraceus) cytoplasmic actin gene, complete cds
855	14032	27093	1.23	2.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1085	14251		1.75	2.5E-01	AE002166.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1145	14310	27367	5.45	2.5E-01	T89837.1	EST_HUMAN	ye11g07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1767	14916		4.53	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2479	15606		11.21	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2563	15688	28814	1.22	2.5E-01	6679216	NT	Mus musculus protein-L-isoaspertate (D-aspartate) O-methyltransferase 1 (Pcmt1), mRNA
2565	15690		1.02	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
2702	15820	28936	1	2.5E-01	X95310.1	NT	B.taurus mRNA for D-aspartate oxidase
3499	16666		3.34	2.5E-01	AW973471.1	EST_HUMAN	EST385464 MAGE resequences, MAGM Homo sapiens cDNA
3639	16803	29815	7.18	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3950	17108	30105	1.25	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3950	17108	30106	1.25	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4438	17578		0.88	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4737	17872	30855	0.7	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4871	18004		1.13	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4878	18009	30993	3.99	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4904	18034	31023	2.3	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4926	18056		3.54	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4954	18084	31060	0.8	2.5E-01	BE896785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4994	18123	31101	0.61	2.5E-01	U83656.1	NT	Rattus norvegicus NF-KB gene, promotor region
5212	18333	31303	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5212	18333	31304	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5337	18450		1.08	2.5E-01	AA419208.1	EST_HUMAN	zv35a05.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:755600 5' similar to gb:M88279 P59 PROTEIN (HUMAN);
5441	18641	31620	12.21	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6080	19262	32591	0.6	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6081	19263		0.81	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6762	19918	33313	0.82	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
7190	20055	33465	0.64	2.5E-01	8394138	NT	Rattus norvegicus rabin 3 (RABIN3), mRNA
7507	20581	34054	0.71	2.5E-01	U13992.1	NT	Feline calicivirus CFI/68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7536	20609		1.13	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7770	20828	34319	0.62	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7814	20869	34365	4.23	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8028	21111	34630	2.22	2.5E-01	BF109040.1	EST_HUMAN	7I57a03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8039	21122	34642	0.51	2.5E-01	BE960712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8421	21502	35034	1.9	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
8591	21672	35210	0.8	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8837	21916	35454	4.07	2.5E-01	H53236.1	EST_HUMAN	yq84f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
9076	22155	35699	1.05	2.5E-01	M88626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9716	22781	36351	16.85	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9716	22781	36352	16.85	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9772	22768	36339	2.44	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9772	22768	36340	2.44	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10303	23338	36943	1.31	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10550	23585	37193	0.51	2.5E-01	11465652	NT	Porphyra purpurea chloroplast, complete genome
10763	23798	37416	1.4	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
10767	23800	37422	1.61	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
11332	24395	38043	2.96	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
12204	25158	38834	5.16	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds
12233	26167		6.12	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13024	25674		1.22	2.5E-01	AF325363.1	NT	Delia brassica cytochrome oxidase subunit II (COII) gene, partial cds; mitochondrial gene for mitochondrial product
567	13759	26783	1.41	2.4E-01	AA936316.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
871	14047	27113	4.4	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271678 5'
1332	14489	27557	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1332	14489	27558	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1415	14569	27642	0.97	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1898	15041		29.78	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1949	15092	28193	1.43	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2091	15231	28353	1.64	2.4E-01	AI742958.1	EST_HUMAN	wg76d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:O60267 O60267 KIAA0512 PROTEIN. ;
2206	15340	28467	1.17	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2237	15370		1.25	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2336	15467	28602	2.29	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2602	15726	28845	3.13	2.4E-01	Z36534.1	NT	D.discoideum (Ax3-K) ponA gene
2820	15934	29045	2.22	2.4E-01	X71783.1	NT	S.pombe swi6 gene
2846	15960	29069	6.27	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3202	16377		3.03	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3217	16391	29402	1.51	2.4E-01	X74209.1	NT	H.sapiens AGT gene, PstI fragment of intron 4
3856	17016	30016	0.97	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4141	17293		0.65	2.4E-01	D29960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5181	18303	31266	0.65	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5181	18303	31267	0.65	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5334	18447	31415	1.89	2.4E-01	U89914.1	NT	Bacillus firmus hypothetical 34.0 kDa protein, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thiosulfate sulfurtransferase, hypothetical 16.1 kDa transcriptional regulator and hypothetical 18.2 kDa>
5335	18448	31416	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5335	18448	31417	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5578	18773	31818	0.9	2.4E-01	AI925707.1	EST_HUMAN	wc33d05.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5578	18773	31819	0.9	2.4E-01	AI925707.1	EST_HUMAN	wc33d05.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5602	18797	31847	0.59	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5772	18964	32266	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wrn protein (Wrn) gene, complete cds
5772	18964	32267	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wrn protein (Wrn) gene, complete cds

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5800	18990		0.7	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6010	25815		0.97	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (caM2 gene)
6016	19200	32517	2.54	2.4E-01	BF592336.1	EST_HUMAN	7i54d04.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element ;
6106	19286	32620	2.47	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6215	19390	32738	2.49	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6269	19443	32792	0.94	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cdA Homo sapiens cDNA clone cdAADE11 5'
6516	19681	33051	0.87	2.4E-01	AA398672.1	EST_HUMAN	zt70d02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727683 3'
6665	19824	33212	1.59	2.4E-01	AI698989.1	EST_HUMAN	wc62c11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7498	20573	34046	7.79	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7902	20954	34461	0.68	2.4E-01	AF229644.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8271	21353	34868	0.5	2.4E-01	X97252.1	NT	M.musculus pah gene and promotor
8271	21353	34869	0.5	2.4E-01	X97252.1	NT	M.musculus pah gene and promotor
8392	21473	34999	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae rr08 and hk08 genes; two component system 08
8392	21473	35000	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae rr08 and hk08 genes; two component system 08
8544	21625	35162	1.29	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8798	21877	35416	1.18	2.4E-01	BF242794.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
9332	22408	35961	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9332	22408	35962	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9763	22701	36267	8.39	2.4E-01	AI693515.1	EST_HUMAN	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22.b1 TAR1 repetitive element ;
9905	22945	36530	0.66	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
9905	22945	36531	0.66	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10654	23688	37297	1.8	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11006	24085	37722	2.15	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11074	24149	37788	1.96	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11447	24508	38174	1.8	2.4E-01	BE296917.1	EST_HUMAN	601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11447	24508	38175	1.8	2.4E-01	BE296917.1	EST_HUMAN	601176416F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11478	24537		8.04	2.4E-01	Z21547.1	NT	P.asiatica mosaic virus genomic RNA
12159	25127	38827	1.75	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
12299	25932		1.35	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12360	25258		1.62	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12588	25914		1.95	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12839	26151		1.37	2.4E-01	BF229975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
13072	25701		1.4	2.4E-01	AJ238044.1	NT	Homo sapiens mRNA for bradykinin B1 receptor (B1BKR gene)
13102	25718		4.16	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
400	13597	26633	1.39	2.3E-01	S75898.1	NT	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]
654	13840		5.53	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
684	13869	26900	29.31	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
957	14130	27188	3.57	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1634	14786	27872	1.11	2.3E-01	AJ245480.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
1661	14813	27898	1.72	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2103	15242		1.78	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2517	15643	28764	1.85	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2717	15835	28945	0.98	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2885	14573	27646	1.5	2.3E-01	AB015033.1	NT	Marinilabilia agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
3028	16204	29227	1.08	2.3E-01	AA601379.1	EST_HUMAN	no16d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element;contains element THR repetitive element ;
3153	16328		7.06	2.3E-01	R21732.1	EST_HUMAN	yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3456	16623	29644	1.32	2.3E-01	H69836.1	EST_HUMAN	yr97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3944	17103	30100	0.98	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit {5' region, intron 1} [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
4046	17202		5.15	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4470	17610	30588	0.86	2.3E-01	R82252.1	EST_HUMAN	yj17f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4520	17659		1.91	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4573	17710	30693	1.12	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4611	17748	30728	2.76	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4676	17811	30800	5.65	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5159	18281	31246	0.87	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5223	18345		1.03	2.3E-01	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
5260	18379	31345	0.83	2.3E-01	BF574804.1	EST_HUMAN	602132210F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271547 5'
5419	18620	31596	2.47	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5545	18742	31776	2.03	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5647	18841	32122	5.25	2.3E-01	X96587.1	NT	C.familiaris rom1 gene
5766	18958		0.99	2.3E-01	L39112.1	NT	Vittaforma corneum small subunit ribosomal RNA gene
5870	19060	32367	1.32	2.3E-01	S60371.1	NT	23S rRNA [Leuconostoc camosum, Genomic, 2866 nt]
6062	19244	32569	1.98	2.3E-01	AI708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6062	19244	32570	1.98	2.3E-01	AI708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6794	19949	33348	0.66	2.3E-01	AF198089.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product
7017	20153	33573	4.63	2.3E-01	AI718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
7260	20343	33795	0.86	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7440	20517	33989	0.76	2.3E-01	AF000227.1	NT	Secale cereale omega secalin gene, complete cds
7573	20645	34123	2.54	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7576	20648	34125	5.37	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDGB08 5'
7576	20648	34126	5.37	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDGB08 5'
7784	20840		4.26	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
7789	20845	34338	1.56	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7931	20981		2.8	2.3E-01	N80983.1	EST_HUMAN	za12e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292358 5'
7968	21018	34530	0.71	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
7968	21018	34531	0.71	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
8035	21118	34637	0.52	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
8183	21265	34788	1.73	2.3E-01	M68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8690	21770	35300	0.62	2.3E-01	U57999.1	NT	Mus musculus prosaposin (psap\SGP-1) gene, complete cds
8972	22051	35594	0.58	2.3E-01	AW090541.1	EST_HUMAN	xc90e06.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591554 3'
9089	22168	35715	0.52	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
9341	22417	35970	0.64	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9341	22417	35971	0.64	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9780	22820	36398	0.5	2.3E-01	6679318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
9930	22970	36559	0.53	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5'
9985	23024	36616	0.81	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
10037	23075	36675	1.57	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10071	23109	36712	0.63	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281299-001-f04 DT0036 Homo sapiens cDNA
10138	23176	36773	2.62	2.3E-01	BE173060.1	EST_HUMAN	MR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10197	23234	36823	2.48	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10658	23692	37302	0.94	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10671	23705		5.89	2.3E-01	BF133577.1	EST_HUMAN	601646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
11465	24524	38195	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11465	24524	38196	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11633	24713	38404	2.43	2.3E-01	AE002167.2	NT	Chlamydophila pneumoniae AR39, section 4 of 94 of the complete genome
12099	25079		1.36	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
12281	25210		3.07	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12370	25264		48.78	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCoE44 5'
12395	25873		1.23	2.3E-01	AA089819.1	EST_HUMAN	chn1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12464	26086	31657	4.08	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2. ;contains PTR5.b2 TAR1 repetitive element ;
12500	26143	31552	7.05	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
12553	25376		1.77	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12612	25411		2.74	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12708	25470		1.22	2.3E-01	U49845.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12712	25411		1.84	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
13009	25665		2.36	2.3E-01	BF475611.1	EST_HUMAN	nac39h12.x1 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element ;
92	13327	26355	1.13	2.2E-01	AI052190.1	EST_HUMAN	oz14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
1596	14749	27833	2.74	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
2155	15291	28418	2.19	2.2E-01	M34640.1	NT	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2476	15603	28728	7.16	2.2E-01	BF677538.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
2654	15777	28890	1.63	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2654	15777	28891	1.63	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2946	16123	29136	4.94	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2946	16123	29137	4.94	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2987	16163		2.07	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3479	16646		2.35	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3848	17008	30009	0.62	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4211	17360	30349	0.69	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4242	17388		0.6	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4328	17471		1.07	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4335	17478	30460	6.62	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4379	17522	30502	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4379	17522	30503	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4475	17615	30595	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4475	17615	30596	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4947	18077		1.08	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4952	18082	31058	2.2	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'
5156	18278		1.57	2.2E-01	L13299.1	NT	Mus musculus vinculin gene, exon 3
5226	18348	31319	1.34	2.2E-01	BE141035.1	EST_HUMAN	MR0-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA
5863	19053	32360	1.89	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5874	19064		3.75	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6122	19301	32640	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6122	19301	32641	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6845	19998	33405	0.77	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7166	20299	33742	10.63	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7279	20362	33815	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7279	20362	33816	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7442	20519	33991	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7442	20519	33992	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7655	20723	34199	0.62	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7878	20930	34436	0.88	2.2E-01	AF287967.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7905	20957	34463	0.71	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain:C-125
8210	21292		2.45	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8280	21362	34881	2.68	2.2E-01	Z49933.1	NT	E.coli sepA and sepB genes
8748	21827	35363	0.61	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
9083	22162	35705	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9083	22162	35706	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9097	22176	35720	4.58	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
9117	22196	35740	0.48	2.2E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
9224	22302		2.88	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
9315	22391	35942	1.98	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9399	22473	36039	1.13	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
9489	22548	36109	1.42	2.2E-01	W02988.1	EST_HUMAN	za04f08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291591 5'
9507	22773	36345	15.08	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9552	22617	36187	0.76	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9563	22705	36271	1.05	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9576	22718	36286	4.29	2.2E-01	M89643.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
9820	22860	36441	0.65	2.2E-01	Q90980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10020	23058	36654	3.84	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds; nuclear gene for chloroplast product
10159	23196	36792	1.53	2.2E-01	BF206507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10380	23415	37024	1.11	2.2E-01	9625671	NT	Human herpesvirus 5, complete genome
10540	23575	37182	0.65	2.2E-01	T59472.1	EST_HUMAN	yb63d08.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'
10540	23575	37183	0.65	2.2E-01	T59472.1	EST_HUMAN	yb63d08.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'
10580	23615	37220	0.6	2.2E-01	AF068264.1	NT	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquin>
10659	23693		0.79	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10707	23740	37344	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10707	23740	37345	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10853	23886	37505	0.48	2.2E-01	AF049720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 1l and AS
11389	24450	38111	1.65	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11707	24704	38396	5.09	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11748	23934	37560	3.7	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12207	25161		1.33	2.2E-01	BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
12319	26156		1.96	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12407	25286		3.24	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12518	18492	31531	1.86	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12519	25353		1.47	2.2E-01	AW661922.1	EST_HUMAN	hi17b02.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
13115	26148		3.08	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAHB02 5'
993	14165	27226	1.88	2.1E-01	AA569289.1	EST_HUMAN	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
996	14167	27228	0.72	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1148	14312		2.43	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1225	14385	27446	1.45	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1225	14385	27447	1.45	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1540	14692	27771	4.29	2.1E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1963	15106	28206	2.15	2.1E-01	AA906824.1	EST_HUMAN	ok73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765 COMPLEMENT C3 PRECURSOR (HUMAN);
2224	15358	28488	3.55	2.1E-01	BF695073.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2991	16167	29183	2.52	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3533	16698	29709	6.1	2.1E-01	AA639482.1	EST_HUMAN	nq90b10.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1159579 3'
3908	17067		5.61	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
4125	17279		0.67	2.1E-01	AE001793.1	NT	Thermotoga maritima section 105 of 136 of the complete genome
4165	17315	30310	1.57	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4165	17315	30311	1.57	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4495	17635		1.63	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4699	17834	30819	1.82	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
4757	17892	30871	0.93	2.1E-01	X93161.1	NT	P.falciparum mRNA for small GTPase rab11
5138	18261	31228	0.7	2.1E-01	D13567.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
5416	18618	31592	6.31	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
7027	20163	33585	1.05	2.1E-01	AJ223392.1	NT	Dotb fragilis mitochondrial 16S rRNA gene, partial
7038	20091	33508	1.8	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7564	20636	34111	0.77	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID)
7564	20636	34112	0.77	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID)
7575	20647		1.88	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7883	20935	34441	1.54	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
7930	20980	34488	1.38	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7930	20980	34489	1.38	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8263	21345		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1l3), mRNA
8700	21780	35313	4.76	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
8997	22076	35615	0.91	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
8997	22076	35616	0.91	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
9159	22237		0.5	2.1E-01	AB022524.1	NT	Homo sapiens APCL gene, exon 9
9237	22314	35856	6.7	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
9704	22753	36323	0.66	2.1E-01	N42536.1	EST_HUMAN	yy11e10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270954 5'
9704	22753	36324	0.66	2.1E-01	N42536.1	EST_HUMAN	yy11e10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270954 5'
9713	22778	36348	2.72	2.1E-01	X97378.1	NT	A.thaliana mRNA for AtRanBP1b protein
9817	22857	36437	1.02	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10535	23570	37178	1.31	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10569	23604	37209	1.97	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE)
10576	23611	37216	0.72	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11776	24768		1.34	2.1E-01	AI141875.1	EST_HUMAN	qa66f08.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691751 3'
11862	24850		1.68	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11879	24867	38565	2.6	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA
12688	25459		1.92	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12994	25646		1.39	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'
13158	25753	31926	1.19	2.1E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
205	13428	26460	1.92	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avena, complete cds
547	13740		1.97	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
717	13899	26937	1.37	2.0E-01	M77086.1	NT	O.cuniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
833	14011	27067	2.09	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1036	14204	27261	1.83	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1149	14313	27369	2.81	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1283	14439	27508	1.19	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1336	14493	27563	1.99	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1516	14669	27752	22.4	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1582	14734	27815	2.68	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1588	14740	27821	3.48	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1732	14882	27973	0.96	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14904		2.58	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1796	14945		3.87	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1941	15084	28185	1.46	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2423	15552		1.9	2.0E-01	X82877.1	NT	H.sapiens Na+-D-glucose cotransport regulator gene
2955	16132		0.79	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH85A11
3576	16741	29758	0.72	2.0E-01	P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3658	16821		0.91	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element ;
3798	16959	29963	0.86	2.0E-01	P34641	SWISSPROT	CED-11 PROTEIN
3802	16963		0.6	2.0E-01	6680797	NT	Mus musculus bone morphogenetic protein 6 (Bmp6), mRNA
4688	17823		8.71	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5152	18274	31243	6.41	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5243	16959	29963	0.6	2.0E-01	P34641	SWISSPROT	CED-11 PROTEIN
5561	18758	31797	2.55	2.0E-01	X66600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5859	19049	32355	2.08	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5963	19149	32464	0.82	2.0E-01	X91856.1	NT	F.rubripes DNA encoding for valyl-tRNA synthetase
6185	19361	32709	5.99	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6303	19476		0.74	2.0E-01	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
6559	19721	33098	47.65	2.0E-01	X61033.1	NT	M.auretus mu class glutathione transferase gene
6659	19818	33206	3.74	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
7445	20522	33995	1.41	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (Pfkc) gene, exons 3 through 7
7603	20673	34147	0.83	2.0E-01	P54422	SWISSPROT	GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR
8139	21221		6.16	2.0E-01	AF028026.1	NT	Andes virus strain OI23133 glycoprotein G1 and G2 precursor, gene, partial cds
8395	21476	35003	3.12	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
8921	22000		0.48	2.0E-01	BE562247.1	EST_HUMAN	601344648F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9551	22616	36186	1.17	2.0E-01	U82511.1	NT	Dictyostelium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds
9590	22645	36215	0.62	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9756	22694		5.42	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9947	22986	36579	0.52	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9947	22986	36580	0.52	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10095	23133		2.24	2.0E-01	AF146692.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10247	23282	36878	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10247	23282	36879	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10371	23406	37016	0.67	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10371	23406	37017	0.67	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10419	23454		0.8	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppel)
10616	23650	37259	0.88	2.0E-01	X97121.1	NT	R.norvegicus mRNA for NTR2 receptor
11079	24154	37791	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11079	24154	37792	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11908	24895	38597	1.33	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
11908	24895	38598	1.33	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
12666	25443		1.24	2.0E-01	AF206637.2	NT	Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12899	25965		1.64	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12912	25876	31851	1.63	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12952	25662	31956	1.63	2.0E-01	AI023592.1	EST_HUMAN	ov80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12977	25636		17.48	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
113	13344		4.89	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arnt1), mRNA
362	13573	26604	5.58	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
673	13859	26889	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambda/iota protein kinase C-interacting protein mRNA, complete cds
673	13859	26890	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambda/iota protein kinase C-interacting protein mRNA, complete cds
680	13866	26897	8.31	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
681	13866	26897	6.7	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
1010	14181		1.72	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1128	14293	27349	5.63	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1401	14555	27629	2.42	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1466	14620		4.34	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2456	15584	28711	3.66	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2989	16165	29181	3.81	1.9E-01	U66066.1	NT	Sigmodon hispidus p53 gene, partial cds
3004	16179		7.53	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3482	16650	29666	4.07	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3569	16734	29750	4.94	1.9E-01	R16467.1	EST_HUMAN	yf42f10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3907	17066	30065	1.09	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4100	17255	30256	3.68	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4193	17343	30336	1.51	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4251	17397		1.31	1.9E-01	AE001912.1	NT	Deinococcus radiodurans R1 section 49 of 229 of the complete chromosome 1

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4346	17489	30471	0.89	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-d04 FN0010 Homo sapiens cDNA
4592	17729	30711	0.8	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5124	18250		1.08	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5721	18914		5.19	1.9E-01	AW130149.1	EST_HUMAN	xf29a07.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5761	18953	32256	8.03	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5962	19148	32463	1.08	1.9E-01	AF091216.1	NT	Mus musculus Wrn protein (Wrn) gene, complete cds
6006	19191		2.45	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6457	19624	32987	1.03	1.9E-01	AI762391.1	EST_HUMAN	wi54h02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394099 3'
6518	19683	33054	1.1	1.9E-01	AW148452.1	EST_HUMAN	xf14c08.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7112	18638	31495	1.54	1.9E-01	R43212.1	EST_HUMAN	yg09a12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element ;
7138	20273	33712	0.74	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7138	20273	33713	0.74	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7409	20487	33957	0.92	1.9E-01	U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7638	20707	34186	0.78	1.9E-01	U93688.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds
7661	20728	34204	1.38	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7708	20773	34258	2.64	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
8174	21256	34778	1.83	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8885	21964	35500	13.56	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
9146	22225	35768	1.5	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9146	22225	35769	1.5	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
10079	23117	36719	0.77	1.9E-01	AA912486.1	EST_HUMAN	ol96g10.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element;
10447	23482	37090	0.81	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10447	23482	37091	0.81	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10880	23965	37593	1.38	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10880	23965	37594	1.38	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10992	24071	37704	2.18	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12025	25009	38711	2.21	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12047	25028	38735	1.48	1.9E-01	L07344.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
32	13270	26274	1.85	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
270	16009	26519	1.47	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
381	13589	26625	1.9	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
765	13946	26993	0.78	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OlGC1, complete cds
1005	14176	27235	1.8	1.8E-01	AI912212.1	EST_HUMAN	wd71f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1115	14279	27335	2.14	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1317	14473	27540	6.87	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1533	14686	27765	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1533	14686	27766	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1915	15058		1.91	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE ;
1965	15108	28208	2.28	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2756	15873		3.34	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2963	16140		2.3	1.8E-01	AF184589.1	NT	Jonopsidium acaule LEAFY protein (LEAFY2) gene, partial cds
2968	16144	29163	1.16	1.8E-01	AW182300.1	EST_HUMAN	xj41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3194	16369	29375	1.61	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3452	16619	29638	0.77	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3712	16873	29877	0.87	1.8E-01	H03369.1	EST_HUMAN	yj45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3712	16873	29878	0.87	1.8E-01	H03369.1	EST_HUMAN	yj45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4453	17593		0.92	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4678	17813	30801	5.61	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4895	18025	31011	2.68	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5129	18254	31219	0.65	1.8E-01	X79794.1	NT	N.tabacum mRNA pNLA-35
5158	18280	31245	1.79	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA
5206	18327	31297	2.55	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5218	18340	31313	0.89	1.8E-01	AI439881.1	EST_HUMAN	ti57e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5291	18409	31376	1.2	1.8E-01	Y08310.1	NT	M.barkeri mtaC and mtaB genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5413	18615	31589	0.61	1.8E-01	BE082626.1	EST_HUMAN	RC6-BT0641-300300-011-H03 BT0641 Homo sapiens cDNA
5929	19115	32428	1.19	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6047	19230	32554	0.95	1.8E-01	N28629.1	EST_HUMAN	yx38h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264063 5'
6256	19430	32776	0.89	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6256	19430	32777	0.89	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6641	19800	33189	1.16	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6688	19846		2.12	1.8E-01	N94853.1	EST_HUMAN	yy62h02.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278163 5'
7146	20281	33722	1.11	1.8E-01	AB018561.1	NT	Citrullus lanatus mRNA for wsus, complete cds
7146	20281	33723	1.11	1.8E-01	AB018561.1	NT	Citrullus lanatus mRNA for wsus, complete cds
7202	20067	33477	0.67	1.8E-01	BE961353.1	EST_HUMAN	601648361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
7604	20674	34148	0.81	1.8E-01	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
8810	21889	35431	0.58	1.8E-01	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
9543	22608	36176	1.58	1.8E-01	M73268.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9574	22716	36284	1.52	1.8E-01	9626232	NT	Bacteriophage Ike, complete genome
9692	22741		0.6	1.8E-01	AA493751.1	EST_HUMAN	nh02a05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.t3 L1 repetitive element ;
9774	22814	36392	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9774	22814	36393	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9814	22854	36432	1.02	1.8E-01	M26019.1	NT	S.commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9814	22854	36433	1.02	1.8E-01	M26019.1	NT	S.commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9981	23020	36613	0.81	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9986	23025	36617	0.71	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10337	23372		0.67	1.8E-01	AF200252.1	NT	Aquarius amplus cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10578	23613	37218	1.46	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
10785	23818	37441	1.21	1.8E-01	AB011171.1	NT	Homo sapiens mRNA for KIAA0599 protein, partial cds
10873	23958	37588	2.02	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10917	24000	37633	5	1.8E-01	U38906.1	NT	Bacteriophage r1t integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds
10974	20281	33722	3.05	1.8E-01	AB018561.1	NT	Citrullus lanatus mRNA for wsus, complete cds
10974	20281	33723	3.05	1.8E-01	AB018561.1	NT	Citrullus lanatus mRNA for wsus, complete cds
10975	24054	37688	4.41	1.8E-01	AF019107.1	NT	Dictyostelium discoideum unknown (DG1041) gene, complete cds
11270	24338	37976	2.06	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11551	24606	38284	1.41	1.8E-01	AW275728.1	EST_HUMAN	xp40h10.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742883 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11750	23936	37563	8.94	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
12061	25042	38751	3.48	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbxa2r), mRNA
12124	25104	38808	1.77	1.8E-01	AA095094.1	EST_HUMAN	cp2798.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12239	25183		1.79	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12306	25224	32103	1.26	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155318 5'
12719	14473	27540	1.18	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12811	25541		3.28	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12942	25620		20.8	1.8E-01	R24494.1	EST_HUMAN	yh48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12988	25643		4.98	1.8E-01	Y11114.1	NT	E.dispar mRNA for hexokinase (hxk1)
13035	26134	31548	1.7	1.8E-01	9506952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcolce), mRNA
591	13782	26801	6.4	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
828	14006	27063	3.16	1.7E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
983	14156		1.79	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1083	14249	27305	0.89	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome
1083	14249	27306	0.89	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome
1860	15006	28113	2.44	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2038	15179		3.23	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2922	16100	29112	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2922	16100	29113	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2993	16169	29186	1.47	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3061	16237	29257	1.09	1.7E-01	AJ238736.1	NT	Naja naja atra ctx-1 gene, exons 1-3
3061	16237	29258	1.09	1.7E-01	AJ238736.1	NT	Naja naja atra ctx-1 gene, exons 1-3
3174	16349	29355	1.65	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3451	16618	29637	0.81	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3534	16699	29710	1.52	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4049	17205	30215	6.06	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4681	17816		2.49	1.7E-01	X52936.1	NT	Schistocerca gregaria alpha repetitive DNA
4884	18014	30998	0.59	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds

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4961	18090	31066	1.31	1.7E-01	AI247635.1	EST_HUMAN	qh57e09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains OFR.b1 OFR repetitive element ;
5231	18353		1.07	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5272	18391	31359	0.72	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5312	18429	31399	0.91	1.7E-01	D37951.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5524	18721	31737	1.88	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5524	18721	31738	1.88	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5710	18903	32198	0.92	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6459	19626	32988	12.64	1.7E-01	H72118.1	EST_HUMAN	ys02g06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6517	19682	33052	0.72	1.7E-01	AI370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6517	19682	33053	0.72	1.7E-01	AI370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6992	18511	31503	0.75	1.7E-01	BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
7019	20155		1.94	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7140	20275		0.59	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7369	20448	33911	1.38	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7448	20525	33998	8.51	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7649	20718	34195	1.21	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7666	25850	34208	0.64	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
8045	21128	34648	1.26	1.7E-01	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
8150	21232	34752	0.75	1.7E-01	AF150669.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8472	21553	35083	7.35	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8472	21553	35084	7.35	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8895	21974	35511	0.5	1.7E-01	AW992873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8925	22004	35543	1.93	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9045	22124	35666	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neuroligin 3 isoform gene, complete cds, alternatively spliced
9045	22124	35667	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neuroligin 3 isoform gene, complete cds, alternatively spliced
9198	22276	35814	0.51	1.7E-01	R77002.1	EST_HUMAN	yi66g02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144242 5'
9369	22444	36005	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9369	22444	36006	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9789	22829	36407	9.03	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9899	22939	36524	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 MAGE resequences, MAGO Homo sapiens cDNA
9899	22939	36525	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 MAGE resequences, MAGO Homo sapiens cDNA

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9916	22956	36543	2.08	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9992	23031	36621	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9992	23031	36622	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10013	23051	36645	0.93	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10438	23473		2.77	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10605	23639	37247	1.56	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10607	23641	37249	1.66	1.7E-01	AA627972.1	EST_HUMAN	nq60e07.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081 TRANSFORMING PROTEIN RHOC (HUMAN);
10919	24002	37636	9.54	1.7E-01	BE390835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
11045	24122	37756	2.12	1.7E-01	AA814617.1	EST_HUMAN	of43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
11373	24434	38090	6.81	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11373	24434	38091	6.81	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11657	24736	38427	1.71	1.7E-01	AA883375.1	EST_HUMAN	al45f09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460297 3'
12011	24996		1.5	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12042	25023	38727	1.67	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12042	25023	38728	1.67	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12142	25117	38825	2	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
12275	26087		1.45	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12567	25920		1.18	1.7E-01	AI824404.1	EST_HUMAN	tx69g05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12907	25600	31972	7.24	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
128	13356	26388	1.7	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
697	15985	26913	1.16	1.6E-01	R31497.1	EST_HUMAN	yh75f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1551	14703	27783	4.25	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1910	15053		1.27	1.6E-01	AJ235272.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4
1977	15120	28221	2.14	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2041	15182		1.43	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2457	16063	28712	1.09	1.6E-01	X94232.1	NT	H.sapiens mRNA for novel T-cell activation protein
2562	15687	28813	2.73	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2957	16134	29149	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2957	16134	29150	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3723	16884	29889	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3723	16884	29890	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3872	17031	30030	0.82	1.6E-01	AE000962.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4107	17261		2.8	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4144	17296	30288	1.21	1.6E-01	AF084456.1	NT	Crithidia fasciculata tryparedoxin I (txnI) gene, complete cds
4448	17588	30569	10.91	1.6E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4578	17715		2.49	1.6E-01	AW968601.1	EST_HUMAN	EST380677 MAGE resequences, MAGJ Homo sapiens cDNA
4586	17723		4.39	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5060	18188	31162	1.39	1.6E-01	AA088343.1	EST_HUMAN	zl84h09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955 E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
5083	18211	31183	1.8	1.6E-01	AJ006356.1	NT	Lycopersicon esculentum RsaI fragment 2, satellite region
5083	18211	31184	1.8	1.6E-01	AJ006356.1	NT	Lycopersicon esculentum RsaI fragment 2, satellite region
5345	18458		0.93	1.6E-01	AF045283.1	NT	Gallus gallus smooth muscle/non-muscle myosin light chain kinase gene, exon 29
5503	18702	31719	0.81	1.6E-01	L40609.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5639	18833	31909	2.9	1.6E-01	AW197496.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN ;
5639	18833	31910	2.9	1.6E-01	AW197496.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN ;
5651	18845	32126	1.99	1.6E-01	AF034716.1	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6152	19328	32674	0.73	1.6E-01	BE925803.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6558	19720	33096	2.06	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6558	19720	33097	2.06	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6939	20252	33688	0.79	1.6E-01	AB046786.1	NT	Homo sapiens mRNA for KIAA1566 protein, partial cds
6985	20213		0.66	1.6E-01	BF683630.1	EST_HUMAN	602139855F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301004 5'
7103	18530	31485	4.15	1.6E-01	AW291215.1	EST_HUMAN	UI-H-BI2-agi-b-06-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7451	20528	34001	0.71	1.6E-01	Z49632.1	NT	S.cerevisiae chromosome X reading frame ORF YJR132w
7955	21005	34516	1.63	1.6E-01	AW246359.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7982	21031	34544	0.84	1.6E-01	6753237	NT	Mus musculus Ca<2+>dependent activator protein for secretion (Cadps), mRNA
7986	21035		1.03	1.6E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004466 5'
8053	21136	34657	1.62	1.6E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
8215	21297		0.53	1.6E-01	BE244087.1	EST_HUMAN	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8310	21392	34916	0.77	1.6E-01	U38243.1	NT	Bacteroides vulgatus beta-lactamase (cfxA) gene, complete cds and mobilization protein (mobA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8833	21912	35450	1.08	1.6E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
9026	22105	35646	0.77	1.6E-01	R13673.1	EST_HUMAN	yf60h08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:26873 5'
9133	22212		0.74	1.6E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9171	22249	35792	1.85	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9311	22387		0.76	1.6E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9851	22891		1.77	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA
9854	22894	36475	1.99	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9891	22931		1.16	1.6E-01	BE155664.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
10826	23859	37482	0.5	1.6E-01	11128016	NT	Homo sapiens nuclear autoantigen (GS2NA), mRNA
10893	23977	37609	2.34	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11244	24313	37951	1.34	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11244	24313	37952	1.34	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11249	24318	37958	1.62	1.6E-01	BE259649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11377	24438		3.6	1.6E-01	AF106064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11697	24694	38386	7.53	1.6E-01	6671552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12277	25207	38363	3.89	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12597	25402	32043	2	1.6E-01	L14933.1	NT	Rat convertase PC5 mRNA, 5' end
12630	25423		1.38	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12733	25893		11.64	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12933	25615		2.71	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
13029	25678		5.04	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
13054	25690	31964	1.69	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
13060	25694		1.4	1.6E-01	BE267894.1	EST_HUMAN	601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5'
13199	25782		1.29	1.6E-01	BF672698.1	EST_HUMAN	602152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293145 5'
258	13477	26508	1.7	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
258	13477	26509	1.7	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
600	15984		2.5	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
805	13985	27037	1.38	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1116	14281	27337	1.44	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1121	14286	27341	2.7	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1137	14302		1.85	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1243	14402	27463	2.37	1.5E-01	AW195516.1	EST_HUMAN	xn39d11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1304	14460	27526	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1304	14460	27527	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1511	14664	27749	1.38	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1957	15100	28200	0.98	1.5E-01	AW444451.1	EST_HUMAN	UI-H-BI3-akb-b-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733841 3'
2980	16156		0.9	1.5E-01	AW572516.1	EST_HUMAN	xw56a02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_rna1 THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3100	16276	29290	0.91	1.5E-01	M81441.1	NT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3118	16294	29308	0.62	1.5E-01	O78687	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3433	16601	29620	5.78	1.5E-01	AA935049.1	EST_HUMAN	oc68d05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433 RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3454	16621	29641	0.73	1.5E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3454	16621	29642	0.73	1.5E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3851	17011	30011	2.35	1.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3867	17026	30025	0.83	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3881	17040	30037	0.77	1.5E-01	M97882.1	NT	XYNA; Thermoanaerobacterium; xynA; 4182 base-pairs
3970	17128	30131	2.45	1.5E-01	AW665983.1	EST_HUMAN	hj10f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3987	17144	30149	0.68	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3987	17144	30150	0.68	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
4161	17312	30308	1.16	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4210	17359	30348	0.67	1.5E-01	Z12628.1	NT	B.napus mitochondrion DNA for ORF158
4299	17442	30428	9.85	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4847	17980	30969	1.54	1.5E-01	BF687665.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4874	15891	29002	2.33	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
5114	18242	31207	1.5	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5370	18573	31441	1.91	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5399	18601	31571	1.33	1.5E-01	AF256652.1	NT	Caiman crocodilus MHC class II beta chain (hcIIbeta) gene, complete cds
5443	18643		5.95	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5655	18849	32131	4.8	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5697	18891	32182	6.66	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5697	18891	32183	6.66	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6029	19212	32532	0.82	1.5E-01	4506810	NT	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA

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6128	19307	32647	1.71	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6128	19307	32648	1.71	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6168	19344	32690	2.19	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6324	19496	32852	3.49	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6376	19545		1.98	1.5E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6474	19641	33002	1.74	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6631	25828	33179	3.58	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6661	19820	33207	4.73	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6672	19831	33220	1.51	1.5E-01	P48508	SWISSPROT	GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6719	19876	33267	2.35	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6823	19976	33383	0.86	1.5E-01	AA714760.1	EST_HUMAN	nw30d10.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6852	20005	33414	2.24	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7118	18544	31600	6	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE resequences, MAGK Homo sapiens cDNA
7158	25840		0.8	1.5E-01	AA811545.1	EST_HUMAN	ob73f02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element ;
7365	20444		4.73	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7550	20622	34099	1.63	1.5E-01	AI973157.1	EST_HUMAN	wr52c08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2491310 3'
7764	20823	34314	0.88	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7764	20823	34315	0.88	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7775	20832	34322	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7775	20832	34323	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7919	20970	34477	0.79	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds
8248	21330	34846	0.99	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8414	21495	35026	1.1	1.5E-01	AA970317.1	EST_HUMAN	oo85g12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8507	21588		1.06	1.5E-01	BE884799.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8594	21675		14.14	1.5E-01	C16800.1	EST_HUMAN	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09 5'
8628	21708	35245	1.87	1.5E-01	L27835.1	NT	Pangasianodon gigas growth hormone (GH) mRNA, complete cds
8793	21872	35411	2.17	1.5E-01	D84476.1	NT	Homo sapiens mRNA for ASK1, complete cds
8814	21893		0.79	1.5E-01	P43446	SWISSPROT	WNT-10A PROTEIN PRECURSOR
9038	22117	35660	3.12	1.5E-01	4501972	NT	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9305	22381	35932	2.56	1.5E-01	N74226.1	EST_HUMAN	za59e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9394	22469	36033	1.34	1.5E-01	BF585465.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9401	22475		2.52	1.5E-01	AV754819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9605	22660		0.64	1.5E-01	AU130007.1	EST_HUMAN	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9652	21095	34609	6.7	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
10022	23060	36656	0.71	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10125	23163	36761	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10125	23163	36762	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10407	23442	37049	2.59	1.5E-01	X98852.1	NT	P.leniusculus mRNA for integrin beta subunit
10495	23530		0.51	1.5E-01	AB027759.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10516	23551	37161	2.36	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10516	23551	37162	2.36	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10598	23633	37242	1.22	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds.
10761	23794	37413	1.69	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10761	23794	37414	1.69	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10935	24017	37649	1.67	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10935	24017	37650	1.67	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
11063	24139	37773	4.46	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11063	24139	37774	4.46	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11331	24394	38042	1.38	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
11925	24911		1.34	1.5E-01	AI193704.1	EST_HUMAN	qe72e01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to gb:M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12232	25953		38.98	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12629	25422		1.64	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12633	25426		1.23	1.5E-01	AJ238332.1	NT	Mus musculus mRNA for death inducer-obliterator-1 (Dio-1)
12696	25976		6.64	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
12749	25496		1.52	1.5E-01	AP001514.1	NT	Bacillus halodurans genomic DNA, section 8/14
12778	25520	32002	1.41	1.5E-01	9695413	NT	Lymphocystis disease virus 1, complete genome
12807	26000		2.59	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
12932	25896	31857	7.68	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6

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13183	25769	31932	6.61	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
13227	26138		2.26	1.5E-01	9631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
310	13526		1.23	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S5P to TCRBV21S2A2 region
933	14108		3.24	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-)-methyltransferase, complete cds
1288	14444		2.99	1.4E-01	T91864.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1787	14936		1.46	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1790	14939	28032	1.84	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1954	15097		1.27	1.4E-01	AW135741.1	EST_HUMAN	UI-H-BI1-acf-a-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
2042	15183		14.84	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2544	15669	28793	1.02	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2853	15967	29077	3.34	1.4E-01	AI933496.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2441665 3'
4289	17434	30421	9.45	1.4E-01	AI699094.1	EST_HUMAN	tx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4289	17434	30422	9.45	1.4E-01	AI699094.1	EST_HUMAN	tx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4352	17495	30475	4.28	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4531	17669		0.7	1.4E-01	AA776287.1	EST_HUMAN	zj60b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057_rna1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);contains Alu repetitive element;
4798	17933	30920	0.79	1.4E-01	5453861	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
5322	18436	31406	0.62	1.4E-01	AJ005180.1	NT	Lycopersicon esculentum genomic RAPD band 26
5421	18622	31598	5.21	1.4E-01	T90677.1	EST_HUMAN	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5444	18644	31621	4.33	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5444	18644	31622	4.33	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6427	19595	32961	3.17	1.4E-01	BE326891.1	EST_HUMAN	hr67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6611	19771	33161	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6611	19771	33162	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6701	19859	33249	3.7	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6715	19873		1.51	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6739	19895	33286	2.48	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA
7276	20359		0.71	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7545	20617		1.78	1.4E-01	AW015373.1	EST_HUMAN	UI-H-BI0-aat-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7618	20688		0.73	1.4E-01	AI762827.1	EST_HUMAN	wi04f12.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN P49662 CASPASE-4 PRECURSOR ;

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7621	20691	34167	0.63	1.4E-01	T53770.1	EST_HUMAN	ya90f11.r2 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:68973 5' similar to contains Alu repetitive element
7799	20855	34345	0.95	1.4E-01	U85845.1	NT	Oryctolagus cuniculus fructose 1,6, bisphosphate aldolase (AldB) gene, complete cds
7932	20982	34490	1.02	1.4E-01	AI305192.1	EST_HUMAN	qi90b12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8162	21244		0.54	1.4E-01	BF310258.1	EST_HUMAN	601894760F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124199 5'
8670	21750		1.32	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
8984	22063		0.6	1.4E-01	AI436093.1	EST_HUMAN	th92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:O02710 O02710 GAG POLYPROTEIN. ;
9114	22193	35738	4.94	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9194	22272	35810	0.76	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9322	22398	35951	1.07	1.4E-01	R62746.1	EST_HUMAN	yi10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9322	22398	35952	1.07	1.4E-01	R62746.1	EST_HUMAN	yi10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9388	22463	36027	8.52	1.4E-01	BF310959.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9475	22532	36096	1.72	1.4E-01	W93411.1	EST_HUMAN	zd94a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element ;
9547	22612	36180	0.54	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9547	22612	36181	0.54	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9558	22623	36194	1.65	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9558	22623	36195	1.65	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9649	21092	34607	1.81	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducting adaptor protein (STAM), serine threonine kinase lal (IAL), and zinc finger protein (DNZ1) genes, complete cds
10009	23047	36641	0.54	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein
10192	23229	36821	0.89	1.4E-01	AF023813.1	NT	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10293	23328	36931	0.81	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10293	23328	36932	0.81	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10463	23498	37109	0.76	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10463	23498	37110	0.76	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10680	23714		0.51	1.4E-01	T84293.1	EST_HUMAN	yd47d03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111365 5'
10825	23858	37481	0.7	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2590451 to 2812870
10948	24030		1.32	1.4E-01	AA811480.1	EST_HUMAN	oa99a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
11081	24156	37793	2.67	1.4E-01	R53400.1	EST_HUMAN	yj70c05.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154088 5'
11282	24348	37985	1.69	1.4E-01	AW104982.1	EST_HUMAN	xd73e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'
11354	24416	38071	1.58	1.4E-01	T96102.1	EST_HUMAN	ye47g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5'

WO 01/57272

PCT/US01/00663

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11354	24416	38072	1.58	1.4E-01	T96102.1	EST_HUMAN	ye47g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5'
11356	24418	38075	2.36	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11572	24627	38306	1.85	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein
11613	20617		1.57	1.4E-01	AW015373.1	EST_HUMAN	UI-H-BI0-aat-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11757	23943	37570	2.07	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11816	24805		1.51	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
12038	25020	38724	10.18	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
12560	25382	32038	4.68	1.4E-01	X74773.1	NT	P.salina plastid gene secY
12574	25390		3.28	1.4E-01	11968117	NT	Rattus norvegicus deomin (Dco), mRNA
12605	25405		1.71	1.4E-01	BE964835.2	EST_HUMAN	601658490R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885671 3'
12627	26175		2.83	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12724	25482		7.52	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycinamide ribonucleotide transformylase (GART) genes, complete cds
12742	25493		4.02	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
12834	26193		3.2	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12928	25612		1.45	1.4E-01	X69192.1	NT	V.planifolia mRNA for methyltransferase
13084	25977		3.36	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
13178	25765		1.68	1.4E-01	AW377998.1	EST_HUMAN	MR0-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
332	13546	26576	2.27	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
332	13546	26577	2.27	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
542	13735	26759	1.88	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
653	13839	26866	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
653	13839	26867	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
867	14043	27108	1.55	1.3E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
917	14092	27157	1.26	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1052	14218	27274	2.14	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1151	14315		2.04	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1242	14401	27462	1.67	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'

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1475	14628		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1905	15048	28159	1.02	1.3E-01	6680957	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
2014	15154	28259	2.73	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2239	15372		1.09	1.3E-01	AJ243578.1	NT	Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2364	15495		1.38	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2455	15583		3.31	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2653	15776	28889	2.78	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3440	16608	29626	1.21	1.3E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3539	16704	29715	1.11	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3816	16976	29979	0.85	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3816	16976	29980	0.85	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3822	16982	29985	1.55	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodiol dehydrogenase 4 [AKR 1C4], exon 2
3905	17064	30063	0.66	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4096	17251		1.08	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4162	13839	26866	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4162	13839	26867	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4257	17402		0.82	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4274	17419		3.74	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4281	17426	30415	1.82	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose bisphosphate aldolase mRNA, complete cds
4302	17445	30431	21.62	1.3E-01	AW273741.1	EST_HUMAN	xv23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4434	17574		1.19	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4601	17738	30717	0.61	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4656	17792	30776	2.54	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
4748	17883	30865	0.73	1.3E-01	BF679654.1	EST_HUMAN	602154306F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5'
5314	18431	31401	0.78	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994001-1166000 nt. position (5/7)
5440	18640	31619	1.01	1.3E-01	AW466988.1	EST_HUMAN	ha07b06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1 L1 repetitive element ;
5478	18677	31690	1.83	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5618	18812		0.92	1.3E-01	AF107793.1	NT	Emericella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5702	18895		0.67	1.3E-01	AF056880.1	NT	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
5842	19032	32338	0.72	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6107	19287	32621	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6107	19287	32622	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6612	19772	33163	18.92	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6698	19856	33246	2.26	1.3E-01	X88891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6927	20242		0.74	1.3E-01	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6974	20202	33628	0.7	1.3E-01	BE782926.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
6974	20202	33629	0.7	1.3E-01	BE782926.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7155	20289		0.74	1.3E-01	BF529560.1	EST_HUMAN	602044345F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7412	20490		1.97	1.3E-01	H48664.1	EST_HUMAN	yr33d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
8146	21228		0.79	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
8160	21242	34762	1.68	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
8192	21274	34797	1.32	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8469	21550	35080	0.66	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8540	21621		4.24	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8580	21661		4.96	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8725	21805	35342	1.26	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
9149	22227	35770	0.57	1.3E-01	R11172.1	EST_HUMAN	yf39g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9149	22227	35771	0.57	1.3E-01	R11172.1	EST_HUMAN	yf39g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9420	22494	36060	0.69	1.3E-01	11068003	NT	*Plutella xylostella granulovirus, complete genome*
9420	22494	36061	0.69	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9672	22634	36204	4.19	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+,K+-ATPase alpha 2c subunit mRNA, complete cds
9973	23012		0.73	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10257	23292		1.07	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pdi4), mRNA
10335	23370	36980	0.95	1.3E-01	AW851599.1	EST_HUMAN	MR2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA
10603	25864	37244	1.08	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10743	23776	37389	0.65	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10797	23830	37454	0.45	1.3E-01	AW247836.1	EST_HUMAN	2820637.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'
10868	23953		2.31	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
11455	24515		1.34	1.3E-01	BF092708.1	EST_HUMAN	MR4-TN0112-120900-102-e08 TN0112 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11529	24585		3.2	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cfl2), mRNA
11616	24667	38354	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11616	24667	38355	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11895	24883	38581	7.96	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
12000	24985		1.41	1.3E-01	AF012836.1	NT	Thermococcus litoralis trehalose/maltose transporter operon including trehalose/maltose binding protein (malE) and inner membrane proteins MalF (malF) and MalG (malG) genes, complete cds
12023	25007	38708	1.72	1.3E-01	BE619364.1	EST_HUMAN	601473369F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
12052	25033	38739	1.52	1.3E-01	BF683555.1	EST_HUMAN	602139760F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300863 5'
12399	25279	32080	2.13	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
12543	25368		6.39	1.3E-01	AJ242790.1	NT	Gallus gallus scyc1 gene for lymphotactin, exons 1-3
12964	25627		1.31	1.3E-01	AB026829.1	NT	Ephydatia fluviatilis mRNA for sALK-6, complete cds
12995	25647		1.87	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN. ;
394	13631	26668	13.87	1.2E-01	AI421744.1	EST_HUMAN	tf39b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1 ANNEXIN V (HUMAN);
437	13237		1.42	1.2E-01	U66912.1	NT	Dictyostelium discoideum ORF DG1016 gene, partial cds
561	13753		3.82	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1408	14562	27636	2.32	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1408	14562	27637	2.32	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1414	14568		3.35	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cdA Homo sapiens cDNA clone cdAAJB11 5'
1419	14672		0.94	1.2E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1536	14689		0.94	1.2E-01	AA897474.1	EST_HUMAN	al48e09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1660	14812	27897	1.1	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1682	14834	27919	2.88	1.2E-01	AI285402.1	EST_HUMAN	qt69f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
1808	14957		25.75	1.2E-01	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
1970	15113		1.66	1.2E-01	AW449368.1	EST_HUMAN	UI-H-BI3-aki-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2253	15386	28514	1.66	1.2E-01	BF248490.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2450	15578		0.99	1.2E-01	Z21405.1	EST_HUMAN	HSAAAEBZT TEST1, Human adult Testis tissue Homo sapiens cDNA
2656	15779	28893	1.84	1.2E-01	AW996556.1	EST_HUMAN	QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
2905	16083	29098	1.16	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2967	16143	29162	1.9	1.2E-01	AI720470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3001	16177	29198	3.44	1.2E-01	M16364.1	NT	Human creatine kinase-B mRNA, complete cds
3068	16244	29265	0.91	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3302	16476	29498	2.52	1.2E-01	AW370668.1	EST_HUMAN	QV1-BT0259-261099-021-d05 BT0259 Homo sapiens cDNA
3330	16503		0.74	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3568	16733		0.66	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3610	16774	29789	1.12	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3610	16774	29790	1.12	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3694	16733		1.22	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3865	17024		0.95	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053688 3'
4298	17441	30426	2.1	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4298	17441	30427	2.1	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4431	17571	30552	0.59	1.2E-01	M15861.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4942	18072		1.94	1.2E-01	X73416.1	NT	W.suaveolens mitochondrial orf1
5364	18567	31433	0.89	1.2E-01	AA744369.1	EST_HUMAN	ny63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5415	18617	31591	0.93	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5425	18626	31601	2.5	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5484	18683	31700	1.65	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5622	18816	31885	1.14	1.2E-01	Z48234.1	NT	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6329	19500	32858	1.9	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6377	19546	32903	0.81	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6428	19596	32962	2.26	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6493	19659	33022	1.52	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6561	19723	33101	0.58	1.2E-01	AA747535.1	EST_HUMAN	nx85c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
6785	19940	33338	1.18	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158386 5'
7154	20288	33731	0.64	1.2E-01	H47799.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
7154	20288	33732	0.64	1.2E-01	H47799.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
7772	20829	34320	0.62	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp76, drbp76 gamma, drbp76 alpha and ILF3)
8076	21158		1.13	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA
8149	21231	34751	2.45	1.2E-01	AI913753.1	EST_HUMAN	wc99g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II ;
8197	21279	34801	0.64	1.2E-01	Q02369	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
8504	21585	35119	0.66	1.2E-01	AI832681.1	EST_HUMAN	at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8590	21671		10.76	1.2E-01	AW083652.1	EST_HUMAN	xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8611	21691		3.76	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8649	21729	35266	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8649	21729	35267	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8800	21879		1.02	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
8887	21966		1.44	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
8920	21999		0.77	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9771	22767	36338	1.3	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
10209	23245	36835	0.9	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
11125	24197		2.55	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11320	24383		3.03	1.2E-01	BE962324.2	EST_HUMAN	601655576R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11414	24475		1.73	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11533	24589	38264	2.78	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17
11593	24646	38329	1.72	1.2E-01	R40249.1	EST_HUMAN	yf80c02.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28880 3'
11798	24788		2.47	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12161	25128		2.09	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12522	25355		4.37	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
12614	26126	31544	2	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12732	25486		1.65	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12734	13753		18.32	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12863	25574		1.4	1.2E-01	X53981.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12968	25629	31981	4.89	1.2E-01	AI299903.1	EST_HUMAN	qn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12992	25644		3.46	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12997	26050		6.44	1.2E-01	O96433	SWISSPROT	CYCLIN T
13031	25679	31960	1.47	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
13221	25795		1.23	1.2E-01	AF090141.1	NT	Chryseobacterium meningosepticum GOB-1 carbapenemase gene, complete cds
578	13770	26792	1.56	1.1E-01	AI561003.1	EST_HUMAN	tn18d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
630	13815	26838	1.33	1.1E-01	AA569006.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_rna1 HEME OXYGENASE 1 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1079	14245	27302	1.61	1.1E-01	BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1109	14274		1.65	1.1E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1186	16031	27405	3.67	1.1E-01	AW972158.1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo sapiens cDNA
1278	14435	27505	1.88	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
1549	14701	27780	2.75	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2255	15388		1.73	1.1E-01	AJ006701.1	NT	Homo sapiens mRNA for putative serine/threonine protein kinase, partial
2388	15519		2.02	1.1E-01	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
2603	15999		1.08	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2633	15756		1.27	1.1E-01	AW821909.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2917	16095	29107	0.89	1.1E-01	S82418.1	NT	interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5]
3098	16274	29288	0.81	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3422	16591		1.56	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3508	16675	29685	2.09	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3540	16705	29716	1.47	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3580	16745	29763	0.71	1.1E-01	R96946.1	EST_HUMAN	yq62g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element;
3673	16836	29848	0.7	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
3791	16952		0.96	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3800	16961	29965	1.28	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4226	17374	30359	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4226	17374	30360	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4233	17380		0.83	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, comple>
4367	17510		11.45	1.1E-01	AF157066.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4401	17544	30528	0.76	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4762	17897	30877	0.92	1.1E-01	S44957.1	NT	Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4953	18083	31059	1.23	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
5134	17380		0.75	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, comple>
5787	18979		2.59	1.1E-01	AA747216.1	EST_HUMAN	nx76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element;contains element MER35 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5857	19047	32353	1.32	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5894	19082	32393	0.87	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5927	19113	32425	0.95	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
5927	19113	32426	0.98	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
5958	19144	32459	1.79	1.1E-01	X68851.1	NT	S.pombe ste8 gene encoding protein kinase
5992	19177	32498	5.15	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
6150	19326	32671	1.68	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6171	19347	32693	1.37	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
6191	19367	32716	7.73	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
6554	19716	33092	0.61	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6562	19724	33102	1.52	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6602	19762	33150	0.84	1.1E-01	AI216307.1	EST_HUMAN	qg76d06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6742	19898	33289	3.68	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME)
6843	19996		2.73	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6934	20249	33684	2.74	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7193	20058	33468	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7193	20058	33469	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7337	26217		1.01	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050853 5'
7456	25845	34007	0.98	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7)
7706	20771	34255	7.51	1.1E-01	BF884628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7706	20771	34256	7.51	1.1E-01	BF884628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7833	20888	34391	2.16	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7872	20926		0.64	1.1E-01	Z14098.1	NT	B.subtilis gene encoding hypothetical polyketide synthase
7873	20927	34433	3.06	1.1E-01	AA788784.1	EST_HUMAN	ah31b06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483 CHROMOGRANIN A PRECURSOR (HUMAN);
8155	21237	34758	1.58	1.1E-01	U67492.1	NT	Methanococcus jannaschii section 34 of 150 of the complete genome
8403	21484	35012	1.55	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8403	21484	35013	1.55	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8449	21530	35059	1.26	1.1E-01	X91233.1	NT	H.sapiens IL15 gene
8489	21570		0.94	1.1E-01	AW817918.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
8546	21627	35165	2.31	1.1E-01	AL134349.1	EST_HUMAN	DKFZp547P194_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P194 5'
9018	22097	35637	5.67	1.1E-01	U02482.1	NT	Pediococcus acidilactici H plasmid pSMB74 pediocin AcH production (pap) gene cluster papA, papB, papC and papD genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9113	22192	35737	1.04	1.1E-01	AI807474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;
9210	22288	35830	0.5	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
9243	22320	35863	2.25	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9243	22320	35864	2.25	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9335	22411	35964	0.71	1.1E-01	Y12727.1	NT	P.furiosus partial dph5 gene and argF gene
9366	22441	36001	2.78	1.1E-01	T72675.1	EST_HUMAN	yd19h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9392	22467		0.63	1.1E-01	BE893260.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9622	22677		0.99	1.1E-01	BE142305.1	EST_HUMAN	CM3-HT0142-271099-026-g11 HT0142 Homo sapiens cDNA
9696	22745		2.33	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10114	23152		0.77	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10410	23445		1.23	1.1E-01	R80590.1	EST_HUMAN	yi96a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
10544	23579	37188	1.29	1.1E-01	U60529.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10914	23997	37631	1.38	1.1E-01	AF245277.1	NT	Dictyostelium discoideum kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
11044	16274	29288	1.78	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
11162	24233		2.47	1.1E-01	AF169032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
11300	24366	38007	3.11	1.1E-01	R23708.1	EST_HUMAN	yh35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element;contains TAR1 repetitive element ;
11483	24542	38212	2.6	1.1E-01	Z11910.1	NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11483	24542	38213	2.6	1.1E-01	Z11910.1	NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11510	24568	38245	1.69	1.1E-01	BE902974.1	EST_HUMAN	601676924F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959668 5'
11586	24639	38319	3.21	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11971	24956		1.33	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12378	25269		3.78	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
12649	25910		3.18	1.1E-01	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
13136	25738	31947	1.98	1.1E-01	BF239753.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1228	14388		1.51	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1301	14457	27523	2.18	1.0E-01	AI985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.t3 MER7 repetitive element ;
1423	14577	27650	2.3	1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2558	15683	28808	1.01	1.0E-01	AW451366.1	EST_HUMAN	UI-H-BI3-alc-d-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3813	16973	29976	1.11	1.0E-01	BF239818.1	EST_HUMAN	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
4064	17220	30228	2.6	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4527	17665	30651	1.44	1.0E-01	AE002265.2	NT	Chlamydophila pneumoniae AR39, section 91 of 94 of the complete genome
4677	17812		0.76	1.0E-01	AI792349.1	EST_HUMAN	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4834	17967	30955	2.17	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5039	18167	31143	2.17	1.0E-01	AW952344.1	EST_HUMAN	EST364414 MAGE resequences, MAGB Homo sapiens cDNA
5261	18380	31346	0.61	1.0E-01	BE389100.1	EST_HUMAN	601286969F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613552 5'
5436	18636		9.49	1.0E-01	W86490.1	EST_HUMAN	zh62h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5534	18731		0.67	1.0E-01	X54015.1	NT	X.campestris genes for sensor and regulator protein
6001	19186		1.08	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6148	19325	32670	13.08	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6465	19632	32993	0.9	1.0E-01	AA481879.1	EST_HUMAN	zv41g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains L1.t3 L1 repetitive element ;
6479	19646	33008	0.72	1.0E-01	AA406039.1	EST_HUMAN	zu67c12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
7164	20297		1.87	1.0E-01	R23821.1	EST_HUMAN	yh34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
7914	20965		2.39	1.0E-01	Y12488.1	NT	M.musculus whn gene
8118	21200	34721	0.69	1.0E-01	AA861091.1	EST_HUMAN	ak32g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8141	21223	34741	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8141	21223	34742	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8689	21769		0.96	1.0E-01	AW189797.1	EST_HUMAN	xi09b01.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);contains TAR1.t3 TAR1 repetitive element ;
9387	22462	36026	1.12	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synamon mRNA, complete cds
9695	22744	36314	0.87	1.0E-01	R44993.1	EST_HUMAN	yg33h04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34549 3'
9707	22756		1.9	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9750	22688		3.15	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9764	22761	36331	0.55	1.0E-01	W01955.1	EST_HUMAN	zc66c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:327282 3'
10026	23064	36661	1.88	1.0E-01	BF240154.1	EST_HUMAN	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10139	23177	36774	8.92	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10139	23177	36775	8.92	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10347	23382		1.06	1.0E-01	AW957425.1	EST_HUMAN	EST369615 MAGE resequences, MAGE Homo sapiens cDNA
10351	23386	36995	0.62	1.0E-01	T51952.1	EST_HUMAN	yb29a06.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10537	23572	37179	1.27	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5'
10894	23978		1.77	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'

WO 01/57272 PCT/US01/00663

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11286	24352	37991	2.17	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11286	24352	37992	2.17	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11685	24684	38374	3.64	1.0E-01	BE790543.1	EST_HUMAN	601682558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
11814	24803		1.75	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain:RIMD 0509952
12364	25633		1.73	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12609	25408		1.73	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12939	26119		3.11	1.0E-01	U52691.1	NT	*Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds*
12973	25633		1.8	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13045	26085		25.82	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
13117	25729		6.58	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
13219	26106		1.45	1.0E-01	AE002138.1	NT	Ureaplasma urealyticum section 39 of 59 of the complete genome
2839	15953	29060	0.96	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA, complete cds
2847	15961	29070	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2847	15961	29071	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3340	16513	29528	1.31	9.9E-02	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
7110	18536	31492	8.96	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
8099	21181	34699	0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element;contains element MIR MIR repetitive element ;
8099	21181	34700	0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element;contains element MIR MIR repetitive element ;
9457	22573	36139	1.35	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
12132	25112	38816	3.67	9.9E-02	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
577	13769		2.18	9.8E-02	X56338.1	NT	O.sativa RAmy3C gene for alpha-amylase
3214	16388	29398	3.66	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4339	17482	30463	9.93	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4339	17482	30464	9.93	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
7651	20719		0.98	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9454	22570		1.16	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11747	23933	37559	1.73	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12332	25240		1.29	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1381	14536	27611	1.92	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1617	14769		1.01	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2335	15466	28601	2.58	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
4091	17246		4.05	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5461	18661	31639	0.59	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymydilate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5461	18661	31640	0.59	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymydilate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6138	19316	32657	1.39	9.7E-02	AW954476.1	EST_HUMAN	EST366546 MAGE resequences, MAGC Homo sapiens cDNA
7450	20527	34000	3.05	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
8171	21253	34774	1.54	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8171	21253	34775	1.54	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9050	22129	35673	1.49	9.7E-02	AI953984.1	EST_HUMAN	wx78b06.x1 NCI_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
11472	24531		1.72	9.7E-02	U58337.1	NT	Mus musculus ligatin (Lgtn) mRNA, partial cds
2073	15213	28330	1.33	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2073	15213	28331	1.33	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4464	17604	30582	6.67	9.6E-02	Z32686.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
5117	18244	31209	0.95	9.6E-02	AW966230.1	EST_HUMAN	EST378303 MAGE resequences, MAGI Homo sapiens cDNA
6231	19406		2.75	9.6E-02	BE910039.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8017	21068		0.79	9.6E-02	6678753	NT	Mus musculus lymphocyte antigen 78 (Ly78), mRNA
8571	21652		0.65	9.6E-02	AU137084.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
9744	22808	36386	1.49	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
10076	23114		1.34	9.6E-02	BE894895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10245	23280	36876	1.04	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10245	23280	36877	1.04	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10325	23360	36970	0.62	9.6E-02	BF677270.1	EST_HUMAN	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'
10354	23389	36998	1.56	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10354	23389	36999	1.56	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10465	23500	37113	3.43	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
10981	24060	37694	5.27	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
12019	25003	38704	2.8	9.6E-02	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
13015	25668		1.7	9.6E-02	H14599.1	EST_HUMAN	ym19h03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13143	25743	31949	1.41	9.6E-02	AJ295624.1	NT	Gallus gallus ALPHA 10 nAChR gene for alpha 10 subunit of nicotinic acetylcholine receptor, exons 1-5
4217	17366	30355	2.16	9.5E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5782	18974	32280	0.88	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7455	20532	34006	4.64	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7741	20802	34292	7.77	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7876	18974	32280	0.81	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8064	21146	34666	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8064	21146	34667	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37634	4.09	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37635	4.09	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12104	25084		1.82	9.5E-02	7657416	NT	Mus musculus odd Oz/ten-m homolog 3 (Drosophila) (Odz3), mRNA
13097	25715		2.81	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1880	15024	28130	3.95	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
3985	17142	30147	4.64	9.4E-02	Z33059.1	NT	M.capricolum DNA for CONTIG MC073
6447	19614	32978	0.95	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7769	20827	34318	0.68	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds
8799	21878		2.5	9.4E-02	Z46883.1	NT	Acinetobacter sp. cysD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
11174	20827	34318	1.9	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds
12214	26011		7.72	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13198	25780	31936	4.84	9.4E-02	U27699.1	NT	Human pephBGT-1 betaine-GABA transporter mRNA, complete cds
3054	16230		2.37	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3094	16270		8.03	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3329	16502	29521	2.17	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4268	17413	30400	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4268	17413	30401	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4857	17990		1.82	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5779	18971		0.67	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8442	21523	35052	0.56	9.3E-02	AW566007.1	EST_HUMAN	EST69 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9324	22400		0.5	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9911	22951	36537	2.3	9.3E-02	BE962631.2	EST_HUMAN	601655988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10394	23429	37035	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10394	23429	37036	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10526	23561		3.96	9.3E-02	AW206117.1	EST_HUMAN	UI-H-BI1-afx-h-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12485	25933		2.08	9.3E-02	AJ249850.1	NT	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit
12905	25964		22.03	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
13139	26010		2.87	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
238	13460	26486	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26487	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26488	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2302	15434		3.08	9.2E-02	R54156.1	EST_HUMAN	yg98f07.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'
3247	16421	29437	3.7	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3379	16551	29564	1.01	9.2E-02	AA534354.1	EST_HUMAN	nf79e01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926136 3'
3676	16839		1.14	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
4353	17496		1.05	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4425	17565		0.88	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4760	17895	30875	3.44	9.2E-02	X96402.1	NT	G.gallus Mia-CK gene
8198	21280	34802	1.82	9.2E-02	T49920.1	EST_HUMAN	ya99c09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8370	21451	34974	2.18	9.2E-02	X95256.1	NT	H.vulgare xylose isomerase gene
13120	26201		1.2	9.2E-02	11466872	NT	Podospora anserina mitochondrion, complete genome
436	13236	26237	2.23	9.1E-02	X77665.1	NT	O. cuniculus k12 keratin gene
3760	16921		0.97	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
4607	17744	30723	1.78	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5848	19038	32345	1.23	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7459	26218		0.61	9.1E-02	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7546	20618	34094	12.21	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7852	20907	34411	0.95	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7887	20939	34445	1.02	9.1E-02	U39073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
9124	22203	35746	0.96	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10642	23676		1.46	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end
10674	23708	37316	1.02	9.1E-02	S74059.1	NT	Tg616=Cyl actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 5275 nt]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10703	23736	37341	0.8	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
11441	24502	38170	2.13	9.1E-02	AF037625.1	NT	Rana catesbeiana dihydropyridine receptor mRNA, complete cds
12151	25121		7.04	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
12393	26124		1.42	9.1E-02	AA179901.1	EST_HUMAN	zp38h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12473	25326		1.32	9.1E-02	AF052695.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12996	25954		13.49	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
13230	25799		1.27	9.1E-02	AF226688.1	NT	Bombyx mori fibroin heavy chain Fib-H (fib-H) gene, complete cds
763	13944	26990	5.89	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1664	14816	27899	7.33	9.0E-02	BE220482.1	EST_HUMAN	hv39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2454	15582	28710	1.18	9.0E-02	AW801364.1	EST_HUMAN	IL5-UM0067-240300-050-h06 UM0067 Homo sapiens cDNA
2864	15978	29088	4.99	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2864	15978	29089	4.99	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3417	16586	29603	1.11	9.0E-02	AF279135.1	NT	Dictyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
4414	17555	30541	0.6	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4414	17555	30542	0.6	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4790	17925	30913	2.03	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
6118	19298	32634	7.2	9.0E-02	W56037.1	EST_HUMAN	ze68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
6860	20012		0.93	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element;
12819	25546		1.82	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rorf1), rOrf2 (rorf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1469	14623	27706	1.25	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1469	14623	27707	1.25	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2460	15587	28714	1.64	8.9E-02	BE153572.1	EST_HUMAN	PM0-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4316	17459		1.69	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
5972	19158	32474	2.7	8.9E-02	AW452122.1	EST_HUMAN	UI-H-BI3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5972	19158	32475	2.7	8.9E-02	AW452122.1	EST_HUMAN	UI-H-BI3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5987	19172	32494	3.34	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA

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7343	20423	33886	1.6	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE]
7731	20793		1.77	8.9E-02	Z79021.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
8240	21322	34839	1.19	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8323	21405	34932	0.76	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8323	21405	34933	0.76	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8797	21876	35415	5.85	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9819	22859	36439	0.84	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element ;
9819	22859	36440	0.84	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element ;
9934	22973	36565	0.63	8.9E-02	AA339356.1	EST_HUMAN	EST44454 Fetal brain I Homo sapiens cDNA 5' end
12213	25962		1.8	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
12366	25262		3.82	8.9E-02	BF696918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12537	25366		2.75	8.9E-02	6680220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
12584	25393		2	8.9E-02	U29895.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
12827	26199		1.16	8.9E-02	U40493.1	NT	Ceratitis capitata mariner transposon transposase gene, complete cds
12880	26133		1.54	8.9E-02	AE001514.1	NT	Helicobacter pylori, strain J99 section 75 of 132 of the complete genome
1404	14558	27632	0.96	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
4012	17169	30177	1.07	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
4145	17297		5.23	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)
4418	17559		0.75	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7716	20780		0.71	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
9188	22266	35807	2.07	8.8E-02	AA151872.1	EST_HUMAN	zn99a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
11380	24441	38099	2.79	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11380	24441	38100	2.79	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11541	24597	38273	5.25	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
12443	25314	32090	1.19	8.8E-02	Z71661.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285w
3785	16946	29953	4.17	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3785	16946	29954	4.17	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4829	17962	30950	1.4	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5211	18332		1.07	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5429	18629	31605	5.49	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5429	18629	31606	5.49	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6984	20212	33642	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6984	20212	33643	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7188	20053	33463	0.67	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
8046	21129		0.56	8.7E-02	AA284532.1	EST_HUMAN	zt20e03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:713692 3'
8713	21793	35329	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8713	21793	35330	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
10951	24033		2.01	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11591	24644	38326	1.48	8.7E-02	AJ007763.1	NT	Gluconobacter oxydans tRNA-Ile and tRNA-Ala genes
12431	25306		2.2	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12648	25432		2.85	8.7E-02	6679057	NT	Mus musculus nidogen 2 (Nid2), mRNA
13033	25680		2.05	8.7E-02	X65292.1	NT	G.gallus mRNA for vigilin
1281	14437	27506	7.73	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
2317	15449	28581	2.2	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3257	16431	29448	2.35	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3734	16895		3.69	8.6E-02	AF153362.1	NT	Dictyostelium discoideum adenylyl cyclase (acrA) gene, complete cds
3880	17039		0.6	8.6E-02	U29187.1	NT	Mus musculus long incubation prion protein (Prnpb) and prion-like protein (Prnd) genes, complete cds
4609	17746	30725	0.66	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
5330	18443		1.02	8.6E-02	AB011163.1	NT	Homo sapiens mRNA for KIAA0591 protein, partial cds
6219	19394	32743	4.74	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6504	19670	33035	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6504	19670	33036	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7755	20814	34306	0.89	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8115	21197	34716	1.09	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8115	21197	34717	1.09	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8261	21343	34860	0.56	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8324	21408		0.76	8.6E-02	U60168.1	NT	Dictyostelium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9938	22977	36568	1.24	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9975	23014		1.4	8.6E-02	AW662153.1	EST_HUMAN	hi20c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972846 3'
10356	23391	37001	1.07	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11188	24257	37892	1.82	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11188	24257	37893	1.82	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11527	24583	38259	3.02	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11527	24583	38260	3.02	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11724	23910	37534	7.67	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11875	24863	38559	2.29	8.6E-02	AF283660.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2470	15597	28722	2.58	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5292	18410		0.66	8.5E-02	N76915.1	EST_HUMAN	yv46h08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245823 5'
5786	18978	32283	0.73	8.5E-02	AA985491.1	EST_HUMAN	oq83b07.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5826	19016		1.99	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6135	19314	32653	6.61	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8805	21884	35424	1.98	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
10041	23079	36680	3.27	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10041	23079	36681	3.27	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10572	23607	37212	0.64	8.5E-02	X76731.1	NT	V.ammodytes gene for ammodytoxin C
10702	23735	37340	0.82	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11424	24485		8.03	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11446	24507	38173	3.82	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12873	25886		2.76	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
13070	25700		2.44	8.5E-02	AA362934.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2732	16070	28961	4.05	8.4E-02	W69330.1	EST_HUMAN	zd44e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5427	18627	31603	9.84	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6828	19981	33388	1.46	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8218	21300	34821	6.95	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0790-260400-162-d05 BT0790 Homo sapiens cDNA
9043	22122	35664	1.15	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 2

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10571	23606	37211	1.84	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312 O88312 GOB-4. ;
10631	23665		0.48	8.4E-02	AV730682.1	EST_HUMAN	AV730682 HTF Homo sapiens cDNA clone HTFBMG04 5'
12351	25254	32114	1.67	8.4E-02	R79408.1	EST_HUMAN	yl83h12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
3682	16845	29853	7.77	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3709	16870	29873	0.75	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3709	16870	29874	0.75	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4417	17558		0.68	8.3E-02	M54964.1	NT	C.thummi A2b region open reading frame, complete cds
6389	19558	32917	0.74	8.3E-02	AI942338.1	EST_HUMAN	wc79f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
6496	19662	33025	2.87	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8169	21251	34771	3.08	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds
8202	21284		1.06	8.3E-02	AA865285.1	EST_HUMAN	oq88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1 repetitive element ;
8495	21576		1.31	8.3E-02	AA987873.1	EST_HUMAN	oq81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
9738	22803	36377	1.09	8.3E-02	AW583503.1	EST_HUMAN	ia05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
9751	22689		2.02	8.3E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10549	23584		0.72	8.3E-02	AF020409.1	NT	Dictyostelium discoideum DocA (docA) mRNA, complete cds
12448	26128		1.81	8.3E-02	BE958458.1	EST_HUMAN	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929893 5'
1410	14564		9.13	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
1525	14678	27759	2.03	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3141	16317		1.97	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3904	17063		1.35	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4114	17268	30268	0.99	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4399	17542	30523	6.58	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4399	17542	30524	6.58	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4399	17542	30525	6.58	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5192	18314	31282	3.43	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5450	18650	31629	1.46	8.2E-02	BE897030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7165	20298	33741	3.16	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7910	20962		0.58	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
8905	21984		0.59	8.2E-02	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8971	22050	35593	3.24	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
9799	22839	36416	4.88	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9965	23004	36599	2.27	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355596 5'
12454	25318	32094	3.93	8.2E-02	AE002246.2	NT	Chlamydophila pneumoniae AR39, section 73 of 94 of the complete genome
12686	25458	32021	1.43	8.2E-02	AW862195.1	EST_HUMAN	QV4-CT0361-021299-049-b01 CT0361 Homo sapiens cDNA
12909	25875		2.58	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 6 through 28, and complete cds, alternatively spliced
1524	14677	27758	0.96	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds
5873	19063	32371	1.03	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6509	19674	33043	0.89	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7347	20427		0.83	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7756	20815		0.99	8.1E-02	AI692681.1	EST_HUMAN	wd86f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8535	21616	35151	0.56	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8535	21616	35152	0.56	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
10116	23154		1.83	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
10685	23719		0.7	8.1E-02	AW269778.1	EST_HUMAN	xv45b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816061 3'
10858	23891	37511	0.47	8.1E-02	AW450487.1	EST_HUMAN	UI-H-BI3-ako-g-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
10858	23891	37512	0.47	8.1E-02	AW450487.1	EST_HUMAN	UI-H-BI3-ako-g-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
11790	24780	38477	1.99	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	16003	26246	7.61	8.0E-02	AW954653.1	EST_HUMAN	EST366723 MAGE resequences, MAGC Homo sapiens cDNA
959	14132	27191	0.65	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1733	16046	27974	11.83	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1733	16046	27975	11.83	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1952	15095	28196	4.4	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2447	15575	28704	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2447	15575	28705	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2541	15666		3.21	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2881	14280	27336	1.55	8.0E-02	M23449.1	NT	Dictyoselium discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2965	15141	29159	1.05	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3919	17078	30075	0.93	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
4182	17332		0.74	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4935	18065		6.87	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
5038	18166	31142	0.82	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene,s complete cds, and small nuclear RNAs (uRNAs)
6012	19196	32513	3.59	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7330	19196	32513	1.61	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8319	21401	34926	2.41	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9589	22644	36213	1.38	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
9589	22644	36214	1.38	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
10361	23396		0.49	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11032	24111	37747	2.64	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12127	25107	38811	1.69	8.0E-02	4507608	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9) mRNA
12486	25337	32061	3.54	8.0E-02	AJ005376.1	NT	Drosophila orena hunchback region
13134	17332		1.85	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2243	15376	28504	3.37	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
3043	16219	29240	12.63	7.9E-02	AI582029.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
3953	17111	30110	4.47	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3953	17111	30111	4.47	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4932	18062		1.16	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6836	19989		1.14	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
8221	21303	34824	3.1	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
10234	23269	36859	5.6	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611 ;
10234	23269	36860	5.6	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611 ;
13008	25664		1.27	7.9E-02	AI761639.1	EST_HUMAN	wg66h01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
1237	14396	27457	1.49	7.8E-02	AI793275.1	EST_HUMAN	oo59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.t3 L1 repetitive element ;
1237	14396	27458	1.49	7.8E-02	AI793275.1	EST_HUMAN	oo59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.t3 L1 repetitive element ;
4915	18045	31035	0.6	7.8E-02	BE836331.1	EST_HUMAN	PM3-FN0058-140700-005-f09 FN0058 Homo sapiens cDNA
5198	17003		2.97	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
7223	20087	33504	1.1	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7223	20087	33505	1.1	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8985	22064	35604	0.93	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
9081	22160	35702	0.69	7.8E-02	X78344.1	NT	S.cerevisiae CAT8 gene
9253	22330	35877	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9253	22330	35878	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9561	22703	36269	0.9	7.8E-02	AA469354.1	EST_HUMAN	nc68b06.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:771731
10006	23044	36637	0.56	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
10901	23985	37616	2.19	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12910	25602	31973	1.35	7.8E-02	U72847.1	NT	Homo sapiens envoplakin (EVPL) gene, exons 15 through 18
1431	16038	27659	1.22	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3677	16840		2.01	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
8093	21175	34690	5.38	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN. ;
10040	23078	36679	4.88	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10336	23371	36981	0.84	7.7E-02	AI318662.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10336	23371	36982	0.84	7.7E-02	AI318662.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
11262	24331	37972	3.98	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
3474	16641	29660	3.1	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3494	16661	29673	0.98	7.6E-02	AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3649	16812	29825	0.96	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6222	19397	32746	0.69	7.6E-02	AI061275.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
6486	19653	33015	1.14	7.6E-02	BE379328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9570	22712	36280	1.11	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10101	23139		0.99	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10424	23459	37064	0.5	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0545-020800-017-d06 HT0545 Homo sapiens cDNA
10557	23592		1.04	7.6E-02	BE959638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10815	23848	37469	0.97	7.6E-02	X92656.1	NT	L.esculentum mRNA for triose phosphate translocator

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10815	23848	37470	0.97	7.6E-02	X92656.1	NT	L.esculentum mRNA for triose phosphate translocator
11974	24959	38661	1.93	7.6E-02	AW996645.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
807	13987	27039	1.66	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
807	13987	27040	1.66	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1971	15114	28214	0.99	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4630	17766	30748	0.74	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5974	19159	32477	1.45	7.5E-02	AI948714.1	EST_HUMAN	wq24h09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8533	21614	35150	1.28	7.5E-02	AI864367.1	EST_HUMAN	wl52b02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8705	21785	35318	1.36	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
10238	23273		0.49	7.5E-02	BF221730.1	EST_HUMAN	7o61c05.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element MER27 repetitive element ;
10711	23744	37350	0.73	7.5E-02	BF206809.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10816	23849	37471	0.82	7.5E-02	X79460.1	NT	C.fimi DSM 20113 16S rDNA
490	13684	26718	1.41	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1489	14642		1.21	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2648	15771		0.96	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3683	16846	29854	1.21	7.4E-02	AI807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4826	17959	30946	1.19	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4914	18044	31034	2.65	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5056	18184	31159	4.42	7.4E-02	6678492	NT	Mus musculus ubiquintin c-terminal hydrolase related polypeptide (Uchrp), mRNA
6624	19784		1.69	7.4E-02	R17477.1	EST_HUMAN	yg14g06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5'
6717	19875	33266	0.66	7.4E-02	AF030422.1	NT	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
7636	20705	34184	0.64	7.4E-02	AA605132.1	EST_HUMAN	no71d02.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
8085	21167	34683	1.11	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
8699	21779	35312	1.26	7.4E-02	U56089.1	NT	Human periodic tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9367	22442	36002	1.08	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2. ;
9367	22442	36003	1.08	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2. ;
9639	21082	34593	0.58	7.4E-02	AI672939.1	EST_HUMAN	we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9639	21082	34594	0.58	7.4E-02	AI672939.1	EST_HUMAN	we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'

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10019	23057	36653	1	7.4E-02	U62293.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10146	23184	36780	0.49	7.4E-02	BF512678.1	EST_HUMAN	UI-H-BW1-amg-g-06-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
11266	24335	37975	1.46	7.4E-02	AA059167.1	EST_HUMAN	zf64e01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
11914	24901	38604	1.42	7.4E-02	AI125063.1	EST_HUMAN	ao11d07.s1 Barstead aorta HPLRB3 Homo sapiens cDNA clone IMAGE:1726285 3' similar to gb:M86492 GLIA MATURATION FACTOR BETA (HUMAN);
12409	25288		1.22	7.4E-02	11525893	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12892	26101		3.74	7.4E-02	AW379431.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
12870	25580	31995	2.61	7.4E-02	BF035099.1	EST_HUMAN	601453813F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857738 5'
12882	25585	31968	1.44	7.4E-02	AJ223459.2	NT	Aspergillus nidulans prnD, prnX, prnA genes
481	13676	26708	1.15	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
481	13676	26709	1.15	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
702	13885	26917	2.65	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 136 of the complete genome
1510	16040	27748	3.26	7.3E-02	AW900281.1	EST_HUMAN	CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1893	16050		15.79	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5112	18240		1.02	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6582	19744	33126	1.46	7.3E-02	AA779977.1	EST_HUMAN	zj24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7633	20702	34180	2.37	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7633	20702	34181	2.37	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7981	21030		0.58	7.3E-02	BF316067.1	EST_HUMAN	601896047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125515 5'
8361	21442		1.36	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8596	21677	35214	0.5	7.3E-02	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
9411	22485		1.17	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11492	19744	33126	1.78	7.3E-02	AA779977.1	EST_HUMAN	zj24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
122	13352	26382	0.6	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
122	13352	26383	0.6	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1505	14658	27739	2.6	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1505	14658	27740	2.6	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2614	15738		3.34	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3991	17148	30154	0.63	7.2E-02	AW298322.1	EST_HUMAN	UI-H-BW0-ajl-a-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'

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4465	17605	30583	3.07	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5402	18604	31576	2.73	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5403	18605	31577	8.76	7.2E-02	P11120	SWISSPROT	CALMODULIN
6244	19418		1.11	7.2E-02	BF217596.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7318	20400	33863	1.32	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7335	20416	33878	0.7	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7359	20438		1.53	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8382	21463	34987	0.6	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8382	21463	34988	0.6	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9264	22341		0.57	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
9775	22815		0.51	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9811	22851	36430	2.19	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'
9961	23000	36596	4.88	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10118	23156	36754	0.96	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5'
10206	23242	36833	2.34	7.2E-02	AW873187.1	EST_HUMAN	hq24f11.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
10395	23430	37037	0.8	7.2E-02	AA768204.1	EST_HUMAN	oa62c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10560	23595	37201	2.15	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10692	23725	37331	5.57	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10716	23749		3.47	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10837	23870	37492	0.55	7.2E-02	AA706897.1	EST_HUMAN	zj28h05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451641 3'
11153	24224	37853	4.14	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
12315	25230	32104	2.12	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12350	25253		3.63	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
12411	25290		2.05	7.2E-02	AA584465.1	EST_HUMAN	no05h08.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
12474	25327		4.23	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12488	25937		7.37	7.2E-02	AW900962.1	EST_HUMAN	CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
13048	25687		1.63	7.2E-02	AA401779.1	EST_HUMAN	zt57c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 5'
1953	15098	28197	2.05	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds

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2366	15497	28623	6.8	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4092981 5'
8091	21173	34687	1.06	7.1E-02	AI125264.1	EST_HUMAN	qd92a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
10866	23898	37521	0.53	7.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12193	25150		6.48	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
541	13734	26758	1.4	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1529	14682		1.28	7.0E-02	X96677.1	NT	M.artiellia Mtcut-1 gene
1601	14950	28044	1.18	7.0E-02	AA056343.1	EST_HUMAN	zl66f04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
3095	16271	29286	2.02	7.0E-02	AW138152.1	EST_HUMAN	UI-H-BI1-acy-c-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
4004	17161	30167	0.65	7.0E-02	AA815438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
4155	17307	30301	1.19	7.0E-02	BE070264.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4258	17403		1.14	7.0E-02	AW792962.1	EST_HUMAN	CM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4330	17473	30458	1.19	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5045	18173	31150	7.97	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
5493	18692		0.92	7.0E-02	Y09143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7560	20632	34107	0.9	7.0E-02	AV689285.1	EST_HUMAN	AV689285 GKC Homo sapiens cDNA clone GKCCAE06 5'
7762	20838	34331	0.68	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial aczonin, XL spliced variant (acz gene)
9299	22375	35926	1.24	7.0E-02	9628113	NT	African swine fever virus, complete genome
9797	22837	36415	1.31	7.0E-02	K02901.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
10158	23195	36791	0.88	7.0E-02	U27266.1	NT	Human myosin binding protein H (MyBP-H) gene, complete cds
11654	24733	38424	2.6	7.0E-02	AA724295.1	EST_HUMAN	ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837 TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
13022	25673	31958	1.2	7.0E-02	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
527	13720	26744	7.08	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
527	13720	26745	7.08	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1364	14518		1.58	6.9E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3893	17052	30051	1.34	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3893	17052	30052	1.34	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5302	18419	31389	4.11	6.9E-02	Z79163.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA24F7
5316	18433	31403	0.83	6.9E-02	M34956.1	NT	M.hyorhinis 115 kDa protein (p115) gene, complete cds
7793	20849		0.87	6.9E-02	AF164967.1	NT	Canine distemper virus strain A75/17, complete genome
8242	21324		1.14	6.9E-02	U12022.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
8750	21829	35368	1.01	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8750	21829	35367	1.01	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9320	22396	35949	0.67	6.9E-02	U22967.1	NT	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11374	24435	38092	1.46	6.9E-02	S81752.1	NT	DPH2L=candidate tumor suppressor gene {ovarian cancer critical region of deletion} [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
11374	24435	38093	1.46	6.9E-02	S81752.1	NT	DPH2L=candidate tumor suppressor gene {ovarian cancer critical region of deletion} [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
12346	25251		10.94	6.9E-02	X74315.1	NT	X.laevis XFD2 mRNA for fork head protein
12524	25357		1.56	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG
12770	25513		3.37	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1932	15075	28177	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1932	15075	28178	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1956	15099	28199	3.85	6.8E-02	AF156673.1	NT	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds
4675	17810		0.64	6.8E-02	BE141076.1	EST_HUMAN	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
6758	19914		0.65	6.8E-02	P20792	SWISSPROT	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
7040	20093		0.99	6.8E-02	BE061890.1	EST_HUMAN	RC1-BT0254-090300-017-d09 BT0254 Homo sapiens cDNA
7432	20509	33981	8.22	6.8E-02	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
7881	20915	34420	0.6	6.8E-02	U16856.1	NT	Dictyostelium discoideum myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8483	21564	35099	6.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
8483	21564	35100	6.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
12141	26155		1.47	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Stratagene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1
12276	25206		1.64	6.8E-02	AA758014.1	EST_HUMAN	ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
12906	25599		1.34	6.8E-02	AW975839.1	EST_HUMAN	EST387948 MAGE resequences, MAGN Homo sapiens cDNA
12972	25632		2.3	6.8E-02	9910585	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
13203	26091	31660	1.24	6.8E-02	6978885	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1558	14711		2.71	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1942	15035	28186	2.17	6.7E-02	AI220285.1	EST_HUMAN	qg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
3811	16971	29973	4.48	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)
4065	17221	30229	0.74	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
4065	17221	30230	0.74	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
7969	21019	34532	0.66	6.7E-02	W57759.1	EST_HUMAN	zd20g11.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341252 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;
8034	21117	34635	0.74	6.7E-02	X62695.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8034	21117	34636	0.74	6.7E-02	X62695.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8633	21713	35250	0.73	6.7E-02	AW082688.1	EST_HUMAN	xb61c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
9800	22840	36417	0.59	6.7E-02	AW137359.1	EST_HUMAN	UI-H-BI1-acr-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9800	22840	36418	0.59	6.7E-02	AW137359.1	EST_HUMAN	UI-H-BI1-acr-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1379	14534	27608	0.98	6.6E-02	AI735509.1	EST_HUMAN	at12e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
2252	15385	28513	3.73	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcipts
3552	16717	29731	12.38	6.6E-02	R64306.1	EST_HUMAN	yi18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3567	16732	29748	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3567	16732	29749	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4191	17341	30334	1.61	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5093	18221	31191	12.07	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5093	18221	31192	12.07	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5130	18255	31220	0.64	6.6E-02	AA393244.1	EST_HUMAN	zt74a07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
5130	18255	31221	0.64	6.6E-02	AA393244.1	EST_HUMAN	zt74a07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6714	19872	33264	3.92	6.6E-02	X06411.1	NT	P.vulgaris mRNA for chalcone synthase
6749	19905	33298	0.62	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6749	19905	33299	0.62	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6937	19905	33298	0.68	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6937	19905	33299	0.68	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
8133	21215	34736	1.51	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8669	21749	35287	0.77	6.6E-02	AF006055.1	NT	Dictyostelium discoideum darlin (darA) gene, complete cds
8979	22058		0.53	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
9121	22200	35741	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9121	22200	35742	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
10157	23194	36790	0.54	6.6E-02	AI458752.1	EST_HUMAN	tj97g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
10292	23327	36930	1.5	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
10327	23362		0.65	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10710	23743	37349	0.49	6.6E-02	BF694659.1	EST_HUMAN	602080608F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245336 5'
11205	24274	37911	4.95	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
12761	25505		4.64	6.6E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
13124	25733		1.26	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
595	13785	26805	1.57	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1011	14183	27245	1.3	6.5E-02	7706058	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1422	14576	27649	3.38	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1773	14922	28016	2.04	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 95 of 109 of the complete genome
5676	18870	32156	2.07	6.5E-02	AA443991.1	EST_HUMAN	zv46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
6673	19832	33221	0.73	6.5E-02	BF665340.1	EST_HUMAN	602118687F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276029 5'
7113	18539	31496	1.02	6.5E-02	U22661.1	NT	Azotobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
10147	23185	36781	0.57	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10147	23185	36782	0.57	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10683	23717	37323	0.81	6.5E-02	BF106300.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
10876	23960	37589	4.45	6.5E-02	AA195648.1	EST_HUMAN	zr32g05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12163	25129		3.78	6.5E-02	M21496.1	NT	Rabbit microsomal epoxide hydrolase
12533	25363		3.67	6.5E-02	AF102993.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
589	13780	26799	1.49	6.4E-02	X94549.1	NT	A.carterae precursor of peridinin-chlorophylla-protein (PCP) gene
1770	14919	28013	0.99	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
1770	14919	28014	0.99	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
5566	18763	31803	1.11	6.4E-02	AI191956.1	EST_HUMAN	qe07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element ;
6239	19413	32761	2.64	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6239	19413	32762	2.64	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6532	19696	33069	1.23	6.4E-02	AI672895.1	EST_HUMAN	we73g12.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6957	20270	33708	4.11	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
8531	21612		2.47	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
8865	21944	35478	4.17	6.4E-02	AA093305.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9327	22403	35955	0.98	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9785	22825		0.61	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA
9918	22958	36545	1.87	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10468	23503	37116	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10468	23503	37117	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12008	24993	38697	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

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12008	24993	38698	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12427	26048		2.7	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12479	25331	32056	2.61	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1793	14942	28035	2.51	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3692	16854		2.29	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6264	19438	32785	1.12	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7391	20469		1.64	6.3E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
9491	22548	36111	0.99	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exons 1-3
10218	23264	36843	3.52	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10478	23513		1.31	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10954	19438	32785	2.36	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
2549	15674	28797	1.04	6.2E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4365	17508	30489	4.22	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4458	17598		1.03	6.2E-02	AF271235.1	NT	Rattus norvegicus differentation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4705	17840		5.66	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6935	20250	33685	0.78	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds.
7805	20861	34354	0.88	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8016	21067		0.58	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9148	26225		0.92	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9544	22609	36177	0.47	6.2E-02	AA778450.1	EST_HUMAN	af20a06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9681	22730	36300	1.19	6.2E-02	6677898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
11415	24476	38140	1.42	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
11629	24709	38401	1.54	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
12263	26191		3.63	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12617	25415		1.24	6.2E-02	BE793085.1	EST_HUMAN	601583773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5'
12703	25467	32024	3.61	6.2E-02	BF112039.1	EST_HUMAN	7l37h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1] ;
266	13485	26516	3.63	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
4099	17254		2.85	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AtKC1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6240	19414		1.57	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8458	21539	35068	3.65	6.1E-02	X99268.1	NT	H.sapiens mRNA for B-HLH DNA binding protein
8861	21940	35474	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
8861	21940	35475	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10967	24048	37681	3.9	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA
12134	25114	38818	1.66	6.1E-02	AB025333.1	NT	Eptatretus burgeri mRNA for RNA polymerase III largest subunit, partial cds
12218	26093		30.03	6.1E-02	X70969.1	NT	S.japonicum mRNA for serine-enzyme
12836	25957		1.58	6.1E-02	AI886611.1	EST_HUMAN	tz59f07.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292901 3'
12993	25645		6.43	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1291	14447	27513	1.58	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2740	15857	28969	1.17	6.0E-02	AW968848.1	EST_HUMAN	EST380924 MAGE resequences, MAGJ Homo sapiens cDNA
2832	15946		1.43	6.0E-02	AB031289.1	NT	Mesocestoides corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
3002	13335	26362	1.53	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3002	13335	26363	1.53	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3301	16475	29496	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3301	16475	29497	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3725	16886		0.76	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5514	18712		1.01	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6345	19515	32872	1	6.0E-02	AI807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.t1 L1 L1 repetitive element ;
7127	18553	31467	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7127	18553	31468	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7338	20418	33880	2.37	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
7857	20912	34417	1.78	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
8617	21597		0.46	6.0E-02	11466495	NT	Reclinomonas americana mitochondrion, complete genome
9472	22529	36092	1.29	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
9472	22529	36093	1.29	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
9606	22661	36233	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9606	22661	36234	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
10109	23147	36746	0.72	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10109	23147	36747	0.72	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11618	24669		1.42	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X69181 60S RIBOSOMAL PROTEIN L31 (HUMAN);
12921	25606		5.12	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298 O60298 KIAA0551 PROTEIN ;
239	13461	26489	5.86	5.9E-02	AW934719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
3048	16224	29246	2.77	5.9E-02	AF190269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4864	17997		0.77	5.9E-02	AF166111.1	NT	Duck parvovirus strain 90-2193 capsid protein (VP3) gene, partial cds
8817	21896	35435	2	5.9E-02	9055249	NT	Mus musculus iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
9650	21093		0.97	5.9E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
11026	24104		7.39	5.9E-02	6679870	NT	Mus musculus follistatin-like (Fstl), mRNA
11835	24824		1.35	5.9E-02	BF572539.1	EST_HUMAN	602076548F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243834 5'
11850	24839		1.37	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
956	14129		6	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
1693	14845	27929	0.97	5.8E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
3753	16914	29917	1.68	5.8E-02	AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4474	17614	30593	6.79	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4474	17614	30594	6.79	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4669	17804	30792	4.64	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4669	17804	30793	4.64	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4696	17831		2.1	5.8E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7855	20910	34414	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7855	20910	34415	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8866	21945	35479	0.61	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12365	25261		1.65	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12681	26180		4.55	5.8E-02	AA604269.1	EST_HUMAN	no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3123	16299	29312	1.14	5.7E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611 ;
3139	16315	29328	1.09	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3902	17061	30060	2.3	5.7E-02	AW966791.1	EST_HUMAN	EST378865 MAGE resequences, MAGI Homo sapiens cDNA
4807	17941		0.95	5.7E-02	M95099.1	NT	Bos taurus lysozyme gene (cow 3), complete cds

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6000	19185		0.67	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7630	20699	34175	0.68	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7630	20699	34176	0.68	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7710	20775	34260	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7710	20775	34261	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8349	21430	34954	1.45	5.7E-02	AJ296090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
10055	23093	36695	0.82	5.7E-02	6681260	NT	Mus musculus ect2 oncogene (Ect2), mRNA
11464	24523	38193	3.14	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11464	24523	38194	3.14	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11630	24710		1.66	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12586	25969		19.03	5.7E-02	D50320.1	NT	Pig DNA for SPAI-2, complete cds
12769	25512		2.17	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
12853	26042		3.04	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
13012	26165		5.21	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
13171	25759	31929	1.18	5.7E-02	R48513.1	EST_HUMAN	yj64d10.s1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element ;
1556	14709	27789	1.1	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
2362	15493		1.95	5.6E-02	BE904308.1	EST_HUMAN	601494578F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896810 5'
4763	17898	30878	1.37	5.6E-02	AB013100.1	NT	Lycopersicon esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4818	17951	30936	1.31	5.6E-02	AA290599.1	EST_HUMAN	zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6799	19954	33354	5.87	5.6E-02	AW172708.1	EST_HUMAN	xj02c10.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN. ;
7031	20167	33589	1.02	5.6E-02	AA866182.1	EST_HUMAN	od47f12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;
7301	20383	33842	3.3	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA
8010	21060	34572	1.32	5.6E-02	AI183583.1	EST_HUMAN	qd64g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9002	22081	35623	2.52	5.6E-02	BE542663.1	EST_HUMAN	6010671158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9002	22081	35624	2.52	5.6E-02	BE542663.1	EST_HUMAN	6010671158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10017	23055	36651	1.18	5.6E-02	AA482864.1	EST_HUMAN	nf49d07.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11863	24851		2.42	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2720	15838	28948	7.33	5.5E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
3286	16460	29481	3.33	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4332	17475	30459	0.98	5.5E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5776	18968	32272	3.49	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6149	18968	32272	4.32	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7535	20608	34083	1.65	5.5E-02	6755902	NT	Mus musculus tuftelin 1 (Tuft1), mRNA
8311	21393	34917	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8311	21393	34918	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9855	22895	36476	0.76	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9855	22895	36477	0.76	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9951	22990	36583	1.24	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
11271	24339	37977	6.31	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB),>
3084	16260		0.85	5.4E-02	AJ277468.1	NT	Oryza sativa rbbi3-1 gene for putative Bowman Birk trypsin inhibitor
3509	18476		8.19	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
4020	17177	30186	0.61	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8316	21398		1.18	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730
9271	22347	35897	0.51	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10938	24020	37653	1.86	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11453	24513	38180	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
11453	24513	38181	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
12463	25950		3.72	5.4E-02	U44894.1	NT	Rana catesbiana heat shock protein 30 (HSP30) mRNA, complete cds
1078	14244	27300	1.55	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1078	14244	27301	1.55	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1535	14688	27768	20.57	5.3E-02	T94759.1	EST_HUMAN	ye37f12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2566	15691	28816	3.22	5.3E-02	AJ276408.1	NT	Pseudomonas putida ttgS gene
3008	16184	29207	0.97	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3008	16184	29208	0.97	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3221	16395	29406	4.83	5.3E-02	AJ276408.1	NT	Pseudomonas putida ttgS gene
5200	18321	31290	7.98	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds

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5434	18634	31612	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5434	18634	31613	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6228	19403	32753	1.14	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7024	20160	33580	4.02	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7241	20325	33769	1.37	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7517	20590		2.3	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8061	21073	34585	0.68	5.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
8600	21681		0.68	5.3E-02	U10098.1	NT	Mus musculus 129/Sv cystatin C (cst3) gene, complete cds
9325	22401	35954	1.73	5.3E-02	X03127.1	NT	Podospora anserina mitochondrial epsilon-sen DNA
10462	23497		0.61	5.3E-02	Y07907.1	NT	D.rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and postsomitogenesis, 20-28 hpf)
10538	23573	37180	0.79	5.3E-02	X68432.1	NT	B.rerio pou[c] mRNA for transcription factor
13173	25761	31931	1.55	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2358	15489		64.04	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3183	16358	29363	2.39	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3183	16358	29364	2.39	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4050	17208	30216	0.8	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4393	17536	30515	3.31	5.2E-02	U07132.1	NT	Human steroid hormone receptor Ner-I mRNA, complete cds
5287	18406	31373	0.66	5.2E-02	AB035201.1	NT	Ratlus norvegicus mRNA for thyroglobulin, complete cds
6040	19223	32545	0.64	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6233	19408		0.94	5.2E-02	AI830965.1	EST_HUMAN	wj80e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element ;
7424	20501	33972	1.23	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8389	21470		2.39	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9931	22971	36560	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9931	22971	36561	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12725	25483		1.6	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2437	15565		0.98	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D073 5'
5161	18283	31248	0.89	5.1E-02	BE957423.2	EST_HUMAN	601653565R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
5251	18372		0.96	5.1E-02	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
5349	18462		0.74	5.1E-02	U72397.1	NT	Bacteriophage 80 alpha holin and amidase genes, complete cds
6812	19966	33370	0.79	5.1E-02	AF280369.1	NT	HIV-1 patient 96 from Italy protease (pol) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6997	18516	31508	1.73	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8447	21528	35055	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8447	21528	35056	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8542	21623	35160	1.42	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydroecdysone 3beta-reductase
9086	22165	35710	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9086	22165	35711	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10014	23052	36646	4.27	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10384	23419	37026	1.9	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
11068	24143	37778	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11068	24143	37779	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12736	25487		1.81	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
495	13690	26721	2.8	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1231	14390	27452	2.82	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2047	15188	28299	5.08	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2879	14182	27244	10.68	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3418	16587		1.36	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3684	16847		1.01	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3775	16936	29942	5.9	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
4941	18071		1.05	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6258	19432	32779	0.64	5.0E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6438	19605		1.28	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7128	18554	31469	0.58	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7709	20774	34259	10.04	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7913	20964		0.67	5.0E-02	AW062464.1	EST_HUMAN	MR0-CT0064-100899-002-g10 CT0064 Homo sapiens cDNA
10403	23438	37045	1.37	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
10855	23888		0.55	5.0E-02	BF213260.1	EST_HUMAN	601844753F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070101 5'
11782	24772	38468	2.26	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
12229	26004		4.7	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
231	13452		11.82	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
380	13588	26623	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
380	13588	26624	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2937	16114	29126	0.71	4.9E-02	U32636.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3360	16532	29546	1.85	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3660	16823		0.85	4.9E-02	AA188940.1	EST_HUMAN	zq48e12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
3681	16844	29851	0.78	4.9E-02	AA400914.1	EST_HUMAN	zt78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3681	16844	29852	0.78	4.9E-02	AA400914.1	EST_HUMAN	zt78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4964	18093	31069	2.64	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632386 3'
4964	18093	31070	2.64	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632386 3'
5486	18685	31702	1.62	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5486	18685	31703	1.62	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7292	20374	33831	1.79	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8815	21894		1.07	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8942	22021		0.61	4.9E-02	BE931532.1	EST_HUMAN	MR0-HT0408-170800-003-a08 HT0408 Homo sapiens cDNA
8954	22033	35575	0.97	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10500	23535	37145	0.64	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
10802	23835	37459	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
10802	23835	37460	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
11687	24686	38376	3.46	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12957	25624		3.23	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
340	13552	26582	1.19	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
341	13552	26582	2.61	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
501	13696	26726	11.53	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2347	15478	28610	2.08	4.8E-02	W51983.1	EST_HUMAN	zc49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3280	16454	29476	1.79	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4793	17928		1.06	4.8E-02	Z54280.1	NT	S.scrofa gene for skeletal muscle ryanodine receptor
5237	18359	31328	0.98	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
8332	21414	34940	1.41	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA
9329	22405	35957	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9329	22405	35958	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
11219	24288	37928	1.84	4.8E-02	X61236.1	NT	S.cerevisiae NUM1 gene, involved in nuclear migration control
11219	24288	37929	1.84	4.8E-02	X61236.1	NT	S.cerevisiae NUM1 gene, involved in nuclear migration control
12511	25350		1.46	4.8E-02	9632893	NT	Streptococcus thermophilus bacteriophage Sfi19, complete genome
5122	18248	31214	0.74	4.7E-02	6981261	NT	Rattus norvegicus Nestin (Nes), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6969	20197	33623	3.34	4.7E-02	W01153.1	EST_HUMAN	yz97f09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element;
7025	20161	33581	0.69	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7025	20161	33582	0.69	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7058	20111	33527	1.71	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8445	21626	35053	9.44	4.7E-02	X15543.1	NT	B.taurus mRNA for RF-36-DNA-binding protein
9154	22232	35777	1.31	4.7E-02	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
9176	22254		2.97	4.7E-02	AB026678.1	NT	Gallus gallus Wpkci-8 gene, complete cds
9428	22502	36068	7.75	4.7E-02	X15543.1	NT	B.taurus mRNA for RF-36-DNA-binding protein
9936	22975		0.7	4.7E-02	AI873042.1	EST_HUMAN	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11852	24841	38535	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11852	24841	38536	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
12446	26182		4.31	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'
281	13499	26531	0.69	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
758	13939	26984	2.89	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1320	14476		1.49	4.6E-02	AI014255.1	EST_HUMAN	em50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533 P90533 LIMA ;contains element LTR1 repetitive element ;
1390	14544	27620	5.39	4.6E-02	AV727059.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5'
2557	15682	28807	2.34	4.6E-02	AW236023.1	EST_HUMAN	xn24f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1 ;
2869	13499	26531	1.78	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3073	16249	29270	0.64	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3418	16249	29270	0.59	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3585	16249	29270	0.94	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4239	17385		0.92	4.6E-02	AF220365.1	NT	Mus musculus nucleolar RNA helicase II/Gu (ddx21) gene, complete cds
5852	19042	32348	1.57	4.6E-02	AF076962.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds
6359	19529	32887	3.67	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6359	19529	32888	3.67	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6938	20251	33687	1.41	4.6E-02	AI149574.1	EST_HUMAN	qc60b06.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.t3 L1 repetitive element ;
8007	21057	34569	0.63	4.6E-02	6978720	NT	Rattus norvegicus Cathepsin H (Ctsh), mRNA
8856	21935	35472	3.81	4.6E-02	BE154006.1	EST_HUMAN	PM0-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11689	24687	38377	3.39	4.6E-02	AA913328.1	EST_HUMAN	ol27h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'

WO 01/57272 PCT/US01/00663

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13079	25708		3.14	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
460	13655	26693	2.24	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1245	14404	27465	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1245	14404	27466	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1847	14993	28095	4.93	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2177	15312	28440	2.2	4.5E-02	AE003964.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3817	16977	29981	5.04	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6360	19530	32889	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6636	19795	33184	0.84	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7018	20154	33574	0.59	4.5E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhlA) gene; carbon monoxide dehydrogenase small subunit (cdhlB) gene, complete cds
7018	20154	33575	0.59	4.5E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhlA) gene; carbon monoxide dehydrogenase small subunit (cdhlB) gene, complete cds
8587	21668	35207	2.24	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10155	23192	36788	4.2	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to similar to neuro-D4 protein
10305	23340	36945	0.47	4.5E-02	X95508.1	NT	A.europaeum mRNA for legumin-like protein
10421	23456	37061	0.79	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12442	25313	32089	2.61	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
12891	26051	31684	3.79	4.5E-02	AA191097.1	EST_HUMAN	zq43f11.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
227	13449		4.35	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
1050	14216	27273	0.77	4.4E-02	L19295.1	NT	Drosophila melanogaster extradenticle (EXD) mRNA, complete cds
2163	15299		6.82	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2559	15684	28809	1.81	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3730	16891	29895	1.68	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4750	17885	30866	1.33	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4750	17885	30867	1.33	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7267	20350	33802	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7267	20350	33803	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8952	22031	35572	2.34	4.4E-02	AA736969.1	EST_HUMAN	nw13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11326	24389	38034	2.64	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11477	24536	38206	3.08	4.4E-02	AA496739.1	EST_HUMAN	ae33f04.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12158	25126		4.55	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12347	26192		1.65	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
802	13982	27034	7.25	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2634	15757	28871	1.55	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3516	16682	29693	9.18	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3749	16910		1.21	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6625	19785	33172	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6625	19785	33173	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6871	20023	33433	0.8	4.3E-02	AA652266.1	EST_HUMAN	ns69c12.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188886
8711	21791	35327	0.69	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9001	22080	35621	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
9001	-22080	35622	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
12412	25291		1.2	4.3E-02	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
845	14023	27081	1.74	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
889	14065		2.4	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
919	14094	27159	1.51	4.2E-02	AW003645.1	EST_HUMAN	wx34g01.x1 NCI_CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 MRNA ;contains L1.t3 L1 L1 repetitive element ;
1758	14907		1.37	4.2E-02	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1819	14968	28060	0.99	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3754	16915	29918	1.66	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4865	17998	30982	0.59	4.2E-02	BF342995.1	EST_HUMAN	602017105F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4152672 5'
5735	18928	32224	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5735	18928	32225	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7122	18548	31460	0.61	4.2E-02	BE268285.1	EST_HUMAN	601124596F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2989319 5'
7695	20760	34244	4.35	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7717	20781	34267	0.61	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
9010	22089	35631	3.82	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10367	23402	37013	1.46	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)

WO 01/57272 PCT/US01/00663

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11295	24361	38002	1.52	4.2E-02	AA976118.1	EST_HUMAN	on33b11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65290 INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11587	24640	38320	2.83	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11587	24640	38321	2.83	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11795	24785	38483	1.52	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
12729	26109		6.64	4.2E-02	AI983494.1	EST_HUMAN	wt49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
13076	25705		1.17	4.2E-02	D14711.1	NT	Staphylococcus aureus HSP10 and HSP60 genes
523	13716	26743	1.85	4.1E-02	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
2741	15858	28970	1.06	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4005	17162	30168	0.61	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4005	17162	30169	0.61	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4595	17732		8.4	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-164-f06 NN0012 Homo sapiens cDNA
5229	18351		0.61	4.1E-02	X85880.1	NT	L.monocytogenes type 3 partial lap gene (strain 443)
5759	18951	32253	1.06	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5759	18951	32254	1.06	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7022	20158		0.98	4.1E-02	X75881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7248	20331	33778	1.38	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7682	20747	34228	1.79	4.1E-02	7662347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
7778	20834	34325	20.08	4.1E-02	L02110.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7942	20992	34502	2.81	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
8402	21483	35011	0.74	4.1E-02	P97857	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8845	21924	35462	0.79	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9355	22430	35988	0.87	4.1E-02	AA372398.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13112	26110	31666	9.91	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3316	16489	29507	3.85	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3900	17059	30058	1.09	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5495	18694	31710	5.31	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6343	19513	32870	0.98	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75296 O75296 R29124_1. ;
7867	20921	34428	5.99	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7929	20979		0.71	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7943	20993	34503	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7943	20993	34504	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7980	21029	34543	0.61	4.0E-02	AF288153.1	NT	Homo sapiens erythrocyte tropomodulin (E-TMOD) gene, exon 7
8914	21993	35532	2.52	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9844	22884		0.63	4.0E-02	BF679376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9869	22909	36495	2.46	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
10190	23227		1.08	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
12073	25054		1.52	4.0E-02	AJ001018.1	NT	Kluyveromyces lactis gene for Ca++ ATPase
12333	25909	31859	16.34	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1144	14309	27366	2.79	3.9E-02	BF516149.1	EST_HUMAN	UI-H-BW1-anx-h-08-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1375	14530	27603	2.15	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2016	15156	28261	3.22	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2769	15884		1.97	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5246	18367	31334	0.67	3.9E-02	AW392417.1	EST_HUMAN	RC6-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA
5279	18398	31366	0.9	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5279	18398	31367	0.9	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5849	19039	32346	1	3.9E-02	BE968841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
6977	19162	32482	0.65	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7203	20068	33478	0.97	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
8023	21106	34623	1.44	3.9E-02	BF239613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8250	21332	34849	0.6	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8250	21332	34850	0.6	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11695	21071	34582	1.56	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12184	26059		3.54	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds

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12898	25595		2.35	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
13036	25979		64.89	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5556	18754	31792	0.8	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
6212	19387	32736	1.04	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7471	20546	34018	1.72	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8864	21943		1.51	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10789	23822	37446	0.64	3.8E-02	7662563	NT	Homo sapiens PRO0514 protein (PRO0514), mRNA
10888	23972	37603	1.71	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1016	14187	27248	4.05	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2310	15442	28577	6.19	3.7E-02	AI984806.1	EST_HUMAN	wr85e08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2645	15768	28883	0.97	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3115	16291	29306	1.13	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3117	16293	29307	4.33	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3543	16708		0.91	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
7226	26216		0.95	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
7869	20923	34430	0.81	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
10219	23255		1.01	3.7E-02	AA782516.1	EST_HUMAN	ai55c09.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1360912 3'
12227	25175	38837	7.41	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12961	25945	31764	3.71	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
13069	25699		1.23	3.7E-02	11467432	NT	Odontella sinensis chloroplast, complete genome
3744	16905	29909	0.82	3.6E-02	X73221.1	NT	H.vulgare Ss1 gene for sucrose synthase
3752	16913	29916	0.9	3.6E-02	AL096806.1	NT	Homo sapiens genomic region contalning hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5313	18430	31400	0.67	3.6E-02	AL096810.1	NT	Homo sapiens genomic region contalning hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5543	18740	31758	0.61	3.6E-02	X59403.1	NT	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5543	18740	31774	0.61	3.6E-02	X59403.1	NT	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5617	18811	31880	0.66	3.6E-02	AF181722.1	NT	Homo sapiens RU2AS (RU2) mRNA, complete cds
6846	19999	33406	4.48	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6846	19999	33407	4.48	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7234	20318	33761	1.79	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds
7458	20534	34009	2.89	3.6E-02	AA714521.1	EST_HUMAN	nw20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2 TUBULIN BETA-1 CHAIN (HUMAN);
7811	20866	34360	0.94	3.6E-02	BE143078.1	EST_HUMAN	MR0-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA
9591	22646	36216	2.16	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9591	22646	36217	2.16	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9812	22852	36431	0.84	3.6E-02	BF347586.1	EST_HUMAN	602020453F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156116 5'
11456	24516	38183	1.46	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11456	24516	38184	1.46	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
918	14093	27158	0.99	3.5E-02	U09506.1	NT	Drosophila melanogaster tiggrin mRNA, complete cds
1033	14202	27260	2.43	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1595	14748	27831	1.4	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1595	14748	27832	1.4	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4329	17472	30457	1.83	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4435	17575	30556	1.11	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6351	19521	32878	1.76	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAc1), complete cds
8165	21247		0.91	3.5E-02	H29951.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
8824	21903	35443	2.93	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
10224	23260	36848	0.94	3.5E-02	X76642.1	NT	L.lactis MG1363 grpE and dnaK genes
10270	23305	36902	0.51	3.5E-02	BE561042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11785	24775	38471	1.79	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
11785	24775	38472	1.79	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
12876	25583		1.31	3.5E-02	AF009863.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S5P to TCRBV21S2A2 region
12955	25991		2.71	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
592	13783	26802	47.29	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
592	13783	26803	47.29	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
593	13783	26802	3.26	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds

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593	13783	26803	3.26	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1076	14242	27298	2.57	3.4E-02	AW274020.1	EST_HUMAN	xv26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1233	14392		5.43	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2465	15592	28717	1.7	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3517	16683	29694	1.5	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3875	17034	30032	0.81	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
4030	17186	30196	3.72	3.4E-02	AW794952.1	EST_HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4720	17855	30838	2.77	3.4E-02	X59799.1	NT	M.musculus S-antigen gene promoter region
5172	18294		1.9	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5189	18311	31277	1.81	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6993	18512	31504	4.68	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8456	21537		3.15	3.4E-02	AI869629.1	EST_HUMAN	wi99d04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3'
8947	22026	35567	1.18	3.4E-02	AA664886.1	EST_HUMAN	nu70f08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element;contains element MER25 MER25 repetitive element ;
9118	22197		5.28	3.4E-02	AA194306.1	EST_HUMAN	zq04f11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425 IPISGKPLPKVTLSRDGVPLKATMRFNTEITAENLTINLKESVTADAGRYEITAANSSGTTKAFINIVVLDRPG PPT GPVVISDITEESVTLKWEPPKYDGGSQVTNYILLKRETSTAVWTEVSATVARTMMKVMKL ... ;
9980	23019		0.66	3.4E-02	AI092719.1	EST_HUMAN	oz99h08.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 3'
383	13591		6.8	3.3E-02	AA398735.1	EST_HUMAN	zt75e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1193	14355	27413	12.43	3.3E-02	AB035867.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1669	14821	27904	1.23	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1778	14927		1.37	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2149	15285		2.02	3.3E-02	R09112.1	EST_HUMAN	yf25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
3445	16613	29631	0.86	3.3E-02	H02389.1	EST_HUMAN	yj35h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
4293	14821	27904	3.74	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4589	17726	30709	2.24	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
6560	19722	33099	25.73	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6560	19722	33100	25.73	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7677	20742	34223	0.63	3.3E-02	AF124162.1	NT	Nicotiana plumbaginifolia molybdopterin synthase sulphurylase (cnx5) gene, partial cds
9523	22588	36157	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9523	22588	36158	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'

WO 01/57272 PCT/US01/00663

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9624	22679	36248	0.57	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
9624	22679	36249	0.57	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11383	24444	38104	3.28	3.3E-02	BF691107.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12428	26303		3.1	3.3E-02	T96545.1	EST_HUMAN	ye49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
12557	25379		1.6	3.3E-02	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
12591	25398		1.85	3.3E-02	M81890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
134	13360	26394	1.79	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1150	14314	27370	6.32	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1150	14314	27371	6.32	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1812	14961	28054	1.08	3.2E-02	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2187	15322		1.09	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2902	13360	26394	0.87	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3204	16379	29389	13.21	3.2E-02	BE867353.1	EST_HUMAN	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3806	16966	29970	0.94	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4334	17477		16.42	3.2E-02	X94768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4890	18020	31006	3.85	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5310	18427	31397	0.93	3.2E-02	AW850159.1	EST_HUMAN	IL3-CT0219-271099-022-C04 CT0219 Homo sapiens cDNA
5652	18846	32127	1.49	3.2E-02	X68709.1	NT	S.griseocarneum whiG-Stv gene
5652	18846	32128	1.49	3.2E-02	X68709.1	NT	S.griseocarneum whiG-Stv gene
6653	19812	33200	2.4	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
6656	19815		30.91	3.2E-02	T89367.1	EST_HUMAN	yd33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element;contains LTR1 repetitive element ;
6743	19899	33290	3.7	3.2E-02	AF173845.1	NT	Saguinus oedipus tissue kallikrein gene, complete cds
7939	20989	34499	0.92	3.2E-02	11424049	NT	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8496	21577	35113	8.04	3.2E-02	6680565	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9141	22220		0.67	3.2E-02	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
9426	22500	36065	1.2	3.2E-02	AI278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9428	22500	36066	1.2	3.2E-02	AI278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10262	23297		4.51	3.2E-02	AA719795.1	EST_HUMAN	zg54b12.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10566	23601	37207	1.11	3.2E-02	U96762.1	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1289	14445		1.92	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1333	14490	27559	1.46	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1940	15083	28184	1.28	3.1E-02	6671564	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5378	18580	31449	1.29	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5476	18675		2.6	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5764	18956	32259	0.77	3.1E-02	BF687742.1	EST_HUMAN	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
8122	21204		0.58	3.1E-02	AV696098.1	EST_HUMAN	AV696098 GKC Homo sapiens cDNA clone GKCAVH09 5'
9142	22221	35764	0.48	3.1E-02	BE965092.2	EST_HUMAN	601658879R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886291 3'
9339	22415	35968	0.46	3.1E-02	AI872302.1	EST_HUMAN	wm57d09.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2440049 3'
10237	23272	36864	2.67	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1652	14805		2.41	3.0E-02	AF187125.1	NT	Pityokteines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2652	15775	28888	1.08	3.0E-02	AA402242.1	EST_HUMAN	zt65h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3743	16904	29908	2.82	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3839	16998		0.93	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-e09 ST0296 Homo sapiens cDNA
4058	17214		0.94	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
5164	18286	31250	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5164	18286	31251	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5507	18706		3.21	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6384	19553	32910	0.67	3.0E-02	N99615.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element ;
6384	19553	32911	0.67	3.0E-02	N99615.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element ;
6929	20244	33677	2.87	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS gene)
7047	20100	33516	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7047	20100	33517	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7218	20083	33497	1.92	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7218	20083	33498	1.92	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7380	20458	33921	1.22	3.0E-02	M86524.1	NT	Human dystrophin gene
8317	21399		0.48	3.0E-02	BF679706.1	EST_HUMAN	602154364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295654 5'
8821	21900	35439	0.55	3.0E-02	BE512670.1	EST_HUMAN	601171626F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545047 5'
8842	21921	35459	0.74	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-290600-108-c04 HT0704 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8993	22072		1.93	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10677	23711	37319	2.03	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
10770	23803	37425	0.47	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11508	24566	38243	2.26	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11989	24974	38678	7.11	3.0E-02	AA483216.1	EST_HUMAN	ne87f04.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
12536	26168	31556	1.95	3.0E-02	R32019.1	EST_HUMAN	yh63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12943	25621		11.62	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
12989	26161		4.97	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
3650	16813	29826	0.9	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4039	17195	30206	0.81	2.9E-02	H72805.1	EST_HUMAN	yu07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
6188	19364	32712	1.39	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6421	19590	32955	6.58	2.9E-02	BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
7398	20476	33943	9.95	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7584	20656	34133	0.65	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
8187	21269	34793	0.82	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
8187	21269	34794	0.82	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9859	22899	36482	2.14	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9859	22899	36483	2.14	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10078	23116		0.65	2.9E-02	AW976597.1	EST_HUMAN	EST388706 MAGE resequences, MAGN Homo sapiens cDNA
10553	23588	37196	1.25	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomic DNA, section 7/7
11303	16813	29826	1.44	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12538	26057		1.35	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5'
579	13771		0.76	2.8E-02	AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA
3453	16620	29639	1.2	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
3453	16620	29840	1.2	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
4430	17570		0.76	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5605	18800	31866	11	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
6948	20261	33699	1.08	2.8E-02	T78960.1	EST_HUMAN	yd21b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'
8523	21604	35142	1.67	2.8E-02	AJ005820.1	NT	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9219	22297	35840	0.75	2.8E-02	AA280762.1	EST_HUMAN	zs96c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9409	22483	36047	1.41	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9513	22578	36144	0.76	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
9674	22636	36207	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
9674	22636	36208	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
1518	14671	27753	0.96	2.7E-02	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
3518	16684	29695	1.99	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4319	17462	30447	1.93	2.7E-02	N47258.1	EST_HUMAN	yy86h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4319	17462	30448	1.93	2.7E-02	N47258.1	EST_HUMAN	yy86h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
5362	18565	31432	0.6	2.7E-02	BF245672.1	EST_HUMAN	601864811F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5557	18755	31793	1.43	2.7E-02	R12245.1	EST_HUMAN	yf33d09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP:JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6022	19205	32525	0.69	2.7E-02	X61670.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
6734	19890		1.02	2.7E-02	X97580.1	NT	A.bisporus pgkA gene
7213	20078	33491	1.92	2.7E-02	AA993571.1	EST_HUMAN	ot96h03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
8549	21630		1.36	2.7E-02	AI377036.1	EST_HUMAN	tc28g08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
8816	21895	35434	0.55	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
585	13776	26796	2.52	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1399	14553		0.99	2.6E-02	AW850515.1	EST_HUMAN	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
2439	15567	28694	2.6	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2441	15569	28696	4.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2441	15569	28697	4.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2982	16158		2.07	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5025	18154	31131	3.89	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5176	18298	31261	1.22	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5203	18324	31293	2.54	2.6E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
6011	19195		2.94	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6349	19519		6.85	2.6E-02	AI206030.1	EST_HUMAN	qg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6555	19717	33093	2	2.6E-02	BE621748.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6966	20194	33619	0.83	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeth

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6966	20194	33620	0.83	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeth
7050	20103	33520	5.63	2.6E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7449	20526	33999	0.65	2.6E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)
8703	21783	35316	0.73	2.6E-02	AA860946.1	EST_HUMAN	ak22f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9560	22702	36268	1.24	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9915	22955	36541	0.78	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9915	22955	36542	0.78	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10614	23648	37257	5.37	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11670	24747		1.59	2.6E-02	AA279351.1	EST_HUMAN	zs84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
11861	24849	38547	1.35	2.6E-02	AW500547.1	EST_HUMAN	UI-HF-BN0-akj-e-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
12460	26150	31553	1.43	2.6E-02	BF343827.1	EST_HUMAN	602015801F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150944 5'
12583	25392		1.32	2.6E-02	11422936	NT	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
12947	25658		1.39	2.6E-02	R43678.1	EST_HUMAN	yc86f07.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22845 3' similar to contains DBR repetitive element ;
545	13738	26762	1.75	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
545	13738	26763	1.75	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
832	14010	27066	9.54	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
892	14068	27133	5.83	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2821	15935		2.53	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
3021	16197	29219	2.95	2.5E-02	X99697.1	NT	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3021	16197	29220	2.95	2.5E-02	X99697.1	NT	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4156	18468	30302	0.92	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4156	18468	30303	0.92	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4322	17465	30450	4.66	2.5E-02	AW592114.1	EST_HUMAN	hf36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5830	19021	32327	0.72	2.5E-02	AI732776.1	EST_HUMAN	zx83c10.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810354 3'
6322	19494		4.88	2.5E-02	BE670128.1	EST_HUMAN	7e30e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.t1 L1 repetitive element ;
6338	19508		3.72	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6466	19633	32994	0.8	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7843	20898	34400	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
7843	20898	34401	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
8008	21058	34570	0.64	2.5E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8167	21249	34768	0.5	2.5E-02	BE252469.1	EST_HUMAN	601108291F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344278 5'
9025	22104	35645	0.92	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9164	22242	35785	0.57	2.5E-02	AW025821.1	EST_HUMAN	wu08c10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516370 3'
10271	23306		0.63	2.5E-02	X71303.1	NT	D.radicum 28S ribosomal RNA, D2 domain
10810	23843	37486	0.65	2.5E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1699982 3'
11048	24125	37759	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
11048	24125	37760	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
11120	24192		2.93	2.5E-02	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-li>
12065	25046		1.87	2.5E-02	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
12419	26072		2.17	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12621	25934		1.29	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
12716	25476		1.83	2.5E-02	U60169.1	NT	Dictyostelium discoideum putative protein kinase MkcA (mkcA) gene, complete cds
12750	25497	32032	1.58	2.5E-02	BE973327.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
178	13401	26431	1.44	2.4E-02	AI378582.1	EST_HUMAN	tc72c07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1628	14780	27865	1.89	2.4E-02	H65884.1	EST_HUMAN	yr75f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
2102	16054	28363	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2102	16054	28364	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4488	17628	30609	1.69	2.4E-02	J05110.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
6344	19514	32871	0.86	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
7370	20449	33912	1.2	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7386	20464	33928	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP).
7386	20464	33929	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8074	21156		0.75	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-h06 ST0186 Homo sapiens cDNA
8129	21211		0.57	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8636	21716		0.57	2.4E-02	H78376.1	EST_HUMAN	yu12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element;contains A3R repetitive element ;
8728	21808	35344	11.69	2.4E-02	N69442.1	EST_HUMAN	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294596 3' similar to gb|K02909|RATSR7K Rat (rRNA);contains A3R.b1 A3R repetitive element ;
9187	22285	35806	0.78	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
9211	22289	35831	0.81	2.4E-02	AA625660.1	EST_HUMAN	zu91c06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN);contains Alu repetitive element;contains element XTR XTR repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9893	22933	36516	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds
9893	22933	36517	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds
10011	23049	36643	2.75	2.4E-02	AV692954.1	EST_HUMAN	AV692954 GKC Homo sapiens cDNA clone GKCDSC03 5'
10186	23223	36817	2.82	2.4E-02	AA493894.1	EST_HUMAN	nh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element;contains element PTR5 repetitive element ;
10839	23872		0.5	2.4E-02	BE387111.1	EST_HUMAN	601274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615902 5'
11874	24862	38557	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11874	24862	38558	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12210	25163		3.98	2.4E-02	9627909	NT	Bacteriophage bIL67, complete genome
12362	25260	32116	4.45	2.4E-02	6753636	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
12478	25330	32055	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12478	25330	32096	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12668	25445		10.87	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12697	25464		1.26	2.4E-02	N42980.1	EST_HUMAN	yy08a06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270610 5'
12883	25900	31858	1.25	2.4E-02	AA179693.1	EST_HUMAN	zp13h01.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
1921	15064		5.25	2.3E-02	W05340.1	EST_HUMAN	za84g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5'
1936	15079		16.26	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2065	15205	28321	0.99	2.3E-02	AW797355.1	EST_HUMAN	CM2-UM0038-290400-172-b11 UM0038 Homo sapiens cDNA
2426	15554	28681	2.68	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3773	16934	29940	7.02	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
3807	16967		0.67	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3'end
4267	17412	30398	1.17	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4267	17412	30399	1.17	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4540	17678	30660	1.08	2.3E-02	AW899107.1	EST_HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4571	17709	30689	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4571	17709	30690	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4572	18469	30691	1.2	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770671 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4572	18469	30692	1.2	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770671 3'
4717	17852	30835	3.01	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4717	17852	30836	3.01	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5144	18267	31237	0.9	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-290100-011-a07 CN0051 Homo sapiens cDNA
5265	18384	31349	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5265	18384	31350	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5491	18690	31707	3.86	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6365	19535	32894	0.62	2.3E-02	BF106464.1	EST_HUMAN	601822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'
6755	19911	33306	4	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7119	18545	31456	0.69	2.3E-02	BE141475.1	EST_HUMAN	MR0-HT0080-011099-002-c09 HT0080 Homo sapiens cDNA
7619	20689	34164	0.63	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8060	21143	34661	4.52	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8667	21747	35285	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8667	21747	35286	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8894	21973	35509	0.75	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8894	21973	35510	0.75	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9338	22414	35967	0.84	2.3E-02	P41996	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10063	23101	36704	0.94	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10236	23271	36862	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10236	23271	36863	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11022	24101	37739	2.38	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12338	25919		3.61	2.3E-02	BE278331.1	EST_HUMAN	601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12801	25535	32011	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181454 5'
12801	25535	32012	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181454 5'
12919	25604	31974	2.47	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12975	26195		1.88	2.3E-02	U11077.1	NT	Dictyostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
756	13937	26982	3.59	2.2E-02	AF018267.1	NT	Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1786	14935		1.79	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1800	14949	28042	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1800	14949	28043	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2072	15212	28329	2.17	2.2E-02	Z82001.1	NT	S.pneumoniae pcpA gene and open reading frames
3521	16687		2.03	2.2E-02	AA577785.1	EST_HUMAN	nn24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3736	16897		4.09	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3956	17114	30116	0.98	2.2E-02	AW601317.1	EST_HUMAN	PM0-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
4029	17185	30195	0.99	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5177	18299	31262	1.37	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7396	20474	33941	3.43	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8566	21647	35188	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8566	21647	35189	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9009	22088	35630	0.82	2.2E-02	X79468.1	NT	P.vulgata alpha tub 2 mRNA
9856	22896	36478	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9856	22896	36479	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9888	22928	36511	2.73	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9888	22928	36512	2.73	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10409	23444		1.25	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12625	25421		6.8	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element;
432	13627		4.48	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
462	13657		6.62	2.1E-02	AF029726.1	NT	Dictyostelium discoideum histidine kinase C (dhkC) mRNA, complete cds
1292	14448	27514	6.65	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1418	14571	27644	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1418	14571	27645	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1823	14972	28065	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28066	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28067	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2019	15159	28264	0.97	2.1E-02	AF190899.1	NT	Tegula aureotincta major acrosomal protein precursor (TMAP) mRNA, complete cds
2092	15232	28354	1.16	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2092	15232	28355	1.16	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2877	13980	27032	3.12	2.1E-02	N29266.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264541 5'
3674	16837	29847	1.01	2.1E-02	AA461271.1	EST_HUMAN	zx63b09.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4249	17395	30384	0.68	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4427	17567	30549	0.89	2.1E-02	BF343655.1	EST_HUMAN	602015306F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151161 5'
4667	17705	30685	2.14	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4577	17714	30698	1.64	2.1E-02	AI768127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4831	17964	30953	5.95	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4852	17985	30973	0.75	2.1E-02	AA665737.1	EST_HUMAN	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4940	18070	31048	0.89	2.1E-02	AI823432.1	EST_HUMAN	wh54e05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5315	18432	31402	0.91	2.1E-02	BF026405.1	EST_HUMAN	601671411F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954410 5'
5756	18948	32250	0.6	2.1E-02	AW379529.1	EST_HUMAN	CM4-HT0244-111199-040-h05 HT0244 Homo sapiens cDNA
7212	20077	33490	0.73	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
8716	21796	35333	0.66	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9703	22752	36322	0.54	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element;contains element MER11 repetitive element ;
9831	22871	36453	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9831	22871	36454	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10189	23226	36820	1.15	2.1E-02	L29324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
10266	23301	36899	0.75	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element;contains element MER11 repetitive element ;
10856	23889	37508	0.49	2.1E-02	AP001519.1	NT	Bacillus halodurans genomic DNA, section 13/14
11787	24777	38474	1.48	2.1E-02	6754255	NT	Mus musculus heat shock protein, 74 kDa, A (Hspa9a), mRNA
12063	25044	38752	1.42	2.1E-02	AW844320.1	EST_HUMAN	RC4-CN0050-130200-012-h04_1 CN0050 Homo sapiens cDNA
12602	18493		11.16	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
12647	25915	31862	1.22	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
13091	25712	31938	3.82	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
19	13257	26257	1.28	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.t3 MER1 repetitive element ;
20	13258	26258	14.95	2.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
269	13488	26518	5.03	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
306	13522	26556	2.95	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
821	14000	27054	3.63	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1111	14276	27333	0.98	2.0E-02	AL096805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens
1226	14386	27448	0.91	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1226	14386	27449	0.91	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1922	15065	28168	1.84	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1922	15065	28169	1.84	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2859	15973		2.09	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3148	13257	26257	1.56	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.t3 MER1 repetitive element ;
3213	16387		1.13	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3299	16473		1.99	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
4113	17267	30267	1.57	2.0E-02	M18095.1	NT	P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5219	18341		0.74	2.0E-02	AI271995.1	EST_HUMAN	qj83e03.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1866076 3'
6018	19201	32520	0.59	2.0E-02	L35321.2	NT	Dictyostelium discoideum class VII unconventional myosin (myo1) gene, complete cds
7723	20787	34275	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
7723	20787	34276	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
10081	23119		2.39	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10570	23605	37210	1.84	2.0E-02	AI640342.1	EST_HUMAN	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
10879	23964	37592	1.65	2.0E-02	Z73966.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11653	24732	38423	1.91	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11978	24963	38664	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11978	24963	38665	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12149	18499	31535	1.8	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12644	15973		2.26	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13186	25771		5.63	2.0E-02	T80037.1	EST_HUMAN	yd04c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24675 5'
711	13893	26929	2.42	1.9E-02	AA572764.1	EST_HUMAN	nf19a07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.t1 L1 repetitive element ;
2097	15237	28358	4.85	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2097	15237	28359	4.85	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2970	16146	29164	9.15	1.9E-02	AA713856.1	EST_HUMAN	nw04f05.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
3018	16194	29217	1.92	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3332	16505		0.72	1.9E-02	AB033611.1	NT	Urotrichus talpoides mitochondrial gene for cytochrome b, complete cds
3699	16860		1.12	1.9E-02	N52250.1	EST_HUMAN	yz28b02.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284331 3'
3793	16954		8.1	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
3808	16968	29971	0.83	1.9E-02	AI301183.1	EST_HUMAN	qn04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4158	17309	30305	1.3	1.9E-02	AF141940.1	NT	Mycoplasma imitans VlhA1 precursor (vlhA1) and VlhA2 precursor (vlhA2) genes, partial cds
4310	17453	30440	1.58	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4310	17453	30441	1.58	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4663	17798	30785	2.79	1.9E-02	AI452999.1	EST_HUMAN	tj46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5125	15701	28822	4.22	1.9E-02	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5431	18631	31609	0.96	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5585	18780	31825	1.25	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
5908	19097		0.93	1.9E-02	AB019507.1	NT	Drosophila kanekoi gene for glycerol-3-phosphate dehydrogenase, complete cds
7250	20333	33780	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7250	20333	33781	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8769	21848		1.33	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9532	22597	36169	1.21	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9914	22954	36540	0.67	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10251	23288	36882	1.24	1.9E-02	BF895832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10458	23493	37104	0.67	1.9E-02	D64001.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644794
11021	24100	37738	1.91	1.9E-02	AF008938.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12372	25924	31865	4.41	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gliarin mRNA, complete cds
13006	25890		1.46	1.9E-02	L11068.1	NT	Candida albicans lambda Ca3/B fragment
358	13567	26595	1.67	1.8E-02	AW771104.1	EST_HUMAN	hn52c06.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element ;
703	13886	26918	1.81	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1186	14348	27406	1.43	1.8E-02	X17664.1	NT	H.francisci mRNA for myelin basic protein (MBP)
1467	14621	27704	1.38	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
2743	15860	28972	1.74	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3282	16456		0.94	1.8E-02	AI805829.1	EST_HUMAN	te52e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3993	17150	30156	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3993	17150	30157	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4197	17347		1.01	1.8E-02	AA861446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4550	17688	30669	1.52	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
5069	18197	31171	2.02	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845O24.2
6949	20262	33700	4.44	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7624	20694	34170	2.3	1.8E-02	BF125690.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
7650	20694	34170	0.61	1.8E-02	BF125690.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'

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8322	21404	34931	0.88	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8663	21743	35283	0.46	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-159-h09 NN1073 Homo sapiens cDNA
8710	21790	35326	0.76	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Mtap2), mRNA
9693	22742	36311	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9693	22742	36312	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9842	22882		2.23	1.8E-02	AA897543.1	EST_HUMAN	aj52f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN);
10268	23303	36900	1.7	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866963 5'
10431	23466	37072	1.29	1.8E-02	X96933.1	NT	L.stagnalis mRNA for myomodulin neuropeptide precursor
11721	23907	37530	1.76	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11721	23907	37531	1.76	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11912	24899	38602	1.55	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7)
11926	24912	38613	2.45	1.8E-02	U52749.1	NT	Zea mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA, partial cds
13096	25894		1.78	1.8E-02	AF202180.1	NT	Plasmodium falciparum erythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
929	14104	27167	1.34	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1831	14979	28075	2.12	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element ;
1831	14979	28076	2.12	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element ;
1920	15063		2.85	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2181	15316		13.13	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2705	15823		1.36	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3062	16238	29259	0.89	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3602	16766		4.64	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element ;
3716	16877		0.83	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4284	17429		1.23	1.7E-02	AA669618.1	EST_HUMAN	ac19f04.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element;contains element MER24 repetitive element ;
4317	17460		2.02	1.7E-02	R02506.1	EST_HUMAN	ye86f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4576	17713	30697	0.74	1.7E-02	AI305279.1	EST_HUMAN	qm08g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4649	17785	30768	1.32	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element ;

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4836	17969	30957	1.91	1.7E-02	V00641.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4934	18064		5.98	1.7E-02	AI015076.1	EST_HUMAN	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
6253	19427	32773	1.69	1.7E-02	AI769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6709	19867	33256	1.23	1.7E-02	AI038280.1	EST_HUMAN	oy85h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
7195	20060	33471	1.26	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7353	20432	33894	1.9	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7513	20587	34060	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7513	20587	34061	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7921	20972		1.71	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
9636	21079	34591	0.89	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9900	22940	36526	1.28	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434I0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I0314 5'
12093	25073	38780	1.66	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE55), mRNA
12991	26111	31667	2.35	1.7E-02	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-f06 NN1030 Homo sapiens cDNA
13166	25757	31928	1.46	1.7E-02	AA846926.1	EST_HUMAN	oe08d04.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1 repetitive element ;
524	13717		4.05	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1889	14841	27926	1.37	1.6E-02	Y18889.1	NT	Treponema maltophilum flaB2, flaB3 and fliD genes for flagellin subunit proteins and CAP protein homologue
2323	15455	28586	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2323	15455	28587	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2631	15754	28869	0.97	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQT1 gene
2708	15826	28941	1.75	1.6E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2758	15875		1.01	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3614	16778	29793	5.33	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
4291	17436		1.96	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4415	17556	30543	2.04	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-f07 PT0012 Homo sapiens cDNA
5367	18570	31438	0.59	1.6E-02	AI281385.1	EST_HUMAN	qu42b09.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1967417 3'
5741	18934	32234	1.42	1.6E-02	6671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6780	19935	33331	2.16	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7071	20124	33539	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7071	20124	33540	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7888	20940	34446	0.96	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8312	21394	34919	0.74	1.6E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8372	21453		3.37	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10246	23281		2.97	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10633	23667	37276	1.61	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. [1];
10633	23667	37277	1.61	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. [1];
11149	25868	37848	2.9	1.6E-02	Z94828.1	NT	G.gallus microsatellite DNA (LEI0260 (=T16IIIE11))
11488	24547	38219	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11488	24547	38220	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11801	24791	38488	2.16	1.6E-02	AI373558.1	EST_HUMAN	qz96e10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
12348	15455	28586	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12348	15455	28587	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
770	13951		9.38	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2209	15343	28469	3.58	1.5E-02	N39521.1	EST_HUMAN	yv27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243926 3'
2244	15377	28505	1.6	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3128	16304	29317	1.04	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3128	16304	29318	1.04	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3818	16978	29982	1.14	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
4590	17727	30710	0.72	1.5E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6423	19592	32957	2.07	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
7472	20547		1.69	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7561	20633	34108	1.57	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8058	21141	34660	1.38	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8065	21147	34668	3.06	1.5E-02	11417739	NT	Homo sapiens valyl-tRNA synthetase 2 (VARS2), mRNA
9030	22109	35650	1.42	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154504 5'
9668	22630		0.58	1.5E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9770	22766	36337	1.59	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10016	23054	36649	1.3	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10016	23054	36650	1.3	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10860	23893	37514	0.46	1.5E-02	T92196.1	EST_HUMAN	ye17f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118027 3'
11056	24133		1.78	1.5E-02	D26547.1	NT	Rice gene for thioredoxin h, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11442	24503	38171	2.21	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12576	25970		2.38	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
430	13625		1.54	1.4E-02	AE002230.2	NT	Chlamydophila pneumoniae AR39, section 58 of 94 of the complete genome
1142	14307	27363	3.81	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51226), mRNA
1285	14441		2.12	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1326	14483		2.49	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
3284	16458	29478	1.83	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xylR) gene, partial cds
3485	16653	29658	1.23	1.4E-02	AW074212.1	EST_HUMAN	xb09d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3573	16738	29753	6.9	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3573	16738	29754	6.9	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3608	16772	29787	0.75	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3746	16907	29911	12.14	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4612	17749	30729	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cDNA
4612	17749	30730	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cDNA
4998	18127	31102	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4998	18127	31103	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5911	26210		0.74	1.4E-02	X91338.1	NT	H.sapiens La/SS-B pseudogene 3
6545	19707	33083	4.52	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
6545	19707	33084	4.52	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
8333	21415		1.55	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9099	22178	35722	1.44	1.4E-02	M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9356	22431	35989	1.41	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9600	22655	36227	1.66	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10780	23813		0.89	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
12258	25194	38358	8.95	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12640	25430		1.84	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12959	25625		1.45	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
13075	25704		1.51	1.4E-02	AF238059.2	NT	Rheum x cultorum NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product

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1913	15056		1.19	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
2010	15150	28254	2.13	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2512	15638	28759	0.98	1.3E-02	AE002445.1	NT	Neisseria meningitidis serogroup B strain MC58 section 87 of 206 of the complete genome
3285	16459	29479	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3285	16459	29480	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
4076	17232		1.22	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5275	18394		3.02	1.3E-02	D26547.1	NT	Rice gene for thioredoxin h, complete cds
5360	18563	31478	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5360	18563	31479	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6293	19466	32819	1.2	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6327	19499	32856	1.05	1.3E-02	M62962.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7101	18528	31481	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7101	18528	31482	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7752	20812	34303	4.9	1.3E-02	AI031593.1	EST_HUMAN	ow06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8678	21758	35294	1.67	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10411	23446	37051	1.89	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10485	23520	37129	0.95	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
11239	24308	37944	3.35	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11239	24308	37945	3.35	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12645	26127		1.7	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12753	25499		2.56	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
12965	25885		30.16	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
219	13441		0.82	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
365	13575	26606	4.38	1.2E-02	AA059299.1	EST_HUMAN	zf65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element ;
465	13660	26696	1.43	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
757	13938	26983	2.67	1.2E-02	AI183522.1	EST_HUMAN	qd68e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1 repetitive element ;
2246	15379	28507	2.03	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013

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2514	15640	28762	1.02	1.2E-02	AW172350.1	EST_HUMAN	xj37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2701	15640	28762	1.43	1.2E-02	AW172350.1	EST_HUMAN	xj37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3170	16345		7.3	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3359	16531	29545	2.05	1.2E-02	R62805.1	EST_HUMAN	yi11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3362	16534	29548	0.59	1.2E-02	AI668694.1	EST_HUMAN	zb66a07.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element ;
5035	18163	31139	2.02	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5154	18276		1.97	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiqT mRNA, partial cds
5195	18317	31286	1.31	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5871	19061	32368	1.78	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6243	19417	32765	0.72	1.2E-02	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7147	20282	33724	8.67	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7443	20520	33993	1.42	1.2E-02	H02197.1	EST_HUMAN	yj34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7465	20540	34014	8.54	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
7729	20791	34280	0.66	1.2E-02	BF216650.1	EST_HUMAN	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
8186	21268	34792	2.3	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
8321	21403	34929	0.56	1.2E-02	R68831.1	EST_HUMAN	yi43f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8321	21403	34930	0.56	1.2E-02	R68831.1	EST_HUMAN	yi43f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8386	21467	34993	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8386	21467	34994	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
9091	22170		1	1.2E-02	T76987.1	EST_HUMAN	yd72c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'
9839	22879	36461	2.54	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9872	22912	36497	1.24	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12757	25986		1.16	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
12974	25634		6.24	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-557G06 5'
1298	14454	27520	1.22	1.1E-02	AA070364.1	EST_HUMAN	zm69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1743	14892	27986	1.48	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
1743	14892	27987	1.48	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
2096	15236	28357	5.35	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5'

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2942	16119		5.31	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5'
3612	16776	29792	3.59	1.1E-02	AI653508.1	EST_HUMAN	tq95b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPF_HUMAN Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4222	17370		0.66	1.1E-02	AW813796.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
4951	18081	31057	1.27	1.1E-02	AL048383.2	EST_HUMAN	DKFZp586E0924_s1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586E0924
6277	19451	32800	0.89	1.1E-02	U66480.1	NT	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynaB), YnaC (ynaC), YnaD (ynaD), YnaE (ynaE), YnaF (ynaF), YnaG (ynaG), YnaH (ynaH), YnaI (ynaI), YnaJ (ynaJ), xylan beta-1,4-xylosi>
7773	20830	34321	2.19	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
7989	21039	34551	1.25	1.1E-02	9631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
8451	21532	35061	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8451	21532	35062	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8841	21920	35458	0.69	1.1E-02	AW996160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
9022	22101	35641	0.7	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4040
9103	22182	35727	7.44	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10133	23171	36769	2.02	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10299	23334	36939	4.06	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
11224	24293	37934	2.41	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
12195	25152		4.01	1.1E-02	AA668239.1	EST_HUMAN	ab77f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains Alu repetitive element;
7	13245	26247	8.82	1.0E-02	AW846120.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
1552	14705	27785	0.97	1.0E-02	AW368128.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
2638	15761		1.71	1.0E-02	AA806389.1	EST_HUMAN	oc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3159	16334	29344	2.88	1.0E-02	BE835556.1	EST_HUMAN	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3336	16509	29525	1.24	1.0E-02	BE968999.1	EST_HUMAN	601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3598	16762		0.7	1.0E-02	AW845621.1	EST_HUMAN	MR0-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
3986	17143	30148	0.85	1.0E-02	AI065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4002	17159	30165	0.59	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4899	18029	31017	5	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Crhr2), mRNA
4969	18098	31074	4.14	1.0E-02	R96567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
5116	18243	31208	0.83	1.0E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5242	18364	31332	1.96	1.0E-02	P06599	SWISSPROT	EXTENSIN PRECURSOR
5532	18729	31745	0.81	1.0E-02	H52681.1	EST_HUMAN	yu36h11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5865	19055	32362	0.66	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6242	19416	32764	1.29	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Syt2) gene, complete cds
6310	19482	32836	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6310	19482	32837	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6901	20216	33646	1.69	1.0E-02	Z29642.1	NT	Z.mays U3snRNA pseudogene
9593	22648	36219	6.34	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9593	22648	36220	6.34	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11542	24598		2.12	1.0E-02	AF157559.1	NT	Crithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11573	24628		1.7	1.0E-02	AI417961.1	EST_HUMAN	tg55h07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183_cds1 HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN);contains Alu repetitive element;contains element MER5 repetitive element ;
11649	24728	38420	1.95	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12278	26206		1.76	1.0E-02	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12339	25941	31762	3.58	1.0E-02	AW935521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12355	26002		4.31	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12764	25974		1.4	1.0E-02	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12949	26060		2.91	1.0E-02	X62654.1	NT	H.sapiens gene for Me491/CD63 antigen
916	14091	27156	5.69	9.0E-03	AI796126.1	EST_HUMAN	wh42f09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element MER22 MER22 repetitive element ;
1293	14449		1.66	9.0E-03	BE781889.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2469	15598	28721	2.64	9.0E-03	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2971	16147	29165	0.81	9.0E-03	AI251744.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
2971	16147	29166	0.81	9.0E-03	AI251744.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3758	16919	29921	0.66	9.0E-03	J05184.1	NT	S.acidocaldarius thermopsin gene, complete cds
5931	19117		1.19	9.0E-03	AI809792.1	EST_HUMAN	wf77f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
6788	19922		4.01	9.0E-03	BE745988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7623	20693	34169	0.61	9.0E-03	AI242219.1	EST_HUMAN	qh87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7640	20709	34188	0.91	9.0E-03	6922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
8059	21142		0.8	9.0E-03	AL039991.1	EST_HUMAN	DKFZp434L0412_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0412 5'
8443	21524		0.54	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10050	23088	36690	0.54	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)
10066	23104	36707	1.47	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR

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11232	24301		1.68	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
11951	24937	38638	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
11951	24937	38639	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12494	26208		2.07	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
12722	26200		37.58	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12838	25558	32016	1.21	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
13074	25703		17.6	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
514	13708		3.15	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element;
1013	14185	27246	12.69	8.0E-03	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2226	15360	28489	1.87	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2617	15741	28853	3.05	8.0E-03	P10266	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3442	16610	29628	1.02	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3766	16927	29930	1.81	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3766	16927	29931	1.81	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4372	17515	30495	1.15	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4502	17642	30627	5.73	8.0E-03	BF363327.1	EST_HUMAN	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
4839	17972	30961	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4839	17972	30962	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5271	18390	31358	0.94	8.0E-03	AU140261.1	EST_HUMAN	AU140261 PLACE2 Homo sapiens cDNA clone PLACE2000223 5'
5640	18834	31911	2.8	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6328	25823	32857	1.27	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
6889	20041	33450	4.4	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
7059	20112		1.06	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7357	20436	33898	1.43	8.0E-03	M17197.1	NT	A.californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
7714	20779		1.8	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
9084	22163	35707	0.64	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
9111	22190	35734	3.53	8.0E-03	AW808692.1	EST_HUMAN	MR1-ST0111-111199-011-h06 ST0111 Homo sapiens cDNA
9180	22258	35801	0.68	8.0E-03	9789956	NT	Mus musculus fusion 2 (human) (Fus2), mRNA
10154	23191		4.75	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA

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11005	24084	37721	2.01	8.0E-03	BE788441.1	EST_HUMAN	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
11231	24300		2.79	8.0E-03	Z49852.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
11663	24742	38433	1.39	8.0E-03	AA828817.1	EST_HUMAN	od80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11663	24742	38434	1.39	8.0E-03	AA828817.1	EST_HUMAN	od80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12015	24999	38701	4.37	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
12205	25159		1.89	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
12252	25191		7.14	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
13145	25959		1.16	8.0E-03	AI277806.1	EST_HUMAN	qm55c09.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1892752 3'
712	13894	26930	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
712	13894	26931	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
999	14170	27231	3.26	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1140	14305	27361	3.55	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1395	14549		1.03	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1426	14580	27653	3.39	7.0E-03	AA668298.1	EST_HUMAN	ab79b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
1532	14685	27764	3.28	7.0E-03	AW303599.1	EST_HUMAN	xv21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2332	16060	28598	2	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2695	15815		0.98	7.0E-03	AW772132.1	EST_HUMAN	hn67h07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032989 3' similar to contains Alu repetitive element;
3648	16811	29824	0.65	7.0E-03	AI150273.1	EST_HUMAN	qf34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3863	17023	30022	0.71	7.0E-03	AW444463.1	EST_HUMAN	UI-H-BI3-akb-c-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
3914	17073	30071	1.13	7.0E-03	AF196344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4128	17023	30022	0.77	7.0E-03	AW444463.1	EST_HUMAN	UI-H-BI3-akb-c-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4721	17856		0.98	7.0E-03	AW630888.1	EST_HUMAN	hh89a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969936 5'
5103	18231		6.54	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5940	19126		0.72	7.0E-03	H71106.1	EST_HUMAN	yr82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
6238	25821		4.42	7.0E-03	AW861059.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6444	19511	32974	1.67	7.0E-03	W68251.1	EST_HUMAN	zd33f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
6667	19826	33213	2.92	7.0E-03	AA327129.1	EST_HUMAN	EST30674 Colon I Homo sapiens cDNA 5' end

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6695	19853	33243	1.05	7.0E-03	BE857385.1	EST_HUMAN	7g34b10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 Q13387 HYPOTHETICAL PROTEIN 384D8_2. ;contains TAR1.t2 TAR1 TAR1 repetitive element ;
7228	20133	33550	1.93	7.0E-03	BE928133.1	EST_HUMAN	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7689	20754	34238	4.76	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
7689	20754	34239	4.76	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8031	21114	34632	0.59	7.0E-03	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8031	21114	34633	0.59	7.0E-03	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8302	21384	34905	2.48	7.0E-03	BE175667.1	EST_HUMAN	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
8813	21892	35433	0.58	7.0E-03	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
9597	22652		0.64	7.0E-03	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9794	22834	36414	0.68	7.0E-03	N52378.1	EST_HUMAN	yv49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains Alu repetitive element;
9921	22961	36548	2.72	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9921	22961	36549	2.72	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10513	23548		1.34	7.0E-03	AV687379.1	EST_HUMAN	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'
10704	23737		0.82	7.0E-03	AI799734.1	EST_HUMAN	wc37e09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2320840 3'
10800	23833	37456	0.47	7.0E-03	BE154643.1	EST_HUMAN	PM3-HT0344-181199-002-g06 HT0344 Homo sapiens cDNA
11065	24141	37776	2.41	7.0E-03	AB008852.1	NT	Bos taurus mRNA for NDP52, complete cds
11140	24212	37838	1.55	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
11140	24212	37839	1.55	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12792	26189		1.95	7.0E-03	H94065.1	EST_HUMAN	yv15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains Alu repetitive element;
12800	25634		1.46	7.0E-03	BE263253.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
12908	25601		1.76	7.0E-03	Y17455.1	NT	Homo sapiens LSFR2 gene, penultimate exon
13058	26186		1.68	7.0E-03	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
1269	14427	27494	8.76	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR ;
1269	14427	27495	8.76	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR ;
2831	15945	29054	0.94	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2956	16133	29147	3.29	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2956	16133	29148	3.29	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3318	16491		2.27	6.0E-03	H75690.1	EST_HUMAN	yr77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'

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3378	16550		0.63	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3469	16636	29655	1.25	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3469	16636	29656	1.25	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3636	16800		1.11	6.0E-03	W37985.1	EST_HUMAN	zc13a11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3750	16911	29914	3.73	6.0E-03	BF510986.1	EST_HUMAN	UI-H-BI4-apm-c-06-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3877	17036	30034	1.31	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA
4032	17188	30199	0.6	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA
4067	17223		1.26	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4484	17624		1.54	6.0E-03	AI016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4817	17950	30935	7.9	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5305	18422	31392	0.6	6.0E-03	AA889972.1	EST_HUMAN	aj95g09.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 3'
6281	25822	32803	0.68	6.0E-03	9627521	NT	Variola virus, complete genome
6956	20269	33707	0.8	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6994	18513	31505	0.97	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7399	20477	33944	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7399	20477	33945	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7824	20879	34380	0.8	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
8042	21125	34646	6.71	6.0E-03	AI033980.1	EST_HUMAN	ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element ;
8161	21243	34763	2.76	6.0E-03	AW799337.1	EST_HUMAN	RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8236	21318		1.65	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
9754	22692	36262	7.03	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
10249	23284		2.49	6.0E-03	AI432661.1	EST_HUMAN	ti22c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
10365	23400	37011	0.75	6.0E-03	AJ011849.1	NT	Bacillus subtilis fenD gene
10503	23538		0.91	6.0E-03	AF084555.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10615	23649	37258	0.64	6.0E-03	X68366.1	NT	M.thermoformicicum complete plasmid pFV1 DNA
10661	23695		0.54	6.0E-03	AF245505.1	NT	Homo sapiens adlican mRNA, complete cds
10983	24062	37697	1.56	6.0E-03	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
11049	24126		1.94	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11228	24297		4.1	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11229	24298	37938	2.66	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12321	25232		2.04	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12425	25998		1.3	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
12451	25926		4.65	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete genome
12532	25993		2.49	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12590	25397		1.63	6.0E-03	Q62209	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12944	25622		2.41	6.0E-03	AJ245480.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
13095	26018		1.61	6.0E-03	X74807.1	NT	R.norvegicus VEGP2 gene
13147	25746		1.19	6.0E-03	BF110298.1	EST_HUMAN	7n36b11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566564 3'
686	13871	26903	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
686	13871	26904	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
687	13871	26903	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
687	13871	26904	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1136	14301	27357	1.47	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase,RH3
1601	14754		1.08	5.0E-03	AI138977.1	EST_HUMAN	qd79d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2746	15863	28974	2.43	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
3206	16381	29392	3.87	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'
3223	16397		2.72	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3235	16409	29423	1.17	5.0E-03	R71794.1	EST_HUMAN	yj86g02.s1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:155666 3'
3351	16523		0.84	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3790	16951	29957	5.28	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3854	17014	30014	0.61	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4079	17235		1.64	5.0E-03	AA299675.1	EST_HUMAN	EST12218 Uterus tumor I Homo sapiens cDNA 5' end
4241	17387	30374	0.65	5.0E-03	AJ002125.1	NT	Natrix domestica Zfx type gene
4421	17562	30546	0.71	5.0E-03	H78355.1	EST_HUMAN	yu79g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240066 5'
4423	17014	30014	0.76	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4731	17866	30848	0.92	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4841	17974	30964	1.56	5.0E-03	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5286	18405		1.9	5.0E-03	4758747	NT	Homo sapiens myosin-binding protein C, fast-type (MYBPC2) mRNA
5916	19104	32417	5.4	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
6169	19345	32691	2.82	5.0E-03	O00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6204	19379		0.88	5.0E-03	AE002234.2	NT	Chlamydophila pneumoniae AR39, section 62 of 94 of the complete genome
6726	19882		7.34	5.0E-03	BE300091.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6986	18505	31520	7.22	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7185	20050		0.85	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7237	20321	33765	0.61	5.0E-03	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
7654	20722	34198	0.7	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR93 similar to EST containing Alu repeat
7774	20831		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031099-011-f07 CT0255 Homo sapiens cDNA
7944	20994	34505	7.18	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8415	21496	35027	0.81	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8415	21496	35028	0.81	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8433	21514	35045	1.99	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8811	21890		5.83	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
9007	22086	35629	1.21	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
9140	22219	35763	0.52	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10044	23082	36684	1.03	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
10176	23213	36805	0.74	5.0E-03	AW821888.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10360	23395	37006	0.56	5.0E-03	AA533143.1	EST_HUMAN	nj46h10.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:995587
10539	23574	37181	0.47	5.0E-03	7662557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10696	23729		0.47	5.0E-03	AA653261.1	EST_HUMAN	ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3'
10959	24040		4.79	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
11181	24250	37884	2.39	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.t2 L1 repetitive element ;
11181	24250	37885	2.39	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.t2 L1 repetitive element ;
11297	24363	38004	1.76	5.0E-03	T49153.1	EST_HUMAN	yb09e04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11615	24666		3.41	5.0E-03	BE048056.1	EST_HUMAN	tz46c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291622 5'
12070	25051	38759	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12070	25051	38760	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12467	26144		11.86	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12616	25414		21.79	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12718	25478		2.03	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12760	25504		1.94	5.0E-03	AA456597.1	EST_HUMAN	zx75a03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12802	25935		5.99	5.0E-03	BF572332.1	EST_HUMAN	602077774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
13002	25651	31951	2.66	5.0E-03	AW449109.1	EST_HUMAN	UI-H-BI3-akf-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
242	13464	26493	1.54	4.0E-03	AW500196.1	EST_HUMAN	UI-HF-BN0-akc-h-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
331	13545	26575	1.75	4.0E-03	R46482.1	EST_HUMAN	yg51e04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
456	13651	26689	1.36	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
616	13805	26825	4.37	4.0E-03	AA939339.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
900	14075	27142	1.65	4.0E-03	R46482.1	EST_HUMAN	yg51e04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
934	14109		2.85	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
1174	14337	27393	34.06	4.0E-03	AA099777.1	EST_HUMAN	zl81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1196	14358	27417	1.83	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1331	14488	27556	1.48	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1783	14932	28026	2.68	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
2075	15215	28334	17.33	4.0E-03	AA099777.1	EST_HUMAN	zl81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2321	15453		2.06	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2352	15483	28615	1.53	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2639	15762	28875	1.95	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2639	15762	28876	1.95	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2755	15872	28980	2.97	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2755	15872	28981	2.97	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2761	15877	28984	0.97	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3297	16471	29491	1.09	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3297	16471	29492	1.09	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3619	16783	29798	0.83	4.0E-03	AW188426.1	EST_HUMAN	xj98f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3619	16783	29799	0.83	4.0E-03	AW188426.1	EST_HUMAN	xj98f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3714	16875	29880	0.64	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 5I1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4021	16875	29880	0.65	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 5I1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4040	17196	30207	0.72	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
4102	17256		2.18	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5339	18452	31420	0.98	4.0E-03	AW500547.1	EST_HUMAN	UI-HF-BN0-ekj-e-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
5390	18592	31564	1.58	4.0E-03	AF005859.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5515	18713	31726	27.24	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5914	19102	32416	3.1	4.0E-03	P04196	SWISSPROT	(HPRG)
5918	19106	32418	1.8	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR
6003	19188	32507	0.8	4.0E-03	AL133871.1	EST_HUMAN	DKFZp761I1014_r1 761 (syncnym: hamy2) Homo sapiens cDNA clone DKFZp761I1014 5'
6209	19384		4.18	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6363	19533	32892	0.97	4.0E-03	AW590572.1	EST_HUMAN	hg46c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2948652 3'
6439	19606	32969	1.78	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6809	19963	33367	1.07	4.0E-03	AA813222.1	EST_HUMAN	aj32f11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'
6914	20229	33662	1.41	4.0E-03	U76408.1	NT	Lycopersicon esculentum knotted 3 protein (TKn3) mRNA, complete cds
7217	20082	33495	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7217	20082	33496	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7348	20426	33889	3.73	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7589	20660	34136	0.96	4.0E-03	AI681483.1	EST_HUMAN	tx37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7591	20662	34138	0.62	4.0E-03	BE670170.1	EST_HUMAN	7e31b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7693	20758		0.85	4.0E-03	X92109.1	NT	H.sapiens hcgIX gene
8128	21210	34731	0.57	4.0E-03	Q9TT92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8238	21320	34838	4.51	4.0E-03	AF111944.1	NT	Dictyostelium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
8398	21479	35006	2	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8665	21745	35284	0.67	4.0E-03	AF139827.1	NT	Plasmodium falciparum replication factor C subunit 1 (rfc1) gene, complete cds
8761	21840	35381	0.51	4.0E-03	Y12855.1	NT	Homo sapiens P2X7 gene, exon 12 and 13
8911	21990	35529	7.06	4.0E-03	AI553983.1	EST_HUMAN	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element;
9090	22169		3.24	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9100	22179	35723	3.76	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9825	22865	36447	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9825	22865	36448	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10131	23169	36766	0.63	4.0E-03	H30664.1	EST_HUMAN	yp42g12.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190150 5'
10587	23622	37229	1.35	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11283	24349	37986	1.36	4.0E-03	4759101	NT	Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8) mRNA
11394	24455	38117	5	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
12072	25053	38762	1.57	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12434	26163		5.84	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
12457	25321		1.35	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12541	25367		1.95	4.0E-03	AW504273.1	EST_HUMAN	UI-HF-BN0-alp-g-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12814	25543		3.33	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element;contains element MER31 repetitive element ;
12858	26053		2.18	4.0E-03	AW614596.1	EST_HUMAN	hh02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element ;
12871	25581		1.34	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
13202	25784	31918	1.23	4.0E-03	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
382	13590	26626	1.25	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
902	14077	27143	4.87	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1694	14846	27930	3.65	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2367	15498		6.37	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2368	15499	28624	1.14	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2368	15499	28625	1.14	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3056	16232		0.77	3.0E-03	Y09006.1	NT	Arabidopsis thaliana rpoMt gene
3152	16327	29338	3.55	3.0E-03	BE379296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3220	16394	29405	2.53	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3504	16671	29681	2.16	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3513	16679		7.5	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4086	17241	30248	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4086	17241	30249	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4147	17299	30291	1.67	3.0E-03	AI792278.1	EST_HUMAN	ah04f09.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4515	17654	30642	5.53	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4641	17777	30759	4.62	3.0E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4858	17991	30978	0.69	3.0E-03	AL119067.1	EST_HUMAN	DKFZp761B0712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712 5'
4955	18085	31061	2.05	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4978	18107	31083	5.53	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5255	18375	31341	0.9	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5255	18375	31342	0.9	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5262	18381	31347	1.75	3.0E-03	AI193860.1	EST_HUMAN	qe80b10.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745275 3' similar to SW:AP17_MOUSE Q00380 CLATHRIN COAT ASSEMBLY PROTEIN AP17 ;contains MSR1.t2 MER22 repetitive element ;
5380	18582	31451	3.36	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5673	18867	32153	1.09	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5744	18937	32237	0.83	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6683	19841	33231	9.72	3.0E-03	AA456701.1	EST_HUMAN	aa13f10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7168	20301	33744	0.75	3.0E-03	D37977.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7354	20433	33895	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pcpl3 gene for purine-cytosine permease
7691	20756	34241	3.71	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
8124	21206	34726	0.9	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8124	21206	34727	0.9	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8350	21431	34955	1.4	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8490	21571	35108	0.47	3.0E-03	AI866028.1	EST_HUMAN	wi24d09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425841 3'
8510	21591		0.63	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8655	21735	35276	1.34	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8679	21759	35295	1.5	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8786	21865		1.45	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
9192	22270		10.8	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.t1 L1 repetitive element ;
9245	22322	35866	4.26	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9269	22345	35896	9.96	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_rna1 HISTONE H2B.2 (HUMAN);
9280	22356	35906	0.53	3.0E-03	BF338078.1	EST_HUMAN	602035980F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183938 5'
9609	22664		0.78	3.0E-03	D90901.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9646	21089	34804	0.77	3.0E-03	BE154670.1	EST_HUMAN	PM3-HT0344-071299-003-d07 HT0344 Homo sapiens cDNA
9836	22876		0.56	3.0E-03	P03355	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9908	22948		6.51	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
10099	23137	36738	2.31	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10200	23237	36827	1.44	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10344	23379	36990	3.89	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11085	24159		2.67	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11458	20756	34241	1.45	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11722	23908	37532	1.47	3.0E-03	P22531	SWISSPROT	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)
11732	23918	37543	1.9	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11770	24762	38457	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11770	24762	38458	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11849	24838	38532	1.36	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12077	25057		1.46	3.0E-03	AW294812.1	EST_HUMAN	UI-H-BI2-ahi-d-06-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
12199	25948		1.62	3.0E-03	AI525056.1	EST_HUMAN	promrna-5.E07.r bvtumor Homo sapiens cDNA 5'
12235	25179	38346	1.24	3.0E-03	AA993154.1	EST_HUMAN	ot77b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.t3 MER26 repetitive element ;
12296	26090		1.76	3.0E-03	AB009668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12481	25333	32057	1.23	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
528	13721	26746	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
528	13721	26747	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
808	16023		11.88	2.0E-03	T70874.1	EST_HUMAN	yd15h03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1394	14548	27624	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1397	14551	27626	1.42	2.0E-03	AA661605.1	EST_HUMAN	nu86f01.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593
1406	14560	27634	20.85	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1519	14672	27754	1.1	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1546	14698	27776	2.26	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1546	14698	27777	2.26	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1621	14773		6.17	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1811	14960	28053	1.27	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1928	15071		1.09	2.0E-03	BE144908.1	EST_HUMAN	CM2-HT0183-061099-018-d03 HT0183 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2051	15192	28305	1.59	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2324	15456	28588	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2647	15770		4.93	2.0E-03	AW137782.1	EST_HUMAN	UI-H-BI1-adl-g-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3503	16670	29680	4.92	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3510	16676	29686	0.96	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3756	16917	29919	5.48	2.0E-03	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
4062	17218	30226	0.62	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4229	17376	30364	2.39	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4290	17435	30423	1.02	2.0E-03	AA179693.1	EST_HUMAN	zp13h01.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
4336	17479		13.93	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4532	17670		1.99	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4547	17685		1.22	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BW0-air-g-03-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4551	17689	30670	1.05	2.0E-03	AI064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4668	17803	30790	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds
4668	17803	30791	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds
4828	17961	30949	1.02	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4832	17965		1.57	2.0E-03	R87773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4962	18091	31067	1.07	2.0E-03	P11000	SWISSPROT	WALL-ASSOCIATED PROTEIN PRECURSOR
5132	18257	31223	0.84	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5604	18799	31849	1.57	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5745	25810	32238	1.83	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5828	19019	32325	2.08	2.0E-03	U63711.1	NT	Xenopus laevis xefiltin mRNA, complete cds
6236	19411	32758	3.93	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6236	19411	32759	3.93	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6476	19643	33004	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6476	19643	33005	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6478	19645	33007	7.55	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6514	19679	33049	2.16	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6515	19680	33050	0.75	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6544	19706	33082	1.45	2.0E-03	X94451.1	NT	L.esculentum mRNA for lysyl-tRNA synthetase (LysRS)

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6736	19892		1.36	2.0E-03	AI991089.1	EST_HUMAN	wu36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitive element ;
6775	19930	33326	0.7	2.0E-03	AA677831.1	EST_HUMAN	zi13a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
7098	18525	31517	1.35	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7231	20136	33554	3.3	2.0E-03	BE067986.1	EST_HUMAN	CM4-BT0366-061299-054-d01 BT0366 Homo sapiens cDNA
7294	20376	33833	0.65	2.0E-03	AI298883.1	EST_HUMAN	qm99d11.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7444	20521	33994	0.8	2.0E-03	T86569.1	EST_HUMAN	yd77g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114306 5'
7794	20850	34342	1.41	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8241	21323	34840	2.97	2.0E-03	AW592004.1	EST_HUMAN	hf37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY. ;
8412	21493	35023	5.49	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8412	21493	35024	5.49	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8459	21540	35069	0.64	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME I
8481	21562	35097	1.09	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8536	21617	35153	1.04	2.0E-03	6005856	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8536	21617	35154	1.04	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8561	21642	35181	1.03	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8614	21694		0.9	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9396	19018	32323	0.79	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9396	19018	32324	0.79	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9441	22515	36079	1.07	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9726	22791	36362	0.71	2.0E-03	H50832.1	EST_HUMAN	yp85a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194296 3'
9726	22791	36363	0.71	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194296 3'
9758	22696	36264	3.33	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9868	22908	36493	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9868	22908	36494	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9924	22964	36552	0.6	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9924	22964	36553	0.6	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10119	23157	36755	0.96	2.0E-03	AW884269.1	EST_HUMAN	QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA
10248	23283		6.26	2.0E-03	AA251376.1	EST_HUMAN	zs10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
10628	23662	37270	0.49	2.0E-03	BF367386.1	EST_HUMAN	MR2-GN0030-140900-001-e05 GN0030 Homo sapiens cDNA
11265	24334		2.14	2.0E-03	M86524.1	NT	Human dystrophin gene
11778	20850	34342	3.79	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11836	24825		2.36	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11844	24833	38528	9.64	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
12180	25140		3.37	2.0E-03	AI625745.1	EST_HUMAN	ty65h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
12198	25155	38833	4.31	2.0E-03	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
12222	25171	38836	1.71	2.0E-03	AI084325.1	EST_HUMAN	oy43g06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to TR:P97535 P97535 PS-PLA1 PRECURSOR. ;
12245	18497		4.86	2.0E-03	AJ245167.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
12462	26140		4	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
12561	25383	32039	1.29	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12897	25594		1.38	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
13090	25927		2.46	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
452	13648	26684	1.38	1.0E-03	H96471.1	EST_HUMAN	yt98c08.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
852	14029	27091	1.55	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
852	14029	27092	1.55	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1119	14284	27339	2.61	1.0E-03	AI865788.1	EST_HUMAN	wk86a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1139	14304	27360	1.51	1.0E-03	AI954572.1	EST_HUMAN	wx93e10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1192	14354	27412	0.85	1.0E-03	AI692616.1	EST_HUMAN	wd86a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2084	15224	28346	3.42	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2222	15356	28486	9.52	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3044	16220	29241	1.37	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3280	16434	29451	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3260	16434	29452	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3374	16546	29560	0.75	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3632	16796	29813	0.94	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3632	16796	29814	0.94	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3755	16916		1.43	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4034	17190	30200	0.98	1.0E-03	AW170552.1	EST_HUMAN	xn63d07.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to contains TAR1.t1 TAR1 repetitive element ;
4044	17200	30211	0.91	1.0E-03	Z49649.1	NT	S.cerevisiae chromosome X reading frame ORF YJR149w
4556	17694	30673	2.34	1.0E-03	BE939162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4598	17735	30715	4.89	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4785	17920	30908	0.81	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4945	18075	31050	2.54	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4945	18075	31051	2.54	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4946	18076		6	1.0E-03	BE154067.1	EST_HUMAN	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5188	18310	31276	15.5	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5324	18437	31407	4.73	1.0E-03	BE219340.1	EST_HUMAN	hv51f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176955 3'
5423	18624	31600	2	1.0E-03	AA290951.1	EST_HUMAN	zs44f01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5518	18716	31730	3.57	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5572	18768	31809	1.64	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5572	18768	31810	1.64	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5690	18884	32176	0.95	1.0E-03	BE796491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5696	18890	32181	1.77	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5751	18943	32244	0.8	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element ;
5751	18943	32245	0.8	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element ;
6033	19216		0.59	1.0E-03	BF541639.1	EST_HUMAN	602068042F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068907 5'
6144	19322		2.75	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6184	19360	32708	0.85	1.0E-03	BE963939.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6321	19493		8.77	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6464	19631	32992	1.11	1.0E-03	T87761.1	EST_HUMAN	yd93a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
6539	19702		1.68	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6895	20046	33455	1.41	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7302	20384	33843	2.81	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7656	20724		1.12	1.0E-03	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7817	20872	34370	1.98	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7885	20937	34443	3.44	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7934	20984	34492	0.79	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5'
8073	21155	34674	0.66	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8136	21218	34739	5.02	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8337	21418	34944	1.95	1.0E-03	AA122270.1	EST_HUMAN	zk97c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.t1 L1 repetitive element ;
8438	21519	35048	2.35	1.0E-03	AF153980.1	NT	Homo sapiens exostoses-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8625	21705	35241	0.75	1.0E-03	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9144	22223		1.48	1.0E-03	Y11204.1	NT	V.carteri gene encoding volvoxopsin
9170	22248	35791	0.65	1.0E-03	AW840353.1	EST_HUMAN	CM3-LT0079-170200-092-e07 LT0079 Homo sapiens cDNA
9281	22357		0.65	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9319	22395	35947	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9319	22395	35948	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9796	22836		0.47	1.0E-03	AI247482.1	EST_HUMAN	qh56d01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848673 3' similar to gb:M97388 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN);
9807	22847	36424	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9807	22847	36425	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
10025	23063	36660	0.88	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10366	23401	37012	9.37	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10372	23407		0.75	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10522	23557	37165	1.08	1.0E-03	AI024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1 MER39 MER39 repetitive element ;
10823	23856	37478	0.5	1.0E-03	AE004762.1	NT	Pseudomonas aeruginosa PA01, section 323 of 529 of the complete genome
10823	23856	37479	0.5	1.0E-03	AE004762.1	NT	Pseudomonas aeruginosa PA01, section 323 of 529 of the complete genome

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10830	23863		0.53	1.0E-03	AA706202.1	EST_HUMAN	ag93f12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element;
10902	23986	37617	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10902	23986	37618	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10989	24068	37702	2.46	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11062	24138		2.03	1.0E-03	AI583847.1	EST_HUMAN	tt73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195 PVA1 GENE. ;
11425	24486		2.63	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11858	24846	38543	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11858	24846	38544	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11924	24910	38611	1.53	1.0E-03	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
11924	24910	38612	1.53	1.0E-03	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
12175	25136	38831	5.51	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12679	26118		7.37	1.0E-03	AI347355.1	EST_HUMAN	tc05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12812	26142	31551	3.83	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
12889	25590		1.17	1.0E-03	11465934	NT	Nicotiana tabacum chloroplast, complete genome
5327	18440	31409	0.7	9.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5799	18989		2.08	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6388	19557		0.58	9.0E-04	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6615	19775	33166	1.27	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9843	22883		1.46	9.0E-04	AB037203.1	NT	Glycyrrhiza glabra GgbAS1 mRNA for beta-amyrin synthase, complete cds
1517	14670		1.07	8.0E-04	X96469.1	NT	X.laevis mRNA for C4SR protein
4296	17439		4.4	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4887	18017	31002	2.5	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11412	24473		2.59	8.0E-04	AA777084.1	EST_HUMAN	zf24c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11576	24631		1.87	8.0E-04	AI571099.1	EST_HUMAN	tn85a08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2176310 3'
1874	15018	28127	1.11	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2472	15599	28724	1.45	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2778	15894	29004	1.33	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3353	16525	29540	1.4	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

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6221	19396	32745	0.93	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1 repetitive element ;
6642	19801		2.33	7.0E-04	AI769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7376	20455		0.72	7.0E-04	AK024446.1	NT	Homo sapiens mRNA for FLJ00035 protein, partial cds
10008	23046	36639	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10008	23046	36640	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11665	24853		1.7	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11893	24881	38578	3.76	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12723	25481		9.28	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
13001	25650		2.66	7.0E-04	R17336.1	EST_HUMAN	yg13c06.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5'
13038	25682		5.43	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2760	15876		0.97	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149297 5'
4069	17225	30232	1.64	6.0E-04	AI862525.1	EST_HUMAN	wj15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4201	17350	30341	0.65	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4201	17350	30342	0.65	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4301	17444	30430	3.91	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4565	17703	30683	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA
4565	17703	30684	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA
8050	21133		4.58	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
8205	21287		0.51	6.0E-04	H92947.1	EST_HUMAN	yt94c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element ;
10185	23222		3.26	6.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
10215	23251		0.53	6.0E-04	AI858286.1	EST_HUMAN	wl35g02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426930 3'
10285	23320	36922	2.29	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10547	23582		0.84	6.0E-04	AF287478.1	NT	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete cds
11774	24766	38462	2.07	6.0E-04	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11866	24854	38549	2.47	6.0E-04	AW013847.1	EST_HUMAN	UI-H-BI0-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11937	24923		1.62	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
12363	26007		3.31	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-261199-012-d08 HT0269 Homo sapiens cDNA
13226	25797		14.14	6.0E-04	AI817088.1	EST_HUMAN	wj76g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element ;
668	13854	26882	7.88	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1531	14684		2.03	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3500	16667	29677	1.6	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
3809	16969	29972	0.94	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5589	18784	31830	2.51	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6765	19921	33317	7.06	5.0E-04	AA156080.1	EST_HUMAN	zo33b08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588663 5'
7534	20607	34082	9.01	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
8143	21225	34745	5.58	5.0E-04	AI188382.1	EST_HUMAN	qd13f06.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN);contains Alu repetitive element;
8498	21579	35115	0.95	5.0E-04	AA814519.1	EST_HUMAN	ob96e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element ;
9477	22534	36098	1.67	5.0E-04	AA846545.1	EST_HUMAN	aj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9571	22713	36281	0.58	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9718	22783	36354	0.64	5.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9809	22849	36428	4.78	5.0E-04	AW270938.1	EST_HUMAN	xs06e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10484	23519		0.6	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
11220	24289		1.9	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
12012	18784	31830	15	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12301	25936		2.39	5.0E-04	AA568513.1	EST_HUMAN	nf15h02.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:913875
12872	25961		1.33	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
403	13600		0.75	4.0E-04	BF241482.1	EST_HUMAN	601876634F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
690	13874	26907	1.36	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
870	14046	27111	1.55	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
870	14046	27112	1.55	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1493	14646	27728	5.58	4.0E-04	AW753356.1	EST_HUMAN	RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
2148	15284	28410	1.87	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2202	15337		1.1	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2691	15811	28927	2.04	4.0E-04	O96615	SWISSPROT	SERICIN-2 (SILK GUM PROTEIN 2)
3233	16407	29420	2.78	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3397	16567	29583	0.69	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
3443	16611	29629	0.6	4.0E-04	AV696624.1	EST_HUMAN	AV696624 GKC Homo sapiens cDNA clone GKCFFH07 5'
4443	17583	30561	3.24	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4443	17583	30562	3.24	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4659	17795	30781	2.33	4.0E-04	AA086324.1	EST_HUMAN	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
5199	18320	31289	3.62	4.0E-04	BE560660.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
7418	20496	33965	1.55	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7705	20770		0.85	4.0E-04	AL161666.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
7896	20948	34456	0.8	4.0E-04	AU122079.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8733	21813	35348	3.64	4.0E-04	BF240712.1	EST_HUMAN	601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
8741	21820	35354	1.68	4.0E-04	N25507.1	EST_HUMAN	yx39e12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264142 5'
9892	22932	36515	3.37	4.0E-04	AI025699.1	EST_HUMAN	ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
10045	23083		1.12	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
12691	25908		1.56	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
160	13385	26415	3.21	3.0E-04	AL119426.1	EST_HUMAN	DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
200	13423	26454	1.7	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
903	14078	27144	1.63	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1886	15030	28137	1.7	3.0E-04	AI262100.1	EST_HUMAN	qz28d03.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1901	15044		0.97	3.0E-04	AI399674.1	EST_HUMAN	th23a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2119082 3'
3383	16554	29568	4.35	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
4071	17227	30234	4.94	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4167	17317		1.36	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
4205	17354		1.06	3.0E-04	BE140609.1	EST_HUMAN	RC0-HT0014-310599-028 HT0014 Homo sapiens cDNA
4635	17771		1.16	3.0E-04	BE148546.1	EST_HUMAN	MR0-HT0241-030200-008-e01 HT0241 Homo sapiens cDNA
4937	18067		5.2	3.0E-04	BE153778.1	EST_HUMAN	PM0-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
5004	18133	31107	0.65	3.0E-04	AW937723.1	EST_HUMAN	QV3-DT0045-221299-046-d09 DT0045 Homo sapiens cDNA
6271	19445		5.58	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6959	20187	33611	1.54	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7130	18556	31471	0.67	3.0E-04	AW893981.1	EST_HUMAN	RC4-NN0027-060400-011-b08 NN0027 Homo sapiens cDNA
7765	20824	34316	0.73	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8454	21535	35065	2.16	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10124	23162	36760	1.26	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
10381	23416	37025	0.46	3.0E-04	AI992139.1	EST_HUMAN	wt75a11.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513276 3'
10676	23710	37318	1.96	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
12249	26164	31555	2.39	3.0E-04	AA228301.1	EST_HUMAN	nc38e04.r1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.t2 L1 repetitive element ;
12646	25987	31769	2.54	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
13114	25727		4.81	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547L185 5'
180	13403	26432	1.33	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
491	13685	26719	2.67	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
930	14105	27168	5.02	2.0E-04	M86524.1	NT	Human dystrophin gene
930	14105	27169	5.02	2.0E-04	M86524.1	NT	Human dystrophin gene
1206	14368		2.78	2.0E-04	AI286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element ;
1213	14374		2.6	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1879	15023		1.71	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pitx3 gene
2257	15390		1.21	2.0E-04	AA478980.1	EST_HUMAN	zu39b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2641	15764	28878	6.42	2.0E-04	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
3052	16228	29248	1.23	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3415	16584	29600	0.82	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3622	16698	29697	2.56	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
4022	17178	30187	0.98	2.0E-04	AW978441.1	EST_HUMAN	EST390550 MAGE resequences, MAGP Homo sapiens cDNA
4261	17406		5.5	2.0E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4791	17926	30914	1.75	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4791	17926	30915	1.75	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4916	18046		1.22	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5171	18293	31256	1.47	2.0E-04	AB037997.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds
5216	18337	31310	0.92	2.0E-04	AF057019.1	NT	Dictyostelium discoideum interaptin (abpD) gene, complete cds
5661	18855	32138	1.11	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3'
5674	18868	32154	1.83	2.0E-04	AI690862.1	EST_HUMAN	tq03b11.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207709 3'
5868	19058	32365	0.93	2.0E-04	AA296652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6068	19250	32578	0.92	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6368	19538	32897	1.01	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7378	20457		2.57	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7478	20553		0.84	2.0E-04	AW860963.1	EST_HUMAN	QV0-CT0387-180300-167-e10 CT0387 Homo sapiens cDNA
7798	20854		13.66	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7808	20863	34357	1.45	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8142	21224	34743	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8142	21224	34744	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8479	21560	35094	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8479	21560	35095	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8763	21842	35383	2.14	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
8941	22020	35561	0.67	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9535	22600	36173	0.58	2.0E-04	AA725700.1	EST_HUMAN	al22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518 3'
9619	22674	36244	0.47	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF26.1
10180	23217	36808	1.16	2.0E-04	BE148303.1	EST_HUMAN	RC3-HT0254-161099-011-b05 HT0254 Homo sapiens cDNA
10223	23259	36847	2.06	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
11088	24162	37798	3.88	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'
11585	24638	38318	2.68	2.0E-04	AI440282.1	EST_HUMAN	tj01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
11710	24750	38443	2.39	2.0E-04	AW136740.1	EST_HUMAN	UI-H-BI1-adm-c-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
11859	24847		2.71	2.0E-04	BE065781.1	EST_HUMAN	RC2-BT0317-150200-011-h04 BT0317 Homo sapiens cDNA
12106	25086	38790	32.04	2.0E-04	P21733	SWISSPROT	HYPOTHETICAL 29.1 KD PROTEIN IN CRYB1 5'REGION (ORF2)
12121	25101	38806	2.05	2.0E-04	L19248.1	NT	Caenorhabditis elegans homeodomain protein (lin-39) mRNA, complete cds
13191	26179		1.29	2.0E-04	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
788	13967	27018	0.96	1.0E-04	H99646.1	EST_HUMAN	yx26c09.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.t1 L1 repetitive element ;
1100	14265	27322	2.86	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1138	14303	27358	3.79	1.0E-04	AW013847.1	EST_HUMAN	UI-H-BI0-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1138	14303	27359	3.79	1.0E-04	AW013847.1	EST_HUMAN	UI-H-BI0-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1363	14517		2.65	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1657	14810	27894	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamidine synthase, and LAMP (LAMP) genes, complete cds
1657	14810	27895	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamidine synthase, and LAMP (LAMP) genes, complete cds
1909	15052	28164	2.02	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2752	15869	28978	1.06	1.0E-04	BE218833.1	EST_HUMAN	hv45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2752	15869	28979	1.06	1.0E-04	BE218833.1	EST_HUMAN	hv45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3356	16528	29543	1.18	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3829	16989	29992	0.86	1.0E-04	AI440282.1	EST_HUMAN	tj01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
4171	17321	30314	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4192	17342	30335	1.12	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBBD04 3'
5207	18328	31298	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5207	18328	31299	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5980	19165	32485	1.35	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6569	19731	33109	0.95	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:252
6977	20205	33633	0.66	1.0E-04	AA564561.1	EST_HUMAN	nj25a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb:M97252 KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN);contains Alu repetitive element;
7336	20417	33879	12.52	1.0E-04	AI251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
7744	20417	33879	13.49	1.0E-04	AI251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
8184	21266	34789	1.02	1.0E-04	AA630453.1	EST_HUMAN	ab94g08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854654 3'
9538	22603	36175	2.75	1.0E-04	AI806220.1	EST_HUMAN	wf26e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9548	22613	36182	1.54	1.0E-04	O88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9625	22680		0.76	1.0E-04	T77153.1	EST_HUMAN	yd72c08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 5'
9846	22886	36466	1.06	1.0E-04	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10382	23417		3.59	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10420	23455	37060	1.12	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10775	23808	37431	0.46	1.0E-04	P51786	SWISSPROT	ZINC FINGER PROTEIN 157
11622	24673		2.3	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11950	24936	38637	1.81	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11991	24976	38680	1.94	1.0E-04	AW269061.1	EST_HUMAN	xv49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12024	25008	38709	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12024	25008	38710	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
716	13898	26936	2.44	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
4196	17346	30338	1.13	9.0E-05	AI762209.1	EST_HUMAN	wi54c11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394068 3' similar to contains MER6.t1 MER6 repetitive element ;
6084	19266	32595	1.37	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7751	20811	34301	2.44	9.0E-05	AW204958.1	EST_HUMAN	UI-H-BI1-aer-d-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
7751	20811	34302	2.44	9.0E-05	AW204958.1	EST_HUMAN	UI-H-BI1-aer-d-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9677	22639		3.03	9.0E-05	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
9679	22641	36211	3.3	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11402	24463	38127	2.31	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.t2 L1 repetitive element ;
11518	24574	38251	1.61	9.0E-05	AI287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element ;
11916	19266	32595	3.41	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12469	26016		3.37	9.0E-05	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
844	14022	27080	1.22	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
887	14063		3.11	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
3015	16191		1.01	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4604	17741	30719	0.78	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8948	22027	35568	0.51	8.0E-05	Y11666.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11419	24480	38146	2.58	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
13159	26001		1.78	8.0E-05	AA279333.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
357	13568	26596	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
357	13568	26597	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
581	13773	26793	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
581	13773	26794	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1080	14246	27303	1.07	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2783	15899	29008	5.16	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3227	16401	29413	3.9	7.0E-05	AB009080.1	NT	Dictyostelium discoideum gene for TRFA, complete cds
4168	17318		0.85	7.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4492	17632	30614	1.88	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5041	18169	31144	0.68	7.0E-05	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
8420	21501	35033	1.24	7.0E-05	AA505582.1	EST_HUMAN	nh93g01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966096 3'
9753	22691	36261	3.6	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBED60
11430	24491		5.87	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2083	15223	28344	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2083	15223	28345	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2655	15778	28892	1.56	6.0E-05	AI655241.1	EST_HUMAN	wb54h06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2875	13880	26912	2.54	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6034	19217	32538	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6034	19217	32539	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6533	19697	33070	1.5	6.0E-05	N72829.1	EST_HUMAN	yv50g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246212 5'
7073	20126	33542	0.74	6.0E-05	AA897680.1	EST_HUMAN	oj80a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8276	21358	34876	1.03	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8276	21358	34877	1.03	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8638	21718	35255	0.62	6.0E-05	AA150482.1	EST_HUMAN	zl08c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element ;
8643	21723	35260	2.62	6.0E-05	AW896629.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8780	21859	35402	2.93	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9452	22568	36134	1.59	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9452	22568	36135	1.59	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9721	22786	36357	1.77	6.0E-05	T94149.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
9922	22962	36550	0.69	6.0E-05	AW627985.1	EST_HUMAN	hi37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
10987	24066	37701	2.42	6.0E-05	R75639.1	EST_HUMAN	yi59d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element;contains LTR7 repetitive element ;

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11807	24797	38495	2.7	6.0E-05	AA044015.1	EST_HUMAN	zk68f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12699	25999	31773	9.37	6.0E-05	AW890110.1	EST_HUMAN	MR0-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA
1435	14588	27661	20.87	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1912	15055		1.07	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2924	16102	29116	0.64	5.0E-05	AJ251058.1	NT	Homo sapiens MEP1A gene, promoter region and exon 1
4088	17243	30250	3.16	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5642	18836	31913	11.81	5.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6115	19295	32630	3.58	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3'
6297	19470	32825	0.97	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7485	20560		1.4	5.0E-05	AB037964.1	NT	Mus musculus gene for calretinin, exon 1
12466	25503		5.26	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12759	25503		6.9	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2868	13457		2.73	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4605	17742	30720	0.76	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4605	17742	30721	0.76	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4997	18126		0.95	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5131	18256	31222	0.73	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
9723	22788		6.75	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
10617	23651	37260	0.54	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
11007	24086	37723	4.14	4.0E-05	AW627946.1	EST_HUMAN	hi36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element ;
12343	25248	32113	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C062
12426	25302		1.47	4.0E-05	AW117580.1	EST_HUMAN	xd93e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
13189	25773		1.16	4.0E-05	AA417756.1	EST_HUMAN	zv01e11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746252 3'
698	13881	26914	0.8	3.0E-05	AI248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element ;
1084	14250	27307	1.16	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1550	14702	27781	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
1550	14702	27782	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
3365	16537		0.7	3.0E-05	AI288919.1	EST_HUMAN	qi91g11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632 O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN. ;
4501	17641	30625	7.91	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4501	17641	30626	7.91	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4588	17725	30707	1.11	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein

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4588	17725	30708	1.11	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein
4741	17876	30859	0.93	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4959	13881	26914	0.7	3.0E-05	AI248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element ;
5675	18869	32155	1.72	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
6897	20047	33456	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6897	20047	33457	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8082	21164	34681	2.26	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8547	21628	35166	1.55	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9094	22173	35718	1.56	3.0E-05	AW770982.1	EST_HUMAN	hl94e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
9098	22177	35721	1.63	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9102	22181	35726	0.59	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9331	22407		0.51	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9521	22586	36154	1.4	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9863	22903		3.62	3.0E-05	AI769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10755	23788	37403	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
10755	23788	37404	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12353	25255		1.61	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
12551	25374		1.37	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
12913	26196		1.29	3.0E-05	AW518689.1	EST_HUMAN	xs89d06.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2776811 3'
2400	15531	28658	1.49	2.0E-05	AI286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element ;
2650	15773	28886	14.63	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2777	15893		6.99	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element;contains element L1 repetitive element ;
3207	16382	29393	1.29	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3429	16597	29613	1.04	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3455	16622	29643	1.12	2.0E-05	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
3583	16748		0.87	2.0E-05	X95465.1	NT	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3909	17068		0.81	2.0E-05	AL039107.1	EST_HUMAN	DKFZp566l064_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566l064 5'
5003	18132	31106	0.6	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5878	19068	32376	1.84	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6039	19222		0.87	2.0E-05	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6092	19273	32601	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6092	19273	32602	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6286	19459	32811	0.79	2.0E-05	AI149272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1715114 3' similar to contains L1.t3 L1 repetitive element ;
6700	19916	33311	2.11	2.0E-05	AA714330.1	EST_HUMAN	nw06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
7042	20095	33511	1.69	2.0E-05	Y08926.1	NT	P.falciparum mRNA for AARP1 protein, partial
7054	20107	33523	1	2.0E-05	AI492960.1	EST_HUMAN	qz47b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
7062	20115		7.24	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7303	20385	33844	2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7303	20385	33845	2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7524	20597		0.77	2.0E-05	AF128847.1	NT	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
8069	21151	34671	1.58	2.0E-05	AI381040.1	EST_HUMAN	tg20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9467	22524	36087	0.56	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9467	22524	36088	0.56	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10127	23165	36764	0.6	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10339	23374	36984	0.94	2.0E-05	BF055939.1	EST_HUMAN	7f75g09.y1 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340576 5'
10817	23850	37472	3.53	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
10817	23850	37473	3.53	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
10881	20115		2.66	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11738	23924	37549	1.55	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
11981	24966	38668	5.74	2.0E-05	AI912713.1	EST_HUMAN	we12h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340921 3'
12477	25921		3.7	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2 ;
12592	26104		8.13	2.0E-05	AW074604.1	EST_HUMAN	xa89a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12650	25905		3.24	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12825	25551	32014	2.01	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
13206	25787		1.64	2.0E-05	AI200970.1	EST_HUMAN	qf68g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755236 3'
2759	16071	28983	1.86	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3740	16901	29905	1.71	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lamto 120 Suppressor of Hairless (Su(H)) gene, partial cds
3915	17074		0.97	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4074	17230	30236	11.86	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4288	17433	30420	1.45	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4392	17535	30514	2.14	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4975	18104	31080	2.24	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5079	18207	31179	0.86	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5084	18212	31185	0.64	1.0E-05	Z18943.1	NT	H.sapiens repeat region
6891	20043	33451	1.13	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7230	20135	33553	4.24	1.0E-05	AA641846.1	EST_HUMAN	ns19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element ;
7232	20316	33759	5.19	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7837	20892	34394	0.73	1.0E-05	BF222646.1	EST_HUMAN	7p57d01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3 MER10 repetitive element ;
7956	21006		2.03	1.0E-05	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9116	22195		2.39	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9260	22337	35887	2.59	1.0E-05	AA452578.1	EST_HUMAN	zx35h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9487	22544	36107	12.29	1.0E-05	AA236110.1	EST_HUMAN	zs05e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element;contains element TAR1 repetitive element ;
9566	22708	36275	0.81	1.0E-05	AV732190.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'
10043	23081	36682	0.79	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element ;
10043	23081	36683	0.79	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element ;
10120	23158	36756	1.18	1.0E-05	AW291521.1	EST_HUMAN	UI-H-BI2-agk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10120	23158	36757	1.18	1.0E-05	AW291521.1	EST_HUMAN	UI-H-BI2-agk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10387	23422		2.04	1.0E-05	AW466995.1	EST_HUMAN	he07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.t2 L1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11159	24230	37860	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11159	24230	37861	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
13023	26096	31663	1.4	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2737	15854	28968	5.83	9.0E-06	AI583811.1	EST_HUMAN	tf73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3165	16340	29348	6.11	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759191 3'
3698	16859		2.56	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6025	19208	32528	2.48	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7003	20139	33557	0.82	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7598	20668	34144	2.82	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7953	21003	34515	12.35	9.0E-06	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element;
8659	21739	35280	1.17	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9183	22261	35803	3.3	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9183	22261	35804	3.3	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9423	22497	36063	4.43	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11180	24249	37883	3.61	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2596	16065	28839	2.01	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
6728	19884	33276	2.75	8.0E-06	AA284847.1	EST_HUMAN	zt22d05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:713865 3' similar to contains MER9.t1 MER9 repetitive element ;
10751	23784	37397	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10751	23784	37398	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
1002	14173		1.73	7.0E-06	AA669729.1	EST_HUMAN	ab90f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element ;
1470	14624	27708	3.12	7.0E-06	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2936	16113		10.58	7.0E-06	AI368252.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3654	16817		0.85	7.0E-06	AA385542.1	EST_HUMAN	EST99205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5813	19003		5.49	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
5925	19112	32424	0.93	7.0E-06	N98645.1	EST_HUMAN	yy65c07.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278412 5'
8989	22068	35608	0.83	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
10104	23142		0.52	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	26131	31547	1.68	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4093972 5'
2984	16160	29177	1.17	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3784	16945	29952	1.02	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4876	16183	29206	2.13	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4883	18013	30997	2.19	6.0E-06	AI040099.1	EST_HUMAN	ox08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.t2 MER8 repetitive element ;
5465	18665	31644	2.29	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5525	18722	31739	1.16	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
10060	23098		1.98	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
13142	25742	31948	2.39	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
6186	19362	32710	3.74	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6467	19634	32995	1.94	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7382	20460	33923	1.18	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8654	21734	35274	0.58	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8654	21734	35275	0.58	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10307	23342	36947	6.96	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10731	23764	37372	0.51	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
13011	25566	31957	5.49	5.0E-06	AI065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
664	13850	26877	5.47	4.0E-06	R16267.1	EST_HUMAN	ya48c03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element;contains L1 repetitive element ;
869	14045	27110	4.73	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element;contains element MER21 repetitive element ;
1365	14519	27593	3.18	4.0E-06	AI334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1365	14519	27594	3.18	4.0E-06	AI334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1503	14656	27738	1.45	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2339	15470	28605	1.56	4.0E-06	AW015401.1	EST_HUMAN	UI-H-BI0-aat-f-05-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3131	16307	29321	0.89	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4000	17157	30163	0.99	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4929	18059	31041	1.89	4.0E-06	AI886939.1	EST_HUMAN	wl94c10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element ;
8696	21776	35308	0.68	4.0E-06	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9000	22079	35620	4.49	4.0E-06	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9909	22949	36535	1.28	4.0E-06	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11735	23921	37546	3.99	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
13149	26152		1.33	4.0E-06	AW299734.1	EST_HUMAN	xs53e01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773368 3'
2232	15366	28494	1.31	3.0E-06	AA700562.1	EST_HUMAN	zi34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element ;
2232	15366	28495	1.31	3.0E-06	AA700562.1	EST_HUMAN	zi34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element ;
2340	15471		1.48	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2988	16164	29180	0.84	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.t3 LTR1 repetitive element ;
3339	16512		2.67	3.0E-06	AI857779.1	EST_HUMAN	wl22a05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ;contains L1.t2 L1 repetitive element ;
3883	17042	30040	1.47	3.0E-06	BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3883	17042	30041	1.47	3.0E-06	BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4597	17734	30714	0.8	3.0E-06	T50266.1	EST_HUMAN	yb78b10.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4684	17819	30807	5.52	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
6289	19462	32814	0.82	3.0E-06	AU159412.1	EST_HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7377	20456		2.14	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8274	21356	34874	0.81	3.0E-06	BE562964.1	EST_HUMAN	601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5'
8883	21962	35496	0.75	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12656	25435		12.07	3.0E-06	AW385282.1	EST_HUMAN	RC0-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA
207	13430		2.22	2.0E-06	P54366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1599	14752		6.39	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2451	15579	28707	2.58	2.0E-06	AI672138.1	EST_HUMAN	wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element ;
2537	15662	28785	1.69	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2632	15755	28870	1.81	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3607	16771	29786	0.9	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3858	17018	30017	1.54	2.0E-06	AA173518.1	EST_HUMAN	zp02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3868	17027	30026	0.68	2.0E-06	AW450215.1	EST_HUMAN	UI-H-BI3-aky-g-05-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3876	17035	30033	1.7	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6214	19389		0.92	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6246	19420	32766	0.62	2.0E-06	AI539448.1	EST_HUMAN	te51f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
6571	19733	33112	5.64	2.0E-06	AI819424.1	EST_HUMAN	wj90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7635	20704	34183	0.63	2.0E-06	AA688423.1	EST_HUMAN	nv59c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1.t3 L1 repetitive element ;
8102	21184		1.02	2.0E-06	AW869223.1	EST_HUMAN	MR3-SN0067-120400-002-f02 SN0067 Homo sapiens cDNA
8281	21363	34882	0.76	2.0E-06	T12238.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9036	22115		1.05	2.0E-06	AA772497.1	EST_HUMAN	zh27c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9049	22128	35872	1.59	2.0E-06	H62051.1	EST_HUMAN	yu37c04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929 KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9417	22491	36056	0.9	2.0E-06	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9417	22491	36057	0.9	2.0E-06	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9436	22510		0.46	2.0E-06	AI473450.1	EST_HUMAN	tj16g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
9902	22942	36527	0.86	2.0E-06	N30576.1	EST_HUMAN	yw66e03.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:257212 3'
10123	23161		0.7	2.0E-06	AV748969.1	EST_HUMAN	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
12548	26135	31549	1.34	2.0E-06	P23249	SWISSPROT	PROTEIN MOV-10
12711	25473		5.94	2.0E-06	BE328232.1	EST_HUMAN	hs92f02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.t2 L1 repetitive element ;
34	13272	26276	1.16	1.0E-06	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
674	13860	26891	1.8	1.0E-06	AF084364.1	NT	Mus musculus D6MM5E protein (D6Mm5e) mRNA, complete cds
1482	14635	27719	1.8	1.0E-06	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1553	14706	27786	1	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	zi06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1603	14756	27838	1.19	1.0E-06	AA034141.1	EST_HUMAN	zi06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1615	14768		0.99	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2050	15191	28303	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2050	15191	28304	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4489	17629	30610	15.97	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5215	18336	31308	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5215	18336	31309	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5342	18455	31422	0.72	1.0E-06	N65946.1	EST_HUMAN	za27a08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293750 3'
5405	18607	31579	5.14	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5430	18630	31607	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5430	18630	31608	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5592	18787	31834	1.04	1.0E-06	O60813	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
6915	19103		0.72	1.0E-06	BE063527.1	EST_HUMAN	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
7012	20148	33569	7.53	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
7923	26223		0.73	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8190	21272		0.99	1.0E-06	AA912623.1	EST_HUMAN	ol29c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8468	21549	35079	1.12	1.0E-06	AI347010.1	EST_HUMAN	qp54e02.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926842 3'
8685	21765	35297	1.31	1.0E-06	AI287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element ;
9504	22770	36341	0.91	1.0E-06	N74635.1	EST_HUMAN	za55e01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296472 3'
9579	22721	36291	0.61	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9884	22924	36507	3.47	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9884	22924	36508	3.47	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9929	22969	36558	5.22	1.0E-06	AA132611.1	EST_HUMAN	zo17e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
9991	23030		3.55	1.0E-06	AA449257.1	EST_HUMAN	zx04d11.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
10705	23738		2.19	1.0E-06	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11949	24935		3.1	1.0E-06	AW890941.1	EST_HUMAN	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
12589	25396	32041	8.24	1.0E-06	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
371	13580	26613	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
371	13580	26614	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8602	21683		0.69	9.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11525	24581	38257	1.83	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
4893	18023	31008	4.23	8.0E-07	AI288596.1	EST_HUMAN	ql82g07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4893	18023	31009	4.23	8.0E-07	AI288596.1	EST_HUMAN	qi82g07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6007	19192		8.17	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8191	21273		8.44	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11021	24907		5.84	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBEN89
12183	25143		6.1	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1914	15057	28167	0.97	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5636	18830	31906	0.86	7.0E-07	6006700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5636	18830	31907	0.86	7.0E-07	6006700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1962	15105	28205	3.47	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
2561	15686	28812	2.43	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
4080	17236		1.74	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
9342	22418	35972	1.31	6.0E-07	BF001867.1	EST_HUMAN	7g94f07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L. ;
12115	25095	38800	1.45	6.0E-07	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12444	26067		1.72	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
13229	25992		1.32	6.0E-07	BE222390.1	EST_HUMAN	hu11h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166329 3' similar to contains L1.b2 L1 L1 repetitive element ;
336	13549		1.04	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1082	14248		2.39	5.0E-07	AA380630.1	EST_HUMAN	EST93615 Supt cells Homo sapiens cDNA 5' end
3096	16272		0.73	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4769	17904	30886	0.97	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6247	19421	32767	1.33	5.0E-07	U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7210	20075	33487	1.71	5.0E-07	AI393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element;contains element A3R repetitive element ;
7210	20075	33488	1.71	5.0E-07	AI393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element;contains element A3R repetitive element ;
7503	20578	34050	16.93	5.0E-07	AW070885.1	EST_HUMAN	xe31e02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8470	21551	35081	1.02	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8687	21767		0.88	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10577	23612	37217	5.47	5.0E-07	AI908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
11805	24795	38493	5.69	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11880	24868		2.08	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
12256	25968		1.2	5.0E-07	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
12918	25966		3.06	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
4106	17260	30261	1.66	4.0E-07	AW009602.1	EST_HUMAN	ws84h05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
7328	20410		0.8	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7417	20495	33963	0.97	4.0E-07	Q9Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7417	20495	33964	0.97	4.0E-07	Q9Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8107	21189	34709	0.51	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9251	22328	35875	4.9	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10332	23367	36976	0.53	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10332	23367	36977	0.53	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10531	23566	37174	0.56	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11179	24248	37881	3.88	4.0E-07	AI765528.1	EST_HUMAN	wi81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11179	24248	37882	3.88	4.0E-07	AI765528.1	EST_HUMAN	wi81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11495	24553		1.69	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
11919	24905		1.32	4.0E-07	BE967557.1	EST_HUMAN	601649083F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932924 5'
13207	25788		1.71	4.0E-07	11437071	NT	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1), mRNA
454	13650	26686	5.38	3.0E-07	U19719.1	NT	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
596	13786	26806	3.59	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
1405	14559	27633	1.43	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1655	14808		3.62	3.0E-07	M64857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2104	15243		2.32	3.0E-07	AA526763.1	EST_HUMAN	ni56b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element;contains L1.t3 L1 repetitive element ;
2361	15492	28621	1.14	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2540	15665	28789	4.99	3.0E-07	BE005077.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2540	15665	28790	4.99	3.0E-07	BE005077.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3099	16275	29289	0.97	3.0E-07	T84704.1	EST_HUMAN	yd50f12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111605 5'
3228	16402	29414	1.78	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4802	17937		0.64	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVOMACROGLOBULIN)
4849	17982	30970	8.04	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCCD01 3'
4885	18015	30999	0.7	3.0E-07	AI797236.1	EST_HUMAN	we86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5175	18297	31259	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5175	18297	31260	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5783	18975	32281	12.39	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6095	19276	32605	0.7	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6842	19995		5.09	3.0E-07	AA815175.1	EST_HUMAN	oc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7678	20743	34224	3.53	3.0E-07	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
7841	20896		1.3	3.0E-07	AI591065.1	EST_HUMAN	tw28f11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element;contains element MSR1 MSR1 repetitive element ;
9330	22406	35959	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
9330	22406	35960	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
13194	25777		4.26	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
29	13267	26270	7.32	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
158	13383	26413	6.06	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
158	13383	26414	6.06	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
186	13408	26437	35.88	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
767	13948	26995	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
767	13948	26996	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
779	13959		1.36	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
966	14139	27200	2.32	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN);contains Alu repetitive element;
967	14140	27201	2.02	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
1189	14351	27409	1.55	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1630	14782	27868	2.06	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I
3708	16869		0.63	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3779	16940	29946	21.71	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5238	18360		0.6	2.0E-07	AW902219.1	EST_HUMAN	QV3-NN1023-260400-168-h11 NN1023 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5460	18660	31638	1.52	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6681	25829	33229	0.73	2.0E-07	AW448968.1	EST_HUMAN	UI-H-BI3-ake-b-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
6802	19957	33357	3.39	2.0E-07	AI208715.1	EST_HUMAN	qg56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8664	21744		3.87	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
8893	21972	35508	1.11	2.0E-07	AA035198.1	EST_HUMAN	zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
9963	23002		1.44	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10474	23509	37122	6.34	2.0E-07	AW892507.1	EST_HUMAN	CM4-NN0003-280300-124-e06 NN0003 Homo sapiens cDNA
10706	23739	37342	1.01	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
10706	23739	37343	1.01	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
12138	25655		2.96	2.0E-07	BE153717.1	EST_HUMAN	PM0-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
12226	25967		2.38	2.0E-07	AI732462.1	EST_HUMAN	zn85h11.x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element ;
1126	14291		0.76	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2888	14704	27784	2.08	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3838	14291		1.24	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4408	17550	30534	2.91	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4408	17550	30535	2.91	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6832	19791	33180	0.8	1.0E-07	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
7006	20142	33560	4.69	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
7006	20142	33561	4.69	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
7662	20729	34205	7.6	1.0E-07	N55081.1	EST_HUMAN	yv43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7826	20881	34382	0.69	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7826	20881	34383	0.69	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7854	20909	34413	1.24	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8410	21491	35020	2.76	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8410	21491	35021	2.76	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9155	22233	35778	2.7	1.0E-07	AA693576.1	EST_HUMAN	zi51e10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
9470	22527	36090	1.05	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9816	22856	36436	0.6	1.0E-07	BE327843.1	EST_HUMAN	hu28h06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.t3 MER18 repetitive element ;
10140	23178	36776	2.35	1.0E-07	BF674524.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10149	23187	36784	1.23	1.0E-07	AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
10682	23716		1.22	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12085	25065	38771	2.35	1.0E-07	AI341136.1	EST_HUMAN	qx89e03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009692 3'
12506	25939	31761	3.37	1.0E-07	BE048770.1	EST_HUMAN	hr53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722 DJ1163J1.1 ;
12659	25438		1.45	1.0E-07	X64467.1	NT	H.sapiens ALAD gene for porphobilinogen synthase
12852	25566		2.1	1.0E-07	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
7433	20510	33982	0.75	9.0E-08	AI539362.1	EST_HUMAN	te51b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
10091	23129	36732	2.04	9.0E-08	AV734819.1	EST_HUMAN	AV734819 cdA Homo sapiens cDNA clone cdABFB06 5'
11457	24517	38185	1.92	9.0E-08	AI891052.1	EST_HUMAN	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.t2 OFR repetitive element ;
11965	24950	38656	2.38	9.0E-08	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
12456	25320		2.51	9.0E-08	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
622	16017		2.09	8.0E-08	AI911352.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
1075	14241		1.01	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
3634	16798		1.57	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8937	22016	35557	5.35	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8937	22016	35558	5.35	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9827	22867	36449	3.03	8.0E-08	AW970693.1	EST_HUMAN	EST382776 MAGE resequences, MAGK Homo sapiens cDNA
10788	23821	37445	0.48	8.0E-08	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11523	24579		1.73	8.0E-08	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
82	13317	26345	3.91	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1392	14546	27622	19.51	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3666	16829	29839	0.88	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3666	16829	29840	0.88	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
5332	18445	31413	0.62	7.0E-08	T65891.1	EST_HUMAN	yc11e12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5'
11052	24129		1.73	7.0E-08	AI535743.1	EST_HUMAN	cong3.P11.A5 conorm Homo sapiens cDNA 3'
11970	24955	38658	4.1	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds

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12978	16829	29839	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	16829	29840	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
840	14018	27073	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
840	14018	27074	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2436	15564	28693	1.77	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0166-191199-004-g09 HT0166 Homo sapiens cDNA
3129	16305	29319	0.68	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4363	17506	30487	1.15	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8137	21219		0.59	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9529	22594		0.55	6.0E-08	AA827075.1	EST_HUMAN	ob56c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element ;
11701	24698	38390	2.16	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11823	24812		1.43	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
87	13322	26350	2.17	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2309	15441	28576	3.93	5.0E-08	AA493851.1	EST_HUMAN	nh03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
12185	25144		4.55	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12382	25271	32077	1.77	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1799	14948	28040	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1799	14948	28041	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2950	16127		1.06	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
3132	16308		1.01	4.0E-08	AI078417.1	EST_HUMAN	oz05e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
4024	17180	30189	0.65	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6535	19698	33071	1.07	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8998	22077	35617	0.9	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9340	22416	35969	1.13	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9845	22885		1.56	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10536	23571		0.85	4.0E-08	AI016342.1	EST_HUMAN	ot78d12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 3'
10597	23632	37241	4.75	4.0E-08	AI050027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
11328	24391	38037	5.16	4.0E-08	AA393627.1	EST_HUMAN	zt76b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G505579 NA/CA,K-EXCHANGER. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11328	24391	36038	5.16	4.0E-08	AA393627.1	EST_HUMAN	zt76b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G505579 NA/CA,K-EXCHANGER. ;
11349	24411	38064	11.86	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
11349	24411	38065	11.86	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12190	26108		1.93	4.0E-08	W76159.1	EST_HUMAN	zd66g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.t1 L1 repetitive element ;
12904	25598		2.01	4.0E-08	AI343353.1	EST_HUMAN	tb95a11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;
5728	18921	32215	2.27	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17. ;
7115	18541	31498	6.01	3.0E-08	AI792737.1	EST_HUMAN	qs76f11.y5 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1944045 5'
7711	20776	34262	1.43	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7928	20978		3.32	3.0E-08	AI436352.1	EST_HUMAN	th93h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
10102	23140		0.63	3.0E-08	AF055066.1	NT	Homo sapiens MHC class 1 region
11276	24343	37983	1.64	3.0E-08	AI218001.1	EST_HUMAN	qh21a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845294 3'
11957	24942	38646	1.32	3.0E-08	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
12156	25125		33.85	3.0E-08	R18420.1	EST_HUMAN	yg02f04.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
211	13434		4.16	2.0E-08	AW302996.1	EST_HUMAN	xr87f06.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
236	13458		5.76	2.0E-08	AA425598.1	EST_HUMAN	zw48f07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element;contains element MER16 repetitive element ;
509	13703	26732	4.46	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
677	13863	26893	9.7	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
677	13863	26894	9.7	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1014	14186		7.75	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1373	14528	27602	1.46	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1774	14923	28017	0.98	2.0E-08	AW841890.1	EST_HUMAN	IL5-CN0024-030300-026-C01 CN0024 Homo sapiens cDNA
1780	14929		2.06	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1902	15045		6.7	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2608	15732		1.86	2.0E-08	K00216.1	NT	Sheep His-tRNA-GUG
3279	16453	29474	5.61	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3279	16453	29475	5.61	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3962	17120		1.63	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA
4189	17339	30332	0.62	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4525	17664		1.48	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.t2 L1 repetitive element ;
5072	18200		3.5	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
5753	18945	32247	0.85	2.0E-08	AA813204.1	EST_HUMAN	ai80h11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377189 3'
5955	19141	32457	1	2.0E-08	AW088924.1	EST_HUMAN	xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;
8193	21275	34798	1.11	2.0E-08	P10272	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8301	21383	34904	1.5	2.0E-08	AA490121.1	EST_HUMAN	ab02g06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
9286	22362		0.89	2.0E-08	AU139978.1	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10738	23771	37381	0.83	2.0E-08	N78097.1	EST_HUMAN	yw72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
10738	23771	37382	0.83	2.0E-08	N78097.1	EST_HUMAN	yw72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
12476	25329		1.77	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
13065	26159		1.8	2.0E-08	11431676	NT	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA
1539	16041	27770	1.05	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1672	14824	27907	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
1672	14824	27908	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
1816	14965	28058	1.66	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2110	15248		2.97	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA
3261	16435	29453	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3261	16435	29454	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5716	18909	32204	4.51	1.0E-08	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7946	20996	34507	0.94	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8224	21306	34826	0.62	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8320	21402	34927	0.54	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8320	21402	34928	0.54	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8744	21823	35359	2.27	1.0E-08	AI015304.1	EST_HUMAN	oi35a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9405	22479		0.56	1.0E-08	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9406	22480	36043	0.85	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-d02 BT0546 Homo sapiens cDNA
10171	23208	36801	0.84	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN)
10778	23811	37434	0.87	1.0E-08	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11595	24648	38332	3.55	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
12581	25391		3.06	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
13137	25925		1.26	1.0E-08	BF375398.1	EST_HUMAN	MR4-ST0240-240700-013-g04 ST0240 Homo sapiens cDNA
4357	17500	30481	4.17	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4357	17500	30482	4.17	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10267	23302		0.63	9.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7414	20492	33960	8.1	8.0E-09	AI183500.1	EST_HUMAN	qd42e07.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.t1 MSR1 repetitive element ;
8189	21271	34796	2.54	8.0E-09	AW900159.1	EST_HUMAN	CM0-NN1004-100300-273-e06 NN1004 Homo sapiens cDNA
9189	22267		2.53	8.0E-09	AA938892.1	EST_HUMAN	op74d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
3695	16856		1.98	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4115	17269		0.98	7.0E-09	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
8086	21168		0.58	7.0E-09	BF108755.1	EST_HUMAN	7l45e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
8237	21319		0.99	7.0E-09	AA256200.1	EST_HUMAN	zr80c05.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.t2 L1 repetitive element ;
9460	22517	36080	2.86	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10386	23421	37028	1.95	7.0E-09	BE254850.1	EST_HUMAN	601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10554	23589		0.76	7.0E-09	AA058626.1	EST_HUMAN	zf58e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.t2 L1 repetitive element ;
10910	23993		2.01	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2221	15355		0.95	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: hres3) Homo sapiens cDNA clone DKFZp434C0514 5'
5095	18223	31195	6.2	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5496	18695	31711	9.33	6.0E-09	AW195784.1	EST_HUMAN	xn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8775	21854	35396	1.11	6.0E-09	BE161653.1	EST_HUMAN	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA
9377	22452	36014	2.18	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10483	23518		3.4	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10969	24049	37682	1.66	6.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
12089	25069	38776	1.37	6.0E-09	C01803.1	EST_HUMAN	HUMGS0003762 Human adult (K.Okubo) Homo sapiens cDNA
1447	14600	27677	3.47	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1900	15043	28154	7.4	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6540	19703	33075	2.22	5.0E-09	AA359454.1	EST_HUMAN	EST68746 Fetal lung II Homo sapiens cDNA 5' end
6988	18507	31523	0.66	5.0E-09	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
8785	21864	35407	0.63	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10300	23335	36940	3.25	5.0E-09	AW799667.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
11944	24930	38632	1.87	5.0E-09	AA460142.1	EST_HUMAN	zx60e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795880 3'
534	13727		1.64	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
987	14159		2.75	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1497	14650	27732	1.86	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2500	15627	28747	5.32	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
8030	21113	34631	0.53	4.0E-09	AA495747.1	EST_HUMAN	zw04c06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8719	21799	35334	1.02	4.0E-09	T64942.1	EST_HUMAN	yd11a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66804 3'
11330	24393	38041	9.51	4.0E-09	AI886401.1	EST_HUMAN	wm94f10.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443627 3'
11379	24440		1.44	4.0E-09	AA195142.1	EST_HUMAN	zr34a12.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:L07807 DYNAMIN-1 (HUMAN);
2427	15555	28682	4.51	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3 MER18 repetitive element ;
2619	15742	28856	1.06	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3 MER18 repetitive element ;
2716	15834	28944	0.99	3.0E-09	P23249	SWISSPROT	PROTEIN MOV-10
3408	16578	29593	0.9	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3 MER18 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3464	16631		0.7	3.0E-09	AA442272.1	EST_HUMAN	zv54a04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4212	17361		0.62	3.0E-09	X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
4546	17684	30666	3.47	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4AI (EIF4A1) gene, partial cds
4634	17770	30751	1.19	3.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
8084	21166	34682	1.1	3.0E-09	BE465780.1	EST_HUMAN	hx80a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091 O55091 IMPACT PROTEIN. ;
10453	23488	37096	1.87	3.0E-09	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10792	23825	37448	0.46	3.0E-09	Q10940	SWISSPROT	HYPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X
11272	24340	37978	3.15	3.0E-09	BF109943.1	EST_HUMAN	7l72c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
11272	24340	37979	3.15	3.0E-09	BF109943.1	EST_HUMAN	7l72c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
835	14013		0.98	2.0E-09	X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
1287	14443	27511	4.7	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1691	14843		10.71	2.0E-09	AL118573.1	EST_HUMAN	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2403	15534	28661	2.24	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
4048	17204	30214	3.01	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
4119	17273	30272	0.9	2.0E-09	AI263479.1	EST_HUMAN	qi07d09.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
5264	18383	31348	0.62	2.0E-09	M23161.1	NT	Human transposon-like element mRNA
5837	19027	32333	0.67	2.0E-09	AI004062.1	EST_HUMAN	ot47b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6278	19452		0.75	2.0E-09	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6919	20234		0.88	2.0E-09	AA357407.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7609	20679	34155	8.81	2.0E-09	AA461430.1	EST_HUMAN	zx63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7692	20757	34242	0.66	2.0E-09	W28834.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7971	21021	34534	0.59	2.0E-09	AI243732.1	EST_HUMAN	qh88g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854114 3'
8909	21988	35528	1.2	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
10824	23857	37480	0.85	2.0E-09	AV688642.1	EST_HUMAN	AV688642 GKC Homo sapiens cDNA clone GKCACA11 5'
12745	14013		20.06	2.0E-09	X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
12830	26188		1.86	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
1019	14190		1.19	1.0E-09	W78152.1	EST_HUMAN	zd79d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346863 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1133	14298	27353	1.43	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1133	14298	27354	1.43	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

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2571	15696		1.15	1.0E-09	AI356086.1	EST_HUMAN	qy64e11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.t2 MER12 repetitive element ;
2954	16131	29146	2.02	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2992	16168	29184	6.17	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2992	16168	29185	6.17	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3103	16279	29293	0.99	1.0E-09	BE535440.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4920	18050		6.15	1.0E-09	AA719297.1	EST_HUMAN	zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
5341	18454		0.6	1.0E-09	AA921958.1	EST_HUMAN	om44g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543942 3'
5620	18814	31882	0.85	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5952	19138	32454	1.29	1.0E-09	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
6272	19446	32794	3.34	1.0E-09	P26694	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8584	21665	35206	0.92	1.0E-09	AI688474.1	EST_HUMAN	wd39b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25.t1 MER25 repetitive element ;
10520	23555		2.72	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12642	26120	31668	1.71	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12767	25510		1.42	1.0E-09	T57366.1	EST_HUMAN	yb51g12.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74758 3'
13132	26020		1.66	1.0E-09	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
1337	14494	27564	1.52	9.0E-10	AW867740.1	EST_HUMAN	MR0-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2895	16074	29092	3.74	9.0E-10	AI870071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element PTR5 repetitive element ;
6973	20201	33627	4.98	9.0E-10	AI452982.1	EST_HUMAN	tj46b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:O00372 O00372 PUTATIVE P150. ;
151	13376	26408	9.26	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3423	16592	29607	0.65	8.0E-10	BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-f01 BT0631 Homo sapiens cDNA
4318	17461	30446	5.45	8.0E-10	AA376832.1	EST_HUMAN	EST89564 Small intestine I Homo sapiens cDNA 5' end
10170	23207		2.51	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
719	13901	26941	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
719	13901	26942	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1651	14804	27890	2.56	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2626	15749		20.25	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3157	16332	29341	2.25	7.0E-10	X00566.1	NT	H.sapiens DHFR gene, exon 3

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6314	19486	32841	4.06	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
7574	20646	34124	1.37	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7834	20889		1.65	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8163	21245	34764	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8163	21245	34765	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
936	14111	27171	8.44	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2742	15859	28971	1.63	6.0E-10	AI424405.1	EST_HUMAN	tf02d07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095021 3'
4615	17752	30733	1.88	6.0E-10	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
4861	17994		3.15	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
8983	22062	35602	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
8983	22062	35603	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
9834	22874	36458	0.48	6.0E-10	P98073	SWISSPROT	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
12223	25172		1.95	6.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
780	13960		5.29	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219 5'
3564	16729	29745	1.14	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
5105	18233	31202	1.4	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7475	20550		1.85	5.0E-10	BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9736	22801	36374	2.24	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9736	22801	36375	2.24	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
12040	25021	38725	1.31	5.0E-10	AF091415.1	NT	Macaca tonkeana isolate 569tonkpeona NADH dehydrogenase subunit 4L gene, complete cds; and NADH dehydrogenase subunit 4 gene, mitochondrial genes encoding mitochondrial proteins, partial cds
114	13345		1.09	4.0E-10	AI221083.1	EST_HUMAN	qg09f09.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element ;
2052	15193	28306	1.4	4.0E-10	AW594709.1	EST_HUMAN	hg58g03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
2640	15763	28877	6.79	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7327	20409	33871	17.76	4.0E-10	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10398	23433	37039	0.71	4.0E-10	AW293243.1	EST_HUMAN	UI-H-BI2-ahl-a-07-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10662	23696	37305	1.12	4.0E-10	AI267342.1	EST_HUMAN	aq63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10794	23827	37450	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-f08 HT0521 Homo sapiens cDNA
10794	23827	37451	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-f08 HT0521 Homo sapiens cDNA
938	14112	27173	2.24	3.0E-10	N36113.1	EST_HUMAN	yy32f06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.t1 L1 repetitive element ;
1382	14537		5.3	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
4657	17793	30777	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4657	17793	30778	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5350	18463	31428	0.89	3.0E-10	L34079.1	NT	Human XRCC1 DNA repair gene, genomic
5571	18767	31808	0.78	3.0E-10	N50109.1	EST_HUMAN	yz11g08.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:282782 3'
6332	19503	32861	2.06	3.0E-10	P20350	SWISSPROT	RHOMBOID PROTEIN (VEINLET PROTEIN)
6481	19648	33010	3.62	3.0E-10	BE302970.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
7937	20987	34495	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7937	20987	34496	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8928	22007	35546	1.57	3.0E-10	H87208.1	EST_HUMAN	ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element ;
9249	22326	35872	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9249	22326	35873	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9541	22606		0.78	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10679	23713		1.95	3.0E-10	T65891.1	EST_HUMAN	yc11e12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5'
10820	23853		0.96	3.0E-10	AA769294.1	EST_HUMAN	nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
12941	25619	31977	1.87	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
36	13274	26278	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
36	13274	26279	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1946	15089		1.66	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
3051	16227		0.84	2.0E-10	BF675047.1	EST_HUMAN	602136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5924	19111		2.3	2.0E-10	Q28640	SWISSPROT	(HPRG)
6380	19549	32905	1.56	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7537	20810	34084	6.41	2.0E-10	BE791082.1	EST_HUMAN	601586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8203	21285	34807	0.58	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]
8203	21285	34808	0.58	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]

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9502	22558		1.06	2.0E-10	BF434565.1	EST_HUMAN	7o78d08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.t3 L1 repetitive element ;
11609	24662		1.33	2.0E-10	AI862153.1	EST_HUMAN	ta10f12.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2043695 3'
1538	14691		3.09	1.0E-10	AW867767.1	EST_HUMAN	MR0-SN0038-290300-001-f01 SN0038 Homo sapiens cDNA
1637	14789	27874	3.37	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2649	15772		2.16	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA
3589	16753	29768	0.9	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3629	16793		0.67	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3947	16793		0.76	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
4123	17277		7.33	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4245	17391	30378	16.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4245	17391	30379	16.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4253	17399	30388	1.76	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4285	17430		2.28	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5277	18396		1.01	1.0E-10	AI797745.1	EST_HUMAN	we82f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.t1 MER31 repetitive element ;
7644	20713		0.58	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7860	20914	34419	0.69	1.0E-10	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8434	21515	35046	1.14	1.0E-10	AW408990.1	EST_HUMAN	fB_6A4 Fetal brain library Homo sapiens cDNA
8855	21934		1.62	1.0E-10	AI268340.1	EST_HUMAN	qm04e10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.t1 L1 repetitive element ;
10406	23441		6.24	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548314 5'
11154	24225	37854	3.5	1.0E-10	AI038280.1	EST_HUMAN	oy85h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
12165	18503		1.8	1.0E-10	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
272	13490	26521	0.87	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2171	15306	28433	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
2171	15306	28434	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'

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3470	16637	29657	2.98	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3470	16637	29658	2.98	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
4622	17759	30741	0.8	9.0E-11	AA775985.1	EST_HUMAN	ae78f01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5692	18886		3.05	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10357	23392	37002	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10357	23392	37003	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12556	25378	32072	2.45	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506B08 5'
3185	16360		10.53	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element ;
4154	17306	30300	5.37	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Welzmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5913	19101	32415	0.66	8.0E-11	AW674316.1	EST_HUMAN	ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982 3'
6811	19965		0.62	8.0E-11	AW166158.1	EST_HUMAN	xf45h11.x1 NCI_CGAP_Brn50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.t1 MER10 repetitive element ;
1479	14632	27717	2.09	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
8695	21775	35307	2.61	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10434	23469		1.37	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
425	13620	26661	6.19	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
425	13620	26662	6.19	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6862	20014	33424	0.91	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
7870	20924	34431	3.5	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8559	21640	35179	6.99	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5'
9514	22579	36145	0.5	6.0E-11	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12	13250	26250	1	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3450	13250	26250	1.24	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6646	19804	33191	1.92	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7699	20764	34248	11.57	5.0E-11	11416799	NT	Homo sapiens protocadherin beta 3 (PCDHB3), mRNA
1433	14586		1.38	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2851	15965	29074	9.84	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'
3034	16210	29233	1.26	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4740	17875	30858	0.81	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6605	19765	33154	3.29	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

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7141	20276	33716	0.82	4.0E-11	AA442630.1	EST_HUMAN	zv59f10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR:G1055250 G1055250 PHEROMONE RECEPTOR VN4. ;
7532	20605		3.66	4.0E-11	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9595	22650		1.56	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-f08 HT0256 Homo sapiens cDNA
9862	22902	36487	0.79	4.0E-11	AI609753.1	EST_HUMAN	tf82g12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK353.1 CE00385 ;
10859	23892	37513	0.94	4.0E-11	BF367293.1	EST_HUMAN	MR0-GN0024-180900-008-h09 GN0024 Homo sapiens cDNA
12794	25530	32008	1.71	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1521	14674	27756	4	3.0E-11	6679077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4391	17534		1.35	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
982	14165	27215	1.43	2.0E-11	AI150502.1	EST_HUMAN	qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.t3 MER10 repetitive element ;
1212	14373	27434	20.98	2.0E-11	R24807.1	EST_HUMAN	yg43e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1212	14373	27435	20.98	2.0E-11	R24807.1	EST_HUMAN	yg43e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1644	14796	27880	4.44	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes, complete cds
1644	14796	27881	4.44	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes, complete cds
2823	15937	29047	1.09	2.0E-11	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
3266	16440	29461	5.56	2.0E-11	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3403	16573	29588	0.92	2.0E-11	AI478617.1	EST_HUMAN	tm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
3448	16616	29634	0.67	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
3586	16750		1.01	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3797	16958	29962	0.64	2.0E-11	P70213	SWISSPROT	FRIEND VIRUS SUSCEPTIBILITY PROTEIN 1
4566	17704		1.07	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
4728	17863		0.8	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5051	18179		1.85	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA
6142	18265	31234	0.82	2.0E-11	AA307331.1	EST_HUMAN	EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to alpha-2-macroglobulin
6263	19437	32784	1.23	2.0E-11	AW877806.1	EST_HUMAN	QV2-PT0073-280300-109-h08 PT0073 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6440	19607	32970	2	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16. ;
7345	20425	33888	0.85	2.0E-11	BF592945.1	EST_HUMAN	7j97c03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442565 3'
8066	21148		0.59	2.0E-11	P37072	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR6
9424	22498		1.39	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10491	23526	37135	5.13	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR 6I1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10734	23767	37376	1.09	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10734	23767	37377	1.09	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11375	24436	38094	1.64	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11375	24436	38095	1.64	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11408	24469	38133	1.4	2.0E-11	AA261956.1	EST_HUMAN	zs18b04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685519 5'
12122	25102	38807	12.19	2.0E-11	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12297	26105		1.85	2.0E-11	AA704195.1	EST_HUMAN	zj77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12328	25237		1.44	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12354	25256	32115	2.15	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12641	25431		1.43	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12813	25542		3.62	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13180	26767		2.5	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
693	13876	26909	1.57	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
806	13986	27038	1.72	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1244	14403	27464	2.91	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1528	14681		1.82	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2095	15235	28356	0.94	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2195	15330	28455	3.59	1.0E-11	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
2229	15363	28492	1.1	1.0E-11	AA309318.1	EST_HUMAN	EST180186 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3588	16752	29767	0.95	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5447	18647	31625	14.68	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5953	19139	32455	0.78	1.0E-11	BF222646.1	EST_HUMAN	7p57d01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3 MER10 repetitive element ;
8396	21477	35004	2.65	1.0E-11	4885646	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8781	21860	35403	4.61	1.0E-11	R13174.1	EST_HUMAN	yf73d08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28166 5'
9248	22325	35870	1.49	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9248	22325	35871	1.49	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-260900-423-a03 NN1149 Homo sapiens cDNA
10626	23660		0.54	1.0E-11	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
11566	24621	38302	2.02	1.0E-11	BF680078.1	EST_HUMAN	602154607F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
12903	26879		1.37	1.0E-11	Z20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
3017	16193	29216	0.75	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10002	23040	36632	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10002	23040	36633	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9539	22604		0.88	8.0E-12	BE074720.1	EST_HUMAN	iL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
12408	25287		4.68	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
4783	17918	30905	1.57	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11631	24711	38402	6.8	7.0E-12	AA704735.1	EST_HUMAN	zj23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
13225	25903		1.18	7.0E-12	D16473.1	NT	Human mRNA, Xq terminal portion
3637	16801		0.96	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4468	17608	30586	9.23	6.0E-12	AA732516.1	EST_HUMAN	nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;
5336	18449	31418	5.12	6.0E-12	AI459161.1	EST_HUMAN	tj65g12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2146438 3' similar to contains MER10.t2 MER10 MER10 repetitive element ;
9196	22274	35811	1.09	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9675	22637		1.81	6.0E-12	AA847898.1	EST_HUMAN	od10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.t2 MER29 repetitive element ;
13205	25786		1.25	6.0E-12	AW885845.1	EST_HUMAN	RC4-OT0072-060400-012-f11 OT0072 Homo sapiens cDNA
1068	14234	27293	2.37	5.0E-12	T06573.1	EST_HUMAN	EST04462 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDV33
3477	16644	29663	1.28	5.0E-12	BE047779.1	EST_HUMAN	tz42b05.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291217 5'
3821	16981	29984	7.44	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
6145	19323	32666	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6145	19323	32667	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6620	19780	33168	9.96	5.0E-12	AW974760.1	EST_HUMAN	EST386850 MAGE resequences, MAGN Homo sapiens cDNA
7176	20052	33462	1.06	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
7187	20052	33462	0.93	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8424	21505	35038	1.28	5.0E-12	AA033745.1	EST_HUMAN	zf01g12.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.t3 L1 repetitive element ;
8867	21946		0.55	5.0E-12	AW887037.1	EST_HUMAN	RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA
9195	22273		0.77	5.0E-12	AL079581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9308	22384	35936	2.52	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9623	22678	36247	1.22	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10482	23517		4.8	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10573	23608	37213	0.69	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10793	23826	37449	0.6	5.0E-12	6978754	NT	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
254	13474	26505	3.29	4.0E-12	AA700326.1	EST_HUMAN	zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
255	13474	26505	3.42	4.0E-12	AA700326.1	EST_HUMAN	zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4742	17877	30860	0.88	4.0E-12	AI689984.1	EST_HUMAN	tx26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;
7797	20853		0.71	4.0E-12	BF445140.1	EST_HUMAN	nad21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 MER7 repetitive element ;
8437	21518		4.81	4.0E-12	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
11338	24401	38050	4.33	4.0E-12	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12684	25456		2.11	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
631	13816	26839	2.58	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
631	13816	26840	2.58	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
5276	18395	31363	0.78	3.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5568	18765	31806	1.44	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8570	21651	35193	0.5	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
10891	23975	37606	2.32	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10891	23975	37607	2.32	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1685	14837	27921	1.24	2.0E-12	AW802131.1	EST_HUMAN	IL5-UM0071-120400-065-e05 UM0071 Homo sapiens cDNA
3556	16721	29736	0.93	2.0E-12	6754495	NT	*Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA*
4230	17377	30365	1.29	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4230	17377	30366	1.29	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4541	17679		2.03	2.0E-12	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
5018	18147	31123	0.71	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5018	18147	31124	0.71	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
6606	19766		2.08	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGE resequences, MAGL Homo sapiens cDNA
7326	20408	33870	3.85	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7499	20574	34047	1.33	2.0E-12	BE173035.1	EST_HUMAN	MR0-HT0559-200400-015-e08 HT0559 Homo sapiens cDNA
7838	20893	34395	2.19	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9508	22774		1.88	2.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10191	23228		8.32	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10733	23766	37375	0.76	2.0E-12	AI334130.1	EST_HUMAN	qq07f02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN. ;
12129	25109	38813	1.53	2.0E-12	AW242934.1	EST_HUMAN	xn27h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694965 3'
12313	25228		1.34	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12516	25352		1.46	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
125	13354	26385	1.64	1.0E-12	AW627674.1	EST_HUMAN	hh90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.t1 MER18 repetitive element ;
2044	15185		1.78	1.0E-12	AI871726.1	EST_HUMAN	wm51f07.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
3138	16314	29326	1.04	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3138	16314	29327	1.04	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3978	17135	30138	40.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3978	17135	30139	40.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6088	19269		1.6	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6166	19342		1.62	1.0E-12	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6282	19455	32804	0.59	1.0E-12	BF642800.1	EST_HUMAN	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6282	19455	32805	0.59	1.0E-12	BF642800.1	EST_HUMAN	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6662	19821	33208	0.63	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7265	20348	33800	2.53	1.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7300	20382	33840	10.78	1.0E-12	AI248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.t1 MER10 repetitive element ;
7300	20382	33841	10.78	1.0E-12	AI248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.t1 MER10 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8686	21766	35298	0.59	1.0E-12	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
8902	21981	35521	1.25	1.0E-12	AA782323.1	EST_HUMAN	ac26d05.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
12215	25166	38835	2.32	1.0E-12	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
12437	25310		1.54	1.0E-12	AI738592.1	EST_HUMAN	wi33h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
12600	26068		1.93	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
12788	26166		1.19	1.0E-12	P44836	SWISSPROT	PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR
12951	25661		2.82	1.0E-12	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4056	17212	30223	1.21	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9801	22841		2.81	9.0E-13	N69653.1	EST_HUMAN	za26b06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293651 3'
735	13917	26957	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
735	13917	26958	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1885	15029	28136	2.73	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8303	21385	34906	0.63	8.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437601 3'
8303	21385	34907	0.63	8.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437601 3'
10350	23385		2.82	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8429	21510		0.77	7.0E-13	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12713	25474		32	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866813 5'
12976	25635		1.53	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
2168	15303	28430	5.65	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5239	18361	31329	0.93	6.0E-13	AI267928.1	EST_HUMAN	qo44a09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1911352 3'
3399	16569		1.15	5.0E-13	R78338.1	EST_HUMAN	yi82f04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3484	16652		1.56	5.0E-13	AA435773.1	EST_HUMAN	zt77a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726350 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
7016	20152	33572	0.99	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
11100	24173	37808	2.64	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1916	15059		4.86	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2531	15656		1.61	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4869	18002		1.06	4.0E-13	AA454054.1	EST_HUMAN	zx48d07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795469 5'
5704	18897	32189	4.47	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7355	20434	33896	1.09	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7788	20844	34337	1.08	4.0E-13	AA431529.1	EST_HUMAN	zw76g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA. ;
7898	20950		2.62	4.0E-13	N44291.1	EST_HUMAN	yy33g05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995 A32995 t complex sterility protein - mouse ;
9042	22121	35663	1.38	4.0E-13	AL043810.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
9702	22751	36321	0.47	4.0E-13	AA076907.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
10226	23262	36850	4.44	4.0E-13	AI289831.1	EST_HUMAN	qn32d05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu repetitive element;
11439	24500	38167	1.54	4.0E-13	AA435819.1	EST_HUMAN	zt78g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11439	24500	38168	1.54	4.0E-13	AA435819.1	EST_HUMAN	zt78g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
184	13406		4.35	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
888	14064		1.81	3.0E-13	AA430310.1	EST_HUMAN	zw68g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
1502	14655	27737	0.96	3.0E-13	AI904151.1	EST_HUMAN	CM-BT043-090299-075 BT043 Homo sapiens cDNA
2443	15571	28700	1.53	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
2548	15673		2.28	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2729	15847	28957	3.69	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA
3256	16430		2.44	3.0E-13	AA745844.1	EST_HUMAN	ob18d02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
3592	16756	29771	9.73	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3592	16756	29772	9.73	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5657	18851	32133	0.68	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.t2 THR repetitive element ;
5657	18851	32134	0.68	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.t2 THR repetitive element ;
6114	19294	32629	0.73	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139 O75139 KIAA0644 PROTEIN. ;
8067	21149	34869	7.1	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8268	21350	34865	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
8268	21350	34866	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
10401	23436	37043	0.58	3.0E-13	AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10915	23998		3.1	3.0E-13	AI064768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
11301	24367	38008	3.41	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11898	24886	38585	1.62	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
154	13379	26411	3.52	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
249	13470	26502	2.06	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1299	14455	27521	8.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3070	16245	29266	0.61	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3070	16246	29267	0.61	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3596	16760	29776	1.68	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4224	17372		2.07	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6250	19424	32770	4.34	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6335	19506		0.58	2.0E-13	X79417.1	NT	S.scrofa rps12 mRNA for ribosomal protein S12
6954	20267	33704	5.73	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7199	20064	33474	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7199	20064	33475	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10675	23709	37317	2.41	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12388	25274		22.49	2.0E-13	AW892155.1	EST_HUMAN	CM0-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
302	13518	26551	1.34	1.0E-13	S74129.1	NT	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
911	14086	27151	5.53	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1367	14521	27596	1.4	1.0E-13	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
2079	15219	28339	2.61	1.0E-13	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;
4715	17850	30833	1.32	1.0E-13	BF340987.1	EST_HUMAN	602038009F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4185866 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8094	21176	34691	0.97	1.0E-13	AA577812.1	EST_HUMAN	nn24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element;contains element MER24 repetitive element ;
8094	21176	34692	0.97	1.0E-13	AA577812.1	EST_HUMAN	nn24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element;contains element MER24 repetitive element ;
10295	23330		1.04	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10508	23543	37154	0.6	1.0E-13	AF300701.1	NT	Mus musculus osteotesticular protein tyrosine phosphatase mRNA, complete cds
11661	24740	38431	9.74	1.0E-13	BF108755.1	EST_HUMAN	7l45e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
12206	25160		1.38	1.0E-13	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5',
12920	25605		3.46	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
13077	25706		1.85	1.0E-13	X87579.1	NT	H.sapiens CD4 gene
343	13554	26583	3.76	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
344	13555	26584	1.84	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
2569	15694		4.13	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2811	15925	29036	7.9	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3180	16355	29360	7.5	9.0E-14	AW513296.1	EST_HUMAN	xo54h05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2707833 3'
3310	13554	26583	1	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
3898	17057	30057	7.37	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4879	18010	30994	2.23	9.0E-14	AJ002153.1	NT	Saguinus oedipus gene for seminal vesicle secreted protein semenogelin I
3587	16751		1.17	8.0E-14	BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4066	17222		3.64	8.0E-14	R76269.1	EST_HUMAN	yi72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9647	21090	34605	38.93	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
9760	22698	36266	3.22	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
11717	24757		1.79	8.0E-14	BE062558.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA
12611	25410	32048	2.43	8.0E-14	AI688118.1	EST_HUMAN	wc92h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
1658	16044		4.76	7.0E-14	AW151673.1	EST_HUMAN	xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element ;
9120	22199		0.73	7.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
378	13586	26620	12.43	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10027	23065	36662	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10027	23065	36663	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
633	13818	26842	4.17	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5166	18288	31254	1.32	5.0E-14	AW073791.1	EST_HUMAN	xb03b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.t2 L1 repetitive element ;
5650	18844	32125	5.26	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1147	16030		1.61	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1926	15069	28174	10.15	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3847	17007		0.73	4.0E-14	AA046502.1	EST_HUMAN	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4407	17549	30533	1.04	4.0E-14	N46328.1	EST_HUMAN	yy73c12.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.t3 L1 repetitive element ;
8145	21227		0.71	4.0E-14	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12043	25024	38729	5.5	4.0E-14	BE242466.1	EST_HUMAN	TCAAP1D1470 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1470
12986	26203		5.69	4.0E-14	AI886224.1	EST_HUMAN	wm08c03.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
972	14145	27204	1.56	3.0E-14	X95466.1	NT	R.norvegicus mRNA for CPG2 protein
6873	20025	33434	0.93	3.0E-14	AI420786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
6873	20025	33435	0.93	3.0E-14	AI420786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
7173	20306	33749	0.6	3.0E-14	AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
8987	22066	35606	0.86	3.0E-14	N42165.1	EST_HUMAN	yy07b10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270523 5'
11512	18495	31533	5.87	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element;contains element MER9 repetitive element ;
12894	26041		1.88	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
13212	25884	31853	1.51	3.0E-14	BE891550.1	EST_HUMAN	601435233F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920169 5'
401	13598	26634	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
401	13598	26635	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
708	16019	26925	11.36	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2461	15588		1.04	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2535	15660		0.99	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2593	15718	28835	1.63	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5641	18835	31912	0.97	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5738	18931	32229	1.03	2.0E-14	AI312351.1	EST_HUMAN	ta78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.t3 L1 repetitive element ;
5838	19028	32334	3	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7023	20159		1.04	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
7437	20514	33987	1.06	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7676	20741	34221	24.46	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7676	20741	34222	24.46	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
10121	23159	36758	0.56	2.0E-14	AI978795.1	EST_HUMAN	wr59g10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10630	23664	37273	0.51	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBBF04 5'
11019	24098	37736	3.62	2.0E-14	AW139800.1	EST_HUMAN	UI-H-BI1-adw-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12890	26045		2.5	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
13163	15660		1.26	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1092	14257	27313	2.32	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1438	14591	27664	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1438	14591	27665	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2057	16198	28312	8.9	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2258	15391	28517	6.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2480	15607	28731	6.44	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
3010	16186	29210	1.41	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3236	16410	29424	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3236	16410	29425	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3992	17149	30155	1.69	1.0E-14	AA682994.1	EST_HUMAN	ae89c12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4596	17733	30713	2.01	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5930	19116	32429	1.98	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6813	25834	33371	10.9	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6813	25834	33372	10.9	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1607	14760	27839	1.81	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2242	15375		1.38	9.0E-15	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel.a>
7665	20732	34207	4.24	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8206	21288	34810	1.24	9.0E-15	BE903559.1	EST_HUMAN	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
13099	25716		2.87	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2872	13687		1.53	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7331	20412	33874	1.13	7.0E-15	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
10650	23684		2.34	7.0E-15	AW241958.1	EST_HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR.t2 THR repetitive element ;
12270	25203		1.44	7.0E-15	AA284465.1	EST_HUMAN	zs57d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb:L21934 STEROL O-ACYLTRANSFERASE (HUMAN);contains L1.t1 L1 repetitive element ;
1018	14189	27250	7.51	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
5263	18382		0.98	6.0E-15	AW901258.1	EST_HUMAN	CM4-NN1011-100300-110-d10 NN1011 Homo sapiens cDNA
6041	19224	32546	1.02	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6041	19224	32547	1.02	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
11583	26231		1.54	6.0E-15	AW836843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
423	13618	26658	3.57	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2819	15933	29044	1.76	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5233	18355		0.91	5.0E-15	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
440	13240	26240	2.33	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6804	19959	33359	0.9	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11316	21065	34577	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11316	21065	34578	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4333	17476		7.67	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5141	18264	31232	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5141	18264	31233	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6953	20266		1.11	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7430	20507	33978	3.13	3.0E-15	M27685.1	NT	Mus musculus ultra high suffur keratin gene, complete cds
7430	20507	33979	3.13	3.0E-15	M27685.1	NT	Mus musculus ultra high suffur keratin gene, complete cds

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10129	23167		2.38	3.0E-15	AA807128.1	EST_HUMAN	oc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.t1 MER19 repetitive element ;
11033	24112	37748	8.11	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12620	26081		65.8	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
260	13479	26511	3.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13587	26621	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13587	26622	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1559	14712		0.99	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3599	16763	29778	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3599	16763	29779	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4745	17880		2.76	2.0E-15	AI806335.1	EST_HUMAN	wf07f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN. ;
6311	19483	32838	1.11	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6311	19483	32839	1.11	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7263	20346		1.58	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7421	20498	33969	2.73	2.0E-15	AA704195.1	EST_HUMAN	zj77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7554	20626	34102	5.05	2.0E-15	W05064.1	EST_HUMAN	za78d10.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE ;
9107	22186	35730	2.86	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9273	22349	35899	0.91	2.0E-15	AA397758.1	EST_HUMAN	zt77g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9273	22349	35900	0.91	2.0E-15	AA397758.1	EST_HUMAN	zt77g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9604	22659	36231	1.18	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
9604	22659	36232	1.18	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
11077	24152		3.69	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
13016	16763	29778	3.89	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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13016	16763	29779	3.89	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2834	15948		3.09	1.0E-15	AI689984.1	EST_HUMAN	tx26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;
3077	16253	29275	1.42	1.0E-15	BE043584.1	EST_HUMAN	hk40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
3211	16385	29396	1.18	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4479	17619	30601	0.61	1.0E-15	BE182696.1	EST_HUMAN	RC3-HT0649-100500-022-b05 HT0649 Homo sapiens cDNA
6502	19668	33032	1.72	1.0E-15	T95763.1	EST_HUMAN	ye40e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ;
7149	20284		1.96	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
7184	20049	33460	0.79	1.0E-15	P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8427	21508	35040	0.99	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8615	21695	35232	4.94	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8615	21695	35233	4.94	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9239	22316	35858	0.78	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9242	22319	35862	0.96	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9448	22564	36127	0.99	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9832	22872	36455	0.94	1.0E-15	AA864653.1	EST_HUMAN	oh37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.t3 L1 repetitive element ;
11057	24134	37770	3.04	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
13104	25892	31856	13.05	1.0E-15	AI783944.1	EST_HUMAN	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element;
4626	17762	30744	0.93	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
11241	24310	37947	1.41	9.0E-16	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
11995	24980	38685	1.48	9.0E-16	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ;
11995	24980	38686	1.48	9.0E-16	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ;
5819	19009	32315	0.85	7.0E-16	4885120	NT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7496	20571	34043	1.3	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
7496	20571	34044	1.3	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
13043	25995		38.08	7.0E-16	T94149.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'

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2208	15342		9.12	6.0E-16	AW972611.1	EST_HUMAN	EST384702 MAGE resequences, MAGL Homo sapiens cDNA
1522	14875	27757	0.96	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2745	15862	28973	2.21	5.0E-16	AA992176.1	EST_HUMAN	ot80c04.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element ;
11809	24799	38498	2.68	5.0E-16	BF217368.1	EST_HUMAN	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
13152	25749		14.16	5.0E-16	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2312	15444		1.01	4.0E-16	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2,complete and partial cds
2453	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2453	15581	28709	2.87	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3546	16711	29722	5.29	4.0E-16	Q16653	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4260	17405	30391	8.68	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4260	17405	30392	8.68	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5257	18377	31343	0.91	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7890	20942	34448	42.68	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9495	22552	36114	0.72	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
12293	25218		1.95	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12381	25270		8.66	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic Islet Homo sapiens cDNA clone hbc5355
12392	25277	32079	3.23	4.0E-16	6912469	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12682	25454		1.33	4.0E-16	R18591.1	EST_HUMAN	yf96b11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30489 5'
135	13361	26395	1.09	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
135	13361	26396	1.09	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
478	13673		1.56	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
488	13682		2.33	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1483	14636	27720	2.73	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
3041	16217	29237	4.71	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4711	17846	30830	0.59	3.0E-16	AW160828.1	EST_HUMAN	au76b06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to SW:KID1_MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1 ;
5057	18185	31160	1.32	3.0E-16	AV661393.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'
5392	18594		0.99	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5734	18927	32223	1.67	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8858	21937	35473	4.25	3.0E-16	AI002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element ;

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10094	23132		1.09	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10324	23359	36969	2.59	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13187	26171	31557	3.62	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5'
994	14166		1.03	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2459	15586		0.96	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2753	15870		1.14	2.0E-16	J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4294	17437	30424	1.62	2.0E-16	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4603	17740	30718	1.27	2.0E-16	AI208733.1	EST_HUMAN	qg56f03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER29.t3 MER29 repetitive element ;
5299	18416	31385	0.64	2.0E-16	BE061178.1	EST_HUMAN	RC3-BT0046-131199-003-H12 BT0046 Homo sapiens cDNA
6880	20032	33442	0.68	2.0E-16	Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7893	20945	34451	0.96	2.0E-16	AI470723.1	EST_HUMAN	tj16e11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element ;
8154	21236	34757	1.67	2.0E-16	AI732837.1	EST_HUMAN	nz47f06.x5 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 ;contains MER7.t1 MER7 repetitive element ;
8352	21433	34957	0.81	2.0E-16	BE858026.1	EST_HUMAN	7f82h09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3303521 3'
8352	21433	34958	0.81	2.0E-16	BE858026.1	EST_HUMAN	7f82h09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3303521 3'
8724	21804	35340	0.76	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
8724	21804	35341	0.76	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
189	13411	26438	2.28	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
393	13630		22.93	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.t2 OFR repetitive element ;
2028	15169	28276	3.42	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5839	19029	32335	0.6	1.0E-16	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6565	19727		18	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6704	19862	33252	2.96	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7726	19727		5.39	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9483	22540	36103	0.81	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
3832	16992	29994	2.08	9.0E-17	AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6864	20016		2.15	9.0E-17	AI392964.1	EST_HUMAN	tg22c11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.t2 MER28 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8299	21381		3.56	9.0E-17	AW150257.1	EST_HUMAN	xg49g12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.t2 OFR repetitive element ;
10429	23464		2.35	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1043	14209		2.43	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3998	17155		0.78	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5701	25809	32187	4.09	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7425	20502		1.73	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1487	14640		2.58	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA
5438	18638		3.11	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6826	19979	33387	7.91	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
208	13431	26463	5.62	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6443	19610	32973	2.06	6.0E-17	AW662772.1	EST_HUMAN	hi81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.t2 L1 repetitive element ;
10499	23534	37144	0.54	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
434	13234	26234	2.37	5.0E-17	T64110.1	EST_HUMAN	yc05h08.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
7759	20818	34308	1.81	5.0E-17	T81043.1	EST_HUMAN	yd26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
9562	22704	36270	1.32	4.0E-17	AW129165.1	EST_HUMAN	xf20e04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element;contains MER19.b1 MER19 repetitive element ;
11783	24773	38469	2.51	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12308	25226		1.82	4.0E-17	AI073546.1	EST_HUMAN	ov45e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains MER10.t2 MER10 repetitive element ;
2165	15300	28426	1.85	3.0E-17	AW119123.1	EST_HUMAN	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3263	16437		1.17	3.0E-17	P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3732	16893	29897	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
3732	16893	29898	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
8463	21544	35074	1.12	3.0E-17	N68451.1	EST_HUMAN	za14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.t3 PTR5 repetitive element ;
9903	22943	36528	5.19	3.0E-17	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10591	23626	37234	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10591	23626	37235	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
12268	25201		4.2	3.0E-17	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13155	25751		1.23	3.0E-17	AV720204.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLCDIF08 5'
363	13574	26605	2.65	2.0E-17	AI270080.1	EST_HUMAN	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
364	13574	26605	2.78	2.0E-17	AI270080.1	EST_HUMAN	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
1012	14184		1.43	2.0E-17	AA722932.1	EST_HUMAN	zg81d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2518	15644	28765	2.59	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2518	15644	28766	2.59	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2996	16172	29191	6.96	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5482	18681	31696	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5482	18681	31697	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6394	19563		1.92	2.0E-17	AF055066.1	NT	Homo sapiens MHC class 1 region
6619	19779		1.39	2.0E-17	AL134881.1	EST_HUMAN	DKFZp762J0610_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'
8006	21056	34568	0.89	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8275	21357	34875	1.24	2.0E-17	Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8651	21731	35270	1.05	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
10073	23111	36715	2.71	2.0E-17	BE299888.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960615 5'
10108	23146	36744	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10108	23146	36745	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10466	23501	37114	5.02	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10590	23625	37232	0.97	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10590	23625	37233	0.97	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10618	23652	37261	0.93	2.0E-17	AI798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10618	23652	37262	0.93	2.0E-17	AI798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
769	13950	26999	2.79	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1745	14894		2.01	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
1807	14956	28050	4.83	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2184	15319	28445	2.05	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2412	15542	28669	3.16	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3657	16820		1.03	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4256	17401		9.42	1.0E-17	R09942.1	EST_HUMAN	yf30e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6791	19946	33344	1.62	1.0E-17	AI185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6791	19946	33346	1.62	1.0E-17	AI185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7238	20322	33766	1.33	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8792	21871	35410	1.26	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101299-072-d07 BT0263 Homo sapiens cDNA
10210	23246	36836	1.04	1.0E-17	AW996538.1	EST_HUMAN	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11703	24700	38393	1.52	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
9698	22747		3.05	9.0E-18	AI472167.1	EST_HUMAN	tj86d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3886	17045	30044	2.14	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
359	13570	26599	16.47	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
359	13570	26600	16.47	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
7601	20671	34145	1.09	7.0E-18	AW887642.1	EST_HUMAN	RC3-OT0091-170300-011-d03 OT0091 Homo sapiens cDNA
12826	13570	26599	10.65	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
12826	13570	26600	10.65	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3367	16539	29552	1.23	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived nexin/protease nexin I, enhancer region
4868	18001		3.99	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8444	21525		3.47	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8543	21624	35161	0.78	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9291	22367	35916	0.48	6.0E-18	AI908256.1	EST_HUMAN	RC-BT166-020499-014 BT166 Homo sapiens cDNA
9291	22367	35917	0.48	6.0E-18	AI908256.1	EST_HUMAN	RC-BT166-020499-014 BT166 Homo sapiens cDNA
11399	24460	38124	3.63	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11612	24664	38351	1.69	6.0E-18	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12534	25364	32068	3.91	6.0E-18	U87929.1	NT	Human aconitate hydratase (ACO2) gene, exon 4
1171	14334	27390	12.48	5.0E-18	AI280214.1	EST_HUMAN	qm65g11.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;
4433	17573	30555	0.59	5.0E-18	10946665	NT	Mus musculus gasdermin (Gsdm), mRNA
5387	18589	31561	1.29	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
8917	21996	35535	3.47	5.0E-18	BE143312.1	EST_HUMAN	MR0-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11223	24292	37932	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11223	24292	37933	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12675	25450		6.29	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
13063	25696		28.95	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
127	13355	26386	0.91	4.0E-18	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element ;
127	13355	26387	0.91	4.0E-18	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element ;
1754	14903	27998	52.62	4.0E-18	AA621814.1	EST_HUMAN	nq24f11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1938	15081		1.05	4.0E-18	AI738592.1	EST_HUMAN	wi33h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
2274	15407	28536	1.26	4.0E-18	Q06430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2274	15407	28537	1.26	4.0E-18	Q06430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
3892	17051	30050	0.61	4.0E-18	AI581586.1	EST_HUMAN	ar93b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
5479	18678	31691	2.47	4.0E-18	AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5479	18678	31692	2.47	4.0E-18	AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8029	21112		0.62	4.0E-18	AA746811.1	EST_HUMAN	nx64a08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1.t2 L1 repetitive element ;
11254	24323	37964	7.59	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
872	14048	27114	3.81	3.0E-18	AA814196.1	EST_HUMAN	cb23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5. ;
953	14126	27187	2.25	3.0E-18	BE088634.1	EST_HUMAN	CM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
4060	17216	30225	1.06	3.0E-18	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6968	20196	33622	4.72	3.0E-18	BE001671.1	EST_HUMAN	PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
11167	24238	37869	1.99	3.0E-18	BF218650.1	EST_HUMAN	601984856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
12832	25554		4.55	3.0E-18	AW022015.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
261	13480	26512	4.2	2.0E-18	AW836820.1	EST_HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
1176	14339		74.12	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
3193	16368	29374	0.94	2.0E-18	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5527	18724		4.2	2.0E-18	AA868610.1	EST_HUMAN	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409852 3' similar to TR:O14577 O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE. ;
5623	18817	31886	3.51	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5623	18817	31887	3.51	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5999	19184		1.64	2.0E-18	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
6294	19467	32820	0.91	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6294	19467	32821	0.91	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6408	19577	32938	0.9	2.0E-18	BF352940.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
6448	19615	32979	2.93	2.0E-18	AW665853.1	EST_HUMAN	hi94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER19.t2 MER19 repetitive element ;
7594	20665	34141	0.59	2.0E-18	AA457619.1	EST_HUMAN	aa89d11.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77 ;
8341	21422	34947	0.5	2.0E-18	BE439524.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA
10253	23288	36884	0.95	2.0E-18	AW151673.1	EST_HUMAN	xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element ;
10253	23288	36885	0.95	2.0E-18	AW151673.1	EST_HUMAN	xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element ;
11217	24286	37925	2.91	2.0E-18	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
12031	25014	38716	4.46	2.0E-18	AW151299.1	EST_HUMAN	xg47e09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element ;
12465	14339		12.67	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4537	17675		0.75	1.0E-18	T95406.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element ;
5471	18671	31651	2.64	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCDKE11 3'
5688	18882	32174	3.08	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5688	18882	32175	3.08	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6584	19746	33128	1.31	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8637	21717	35254	1.05	1.0E-18	AI148288.1	EST_HUMAN	oz69d09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.t1 L1 repetitive element ;
10103	23141	36740	4.93	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12416	25294	32084	4.65	1.0E-18	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
559	13752	26780	5.1	9.0E-19	AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
560	13752	26780	3.91	9.0E-19	AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
8032	21115		3.69	9.0E-19	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8886	21965	35501	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8886	21965	35502	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11392	24453	38116	3.15	9.0E-19	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12171	13752	26780	19.34	9.0E-19	AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
1073	14239		1.58	8.0E-19	AW974902.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
8342	21423	34948	1.12	8.0E-19	BE158936.1	EST_HUMAN	MR0-HT0404-210200-001-g06 HT0404 Homo sapiens cDNA
2319	15451	28583	1.74	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
6585	19747	33129	2.11	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7452	20529	34002	0.94	7.0E-19	P26444	SWISSPROT	BETA CRYSTALLIN A2
10216	23252	36841	0.54	7.0E-19	AI344951.1	EST_HUMAN	tb01c08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
12316	26183		1.72	7.0E-19	AA705684.1	EST_HUMAN	zi60b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3879	17038		1.16	6.0E-19	AW852930.1	EST_HUMAN	PM0-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4585	17722	30705	1.56	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4585	17722	30706	1.56	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4921	18051		1.2	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
5978	19163	32483	5.17	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
6346	19516	32873	0.59	5.0E-19	AW663302.1	EST_HUMAN	hh77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
10639	23673	37283	1.18	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11829	24818	38509	8.14	5.0E-19	AW183725.1	EST_HUMAN	xj87b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element ;
13083	25895		1.34	5.0E-19	U66060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
568	13760	26784	0.96	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2747	15864	28975	1.15	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5512	18710	31725	1.2	4.0E-19	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3955	17113	30114	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3955	17113	30115	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4400	17543	30526	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4400	17543	30527	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4569	17707	30686	1.42	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5394	18696		0.69	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7543	20615		1.88	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9658	21101	34614	1.09	3.0E-19	X89685.1	NT	M.musculus mRNA for TPCR33 protein
12563	25385		16.36	3.0E-19	AF165520.1	NT	Homo sapiens phorbolin I protein (PBI) mRNA, complete cds
2627	15750	28863	20.06	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4568	17706		1.34	2.0E-19	AI311783.1	EST_HUMAN	qo91e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE ;
6179	19355	32703	0.81	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7493	20568	34040	0.63	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8525	21606	35145	10.24	2.0E-19	AA012854.1	EST_HUMAN	ze34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10113	23151	36753	0.64	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
494	13689		1.86	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2233	15367	28496	1.64	1.0E-19	H30795.1	EST_HUMAN	yo79g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element ;
2782	15898		2.4	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2909	16087		6.72	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3488	16655	29869	1.18	1.0E-19	AA834967.1	EST_HUMAN	aj49b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.t2 MER37 repetitive element ;
5452	18652	31631	0.73	1.0E-19	AI890866.1	EST_HUMAN	wm91b08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443287 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;
6199	19374	32725	2.6	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6337	26213		0.63	1.0E-19	AA595527.1	EST_HUMAN	nh22d03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:953093 similar to contains L1.t1 L1 repetitive element ;
7806	20862	34355	1.05	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7806	20862	34356	1.05	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7977	25856		0.75	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8644	21724	35261	1.94	1.0E-19	M64657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
8939	22018		2.72	1.0E-19	T99920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element ;
9950	22989		0.69	1.0E-19	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10390	23425	37032	25.12	1.0E-19	AW812259.1	EST_HUMAN	RC0-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
10400	23435	37042	1.59	1.0E-19	N44631.1	EST_HUMAN	yy31e09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272872 5'
11184	24253	37888	1.87	1.0E-19	BE616026.1	EST_HUMAN	601279682F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611493 5'
6784	19939	33336	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6784	19939	33337	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7687	20752	34234	1.46	8.0E-20	AI221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7687	20752	34235	1.46	8.0E-20	AI221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3349	16521	29537	0.71	7.0E-20	BF326455.1	EST_HUMAN	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
7134	18560	31474	5.66	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D092 5'
8693	21773	35305	8.83	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
8693	21773	35306	8.83	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
12014	24998		2.89	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3645	16808	29822	3.64	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4387	17530	30511	4.58	6.0E-20	BE622434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4718	17853		1.8	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTCBTA01 5'
7264	20347	33799	1.42	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8131	21213	34733	6.96	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
8131	21213	34734	6.96	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
8295	21377	34898	0.79	5.0E-20	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9035	22114	35657	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9035	22114	35658	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9644	21087		1.13	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845O24.1
1649	14802	27889	0.94	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5765	18957		1.13	4.0E-20	Q99880	SWISSPROT	HISTONE H2B C (H2B/C)
8110	21192		5.61	4.0E-20	AI874352.1	EST_HUMAN	tz64g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293396 3'
10717	23750	37357	1.13	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2207	15341	28468	1.22	3.0E-20	U03888.1	NT	Human BXP21 gene
4325	17468	30455	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I14
4747	17882	30864	1.08	3.0E-20	AA037616.1	EST_HUMAN	zk36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.t3 L1 repetitive element ;
9135	22214		2.69	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10527	23562	37168	0.47	3.0E-20	BF185264.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5'
10900	23984		1.59	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12331	25239	32109	6.09	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
853	14030		5.65	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;
1135	14300	27355	2.49	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN. ;
1135	14300	27356	2.49	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN. ;
2878	14030		5.32	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;
5061	18189	31163	5.15	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5061	18189	31164	5.15	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5256	18376		0.9	2.0E-20	5174538	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
8309	21391	34915	0.97	2.0E-20	AA309457.1	EST_HUMAN	EST180326 Liver III Homo sapiens cDNA 5' end
9391	22466	36030	2.65	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
9391	22466	36031	2.65	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12743	25878	31852	2.17	2.0E-20	H55371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
2070	15995	28327	6.61	1.0E-20	AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
4560	17698	30679	1.02	1.0E-20	BF115158.1	EST_HUMAN	hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.t2 L1 repetitive element ;
7034	20170	33592	0.74	1.0E-20	AF049567.1	EST_HUMAN	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
9364	22439	35998	2.08	1.0E-20	11418491	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
11847	24836	38530	2.03	1.0E-20	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12461	25323		2.91	1.0E-20	AA420453.1	EST_HUMAN	nc60g08.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.t3 L1 repetitive element ;

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2979	16155		1.18	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl12-8J21
12174	25135		3.98	9.0E-21	AW898189.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
9011	22090		0.98	8.0E-21	AW674891.1	EST_HUMAN	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN O95169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR ;
11830	24819	38510	3.91	8.0E-21	AA809411.1	EST_HUMAN	ob71f06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
12345	25250		3.8	8.0E-21	O21330	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2130	15266	28385	3.85	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
2130	15266	28386	3.85	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3792	16953	29958	1.36	7.0E-21	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4369	17512		6.29	7.0E-21	AA046502.1	EST_HUMAN	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
6564	19726	33104	0.94	7.0E-21	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8582	21663	35203	1.46	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-6
8875	21954	35490	4.94	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10319	23354	36963	1.07	7.0E-21	AW856922.1	EST_HUMAN	RC0-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA
10934	24016	37648	1.94	7.0E-21	AA723404.1	EST_HUMAN	zg73d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.t3 OFR repetitive element ;
4220	17369	30358	0.75	6.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9336	22412		1.39	6.0E-21	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
947	14120	27181	1.34	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
2354	15485	28617	1.23	5.0E-21	AA928194.1	EST_HUMAN	om23g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541908 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
4483	17623	30604	3.21	5.0E-21	BE968839.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4809	14120	27181	1.16	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4923	18053	31039	8.33	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
6902	20217		0.77	5.0E-21	AW440864.1	EST_HUMAN	he05e10.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918154 3'
7157	20291	33734	1	5.0E-21	BE856505.1	EST_HUMAN	7f83d11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.t1 OFR repetitive element ;
10801	23834	37457	0.54	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
10801	23834	37458	0.54	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
12259	25195		1.28	5.0E-21	AA393574.1	EST_HUMAN	zt72c04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1772	14921	28015	1.86	4.0E-21	AA970713.1	EST_HUMAN	oo86e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains OFR.t1 OFR repetitive element ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7011	20147	33568	2.61	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
9983	23022	36614	0.82	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10010	23048	36642	0.61	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
1884	15028	28135	1.1	3.0E-21	AA218891.1	EST_HUMAN	zq15d06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2348	15479	28611	1.51	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3149	16324	29335	6.41	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5616	18810	31878	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5616	18810	31879	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5856	19046		0.9	3.0E-21	AV661044.1	EST_HUMAN	AV661044 GLC Homo sapiens cDNA clone GLCGOA10 3'
6308	19480		2.74	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
7215	20080	33493	7.52	3.0E-21	BF361093.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
9894	22934	36518	0.92	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12879	26099	31665	3.58	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
150	13375		24.5	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
958	14131	27189	0.61	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
958	14131	27190	0.61	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1241	14400		3.03	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2703	15821	28937	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2703	15821	28938	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5601	18796	31846	1.66	2.0E-21	AI624582.1	EST_HUMAN	ts30f03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854 HYPOTHETICAL 51.1 KD PROTEIN ;
5694	18888	32178	0.8	2.0E-21	AA027211.1	EST_HUMAN	ze97a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
5694	18888	32179	0.8	2.0E-21	AA027211.1	EST_HUMAN	ze97a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
6157	19333	32679	0.74	2.0E-21	W44493.1	EST_HUMAN	zc28h02.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323667 5'
8467	21548	35078	0.58	2.0E-21	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
8558	21639	35178	8.13	2.0E-21	BE141785.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
9023	22102	35642	3.27	2.0E-21	AU136779.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11313	24377		2.04	2.0E-21	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
11599	24652	38335	2.88	2.0E-21	BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11599	24652	38336	2.88	2.0E-21	BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12572	25389		6.44	2.0E-21	AF176815.1	NT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1284	14440	27509	1.89	1.0E-21	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
1434	14587		4.93	1.0E-21	AI601264.1	EST_HUMAN	ar88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
6616	19776		2.73	1.0E-21	AL079752.1	EST_HUMAN	DKFZp434I0830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I0830 5'
7342	20422	33885	4.7	1.0E-21	AI223104.1	EST_HUMAN	qg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QM PROTEIN (HUMAN);
10448	23483	37092	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10448	23483	37093	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10812	23845		1.31	1.0E-21	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
13014	25667		1.67	1.0E-21	AF046133.1	NT	Homo sapiens chromosome Xp22 410-8
4530	17668	30654	2.38	9.0E-22	AI702438.1	EST_HUMAN	tz94a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
8803	21882	35420	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
8803	21882	35421	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11031	24110	37746	3.1	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCCG05 5'
12007	24992	38696	1.39	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
971	14144		7.93	8.0E-22	BE144748.1	EST_HUMAN	CM0-HT0179-281099-076-h05 HT0179 Homo sapiens cDNA
8080	21162		3.36	8.0E-22	AA046502.1	EST_HUMAN	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
682	13867	26898	3.78	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4398	17541	30522	3.27	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5150	18272	31241	0.91	7.0E-22	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8888	21967		1.24	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
9032	22111	35653	2.77	7.0E-22	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
9802	22842	36419	2.05	7.0E-22	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8436	21517		1.25	6.0E-22	AW029123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
6646	19805	33192	3.27	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10525	23560	37167	2.98	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12833	25555		1.63	5.0E-22	BF476511.1	EST_HUMAN	naa27b06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3726	16887		0.77	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
8608	26224		2.81	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10961	24042	37677	1.97	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13021	25672		3.85	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
981	14154		1.34	3.0E-22	AI469679.1	EST_HUMAN	tm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN);contains L1.t1 L1 repetitive element ;
2636	15759	28873	1.33	3.0E-22	AI859038.1	EST_HUMAN	wl66b04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21. ;
3763	16924		1.65	3.0E-22	D14718.1	NT	Human chromosomal protein HMG1 related gene
4922	18052	31038	3.18	3.0E-22	AI090125.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.t2 MER12 repetitive element ;
8011	21061	34573	0.8	3.0E-22	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8425	21506		1.11	3.0E-22	BE156613.1	EST_HUMAN	QV0-HT0368-090200-099-f12 HT0368 Homo sapiens cDNA
8430	21511	35042	1.88	3.0E-22	BE089841.1	EST_HUMAN	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8555	21636	35172	1.14	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
8555	21636	35173	1.14	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
2008	15148		4.04	2.0E-22	N24942.1	EST_HUMAN	yx73d05.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
2590	15715	28833	1.72	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3507	16674	29684	3.98	2.0E-22	6394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4341	17484	30466	1.41	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA
5973	25814	32476	1.47	2.0E-22	W39456.1	EST_HUMAN	zc20f01.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6306	19478	32833	3.58	2.0E-22	BF092116.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
9904	22944	36529	1.78	2.0E-22	AI276522.1	EST_HUMAN	qj76h06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains MER29.t3 MER29 repetitive element ;
10001	23039	36630	0.85	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219269 3'
10001	23039	36631	0.85	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219269 3'
12056	25037	38745	1.52	2.0E-22	AW418960.1	EST_HUMAN	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
12139	25656	31954	2.33	2.0E-22	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1927	15070	28175	2.05	1.0E-22	AW865517.1	EST_HUMAN	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
2651	15774	28887	2.36	1.0E-22	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3497	16664	29676	1.53	1.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
7920	20971	34478	1.09	1.0E-22	BE084667.1	EST_HUMAN	MR0-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
10776	23809	37432	1.05	1.0E-22	AI365435.1	EST_HUMAN	qz09b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2 MER29 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10776	23809	37433	1.05	1.0E-22	AI365435.1	EST_HUMAN	qz09b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2 MER29 repetitive element ;
13078	26707		12.31	9.0E-23	AW802801.1	EST_HUMAN	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
3661	16824	29833	0.74	8.0E-23	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3385	16555		2.21	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAWC07 3'
11293	24359	38000	3.74	7.0E-23	5031952	NT	Homo sapiens Not56 (D. melanogaster)-like protein (NOT56L) mRNA
3520	16686		1.83	6.0E-23	AF199333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4383	17526	30507	1.15	6.0E-23	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
12283	25211	32097	4.93	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12283	25211	32098	4.93	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12483	25335	32058	3.18	6.0E-23	AI209130.1	EST_HUMAN	qg59c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MV10_MOUSE P23249 PROTEIN MOV-10. ;
5560	18757	31796	4.01	5.0E-23	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6369	25824	32898	3.69	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7695	25824	32898	2.78	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6570	19732	33110	0.67	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6570	19732	33111	0.67	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8022	21105	34622	3.26	3.0E-23	AA130165.1	EST_HUMAN	zl35g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.t2 MER29 repetitive element ;
9450	22566	36130	3.72	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
9450	22566	36131	3.72	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
10523	23558		1.42	3.0E-23	AW897927.1	EST_HUMAN	RC3-NN0066-270400-011-h01 NN0066 Homo sapiens cDNA
11372	24433		1.35	3.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
683	13868	26899	3.69	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1166	15988		3.46	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2856	15970	29079	1	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2856	15970	29080	1	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3457	16624		1.11	2.0E-23	AI201458.1	EST_HUMAN	qs73f11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
3810	16970		3.53	2.0E-23	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
4085	17240	30246	4.43	2.0E-23	H59931.1	EST_HUMAN	yr16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
4085	17240	30247	4.43	2.0E-23	H59931.1	EST_HUMAN	yr16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
8057	21140		5.28	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
9044	22123	35665	0.95	2.0E-23	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12265	25199		6.7	2.0E-23	M32658.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12844	25561		3.68	2.0E-23	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12983	26103		2.3	2.0E-23	AU133931.1	EST_HUMAN	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4650	17786	30769	1.57	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4888	18018		5.42	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6861	20013		3.27	1.0E-23	BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
8551	21632	35169	4.61	1.0E-23	AA448097.1	EST_HUMAN	zw82c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.t2 PTR5 repetitive element ;
10909	23992	37625	2.19	1.0E-23	BE409643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
10909	23992	37626	2.19	1.0E-23	BE409643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
13082	26074	31654	1.35	1.0E-23	AW901816.1	EST_HUMAN	QV0-NN1020-170400-195-a11 NN1020 Homo sapiens cDNA
566	13758		1.67	9.0E-24	AA663213.1	EST_HUMAN	ab75a08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TR:E19822 E19822 CA PROTEIN. ;
4771	17906	30888	1.12	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
4771	17906	30889	1.12	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
6578	19740	33121	0.95	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3976	17133		0.94	7.0E-24	AW937954.1	EST_HUMAN	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
5281	18400		16.79	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A2311 5'
10876	23961		1.61	7.0E-24	AW303317.1	EST_HUMAN	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element;contains MER19.t2 MER19 repetitive element ;
724	13906		2.21	6.0E-24	AB001421.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
861	14038	27100	12.8	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
4078	17234	30241	9.39	5.0E-24	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
7935	20985	34493	1.27	5.0E-24	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4371	17514		0.9	4.0E-24	BF369469.1	EST_HUMAN	RC0-GN0090-250900-022-h09 GN0090 Homo sapiens cDNA
6052	19234	32559	2.77	4.0E-24	AA594178.1	EST_HUMAN	nn31h05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN ;
8880	21959	35494	0.71	4.0E-24	AW813711.1	EST_HUMAN	RC3-ST0197-130100-014-f06 ST0197 Homo sapiens cDNA
11454	24514	38182	2.05	4.0E-24	BE544822.1	EST_HUMAN	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464498 5'
12669	25446	32054	4.02	4.0E-24	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
7229	20134	33551	0.73	3.0E-24	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
7229	20134	33552	0.73	3.0E-24	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
8618	21698		2.94	3.0E-24	AW614871.1	EST_HUMAN	hh68c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MER29.b2 MER29 repetitive element ;
8673	21753		1.24	3.0E-24	AW962076.1	EST_HUMAN	EST374149 MAGE resequences, MAGG Homo sapiens cDNA
9665	22627	36198	3.79	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
12756	25501	32034	1.34	3.0E-24	BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
2422	15551	28678	2.55	2.0E-24	AA167539.1	EST_HUMAN	zp11f09.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
3899	17058		0.82	2.0E-24	AW898189.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
7515	26219		0.63	2.0E-24	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7643	20712	34191	0.9	2.0E-24	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
7648	20717	34194	0.58	2.0E-24	AJ003536.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl12-5H13
8938	22017	35559	3.81	2.0E-24	AL119158.1	EST_HUMAN	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
8977	22056		0.9	2.0E-24	H69214.1	EST_HUMAN	yr92b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element ;
10058	23096	36698	1.06	2.0E-24	AI521759.1	EST_HUMAN	ti77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
10058	23096	36699	1.06	2.0E-24	AI521759.1	EST_HUMAN	ti77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12580	26153		21.43	2.0E-24	M28877.1	NT	Human O family dispersed repeat element
1731	14881	27972	4.81	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51646), mRNA
2738	15855		1.65	1.0E-24	AW820194.1	EST_HUMAN	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
3085	16261	29278	0.72	1.0E-24	D85423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4385	17528		1.93	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6531	19695	33068	1.13	1.0E-24	7106336	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
7720	20784	34272	4.85	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7907	20959	34465	5.07	1.0E-24	BE144526.1	EST_HUMAN	MR0-HT0168-271199-005-d09 HT0168 Homo sapiens cDNA
8130	21212	34732	2.29	1.0E-24	AW901164.1	EST_HUMAN	CM0-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA
11999	24984	38689	1.37	9.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5111	18239	31206	2.7	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element ;
8413	21494	35025	3.7	7.0E-25	AA468646.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
12003	24988	38693	3.64	7.0E-25	AA583540.1	EST_HUMAN	nf25h06.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
7131	18557		5.04	6.0E-25	W87623.1	EST_HUMAN	zh65h07.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
7899	20951	34458	11.72	6.0E-25	7305360	NT	Mus musculus otogelin (Otog), mRNA
1683	14835	27920	1.61	5.0E-25	AW850271.1	EST_HUMAN	IL3-CT0219-161199-031-D04 CT0219 Homo sapiens cDNA
11596	24649	38333	3.12	5.0E-25	AW979107.1	EST_HUMAN	EST391217 MAGE resequences, MAGP Homo sapiens cDNA
1478	14631	27716	2.66	4.0E-25	T98107.1	EST_HUMAN	ye56h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3489	16656		2.81	4.0E-25	AW887671.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
4436	17576		4.06	4.0E-25	BE170957.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
10144	23182	36779	0.83	4.0E-25	AA383873.1	EST_HUMAN	EST97317 Thymus I Homo sapiens cDNA 5' end similar to EST containing O family repeat
2256	15389	28516	1.02	3.0E-25	BE068922.1	EST_HUMAN	RC5-BT0377-131299-031-F02 BT0377 Homo sapiens cDNA
3396	16566	29581	3.12	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
3396	16566	29582	3.12	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
5015	18144	31119	0.7	3.0E-25	P29622	SWISSPROT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
8532	21613	35149	5.42	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11287	24353	37993	2.7	3.0E-25	AA579013.1	EST_HUMAN	nf30h10.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.t1 L1 repetitive element ;
1378	14533	27607	4.9	2.0E-25	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2382	15513	28641	7.33	2.0E-25	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2893	15731	28848	3.71	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4307	17450	30436	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4307	17450	30437	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
9967	23006	36601	2.13	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
375	13583	26617	0.81	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'
1277	14434		2.07	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4983	18112	31089	2.71	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
5298	18415	31383	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
5298	18415	31384	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
6697	19855		0.95	1.0E-25	AA189080.1	EST_HUMAN	zq45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
6936	25838	33686	2.95	1.0E-25	AA582690.1	EST_HUMAN	nn54h11.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
8098	21180	34698	3.56	1.0E-25	AA709079.1	EST_HUMAN	zf96g04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.t3 PTR5 repetitive element ;
9746	22810	36388	1.32	1.0E-25	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
9746	22810	36389	1.32	1.0E-25	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
11212	24281	37920	3.11	1.0E-25	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12280	25209	38364	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12280	25209	38365	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
2553	15678	28802	1.94	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11252	24321		2.35	9.0E-26	AI905368.1	EST_HUMAN	QV-BT087-301298-006 BT087 Homo sapiens cDNA
12140	25901		5.33	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5811	19001		1.51	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1608	14761	27840	5.61	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4089	17244	30251	1.68	7.0E-26	X89211.1	NT	H.saplens DNA for endogenous retroviral like element
4275	17420	30407	1.92	7.0E-26	AW340153.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366 3'
5755	18947	32249	0.84	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11966	24951		6.85	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12901	25596		5.49	7.0E-26	AW954559.1	EST_HUMAN	EST386629 MAGE resequences, MAGC Homo sapiens cDNA
2300	15432	28565	3.83	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3427	16595	29611	0.69	6.0E-26	AA206131.1	EST_HUMAN	zq52h04.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
10753	23786	37400	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10753	23786	37401	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11979	24964	38666	2.15	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1204	14366	27426	0.89	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1204	14366	27427	0.89	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
9612	22667		3.29	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10897	23981	37613	2.84	4.0E-26	BE266187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
11604	24657	38342	1.38	4.0E-26	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1797	14946	28038	1.25	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
2059	15200	28314	1.14	3.0E-26	AL045855.2	EST_HUMAN	DKFZp434I066_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I066 5'
2088	15228		3.34	3.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3878	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	zo30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR ;
3878	17037	30036	1.41	3.0E-26	AA152464.1	EST_HUMAN	zo30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR ;
7051	20104	33521	6.09	3.0E-26	BF245458.1	EST_HUMAN	601864963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
11867	24855	38550	1.97	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11867	24855	38551	1.97	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11902	24890	38591	7.79	3.0E-26	AA583173.1	EST_HUMAN	nn37d05.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1 OFR repetitive element ;
699	13882	26915	6.84	2.0E-26	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1917	15060		3.07	2.0E-26	AL038099.2	EST_HUMAN	DKFZp566L171_s1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566L171 3'
3303	16477	29499	5.22	2.0E-26	X86694.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
10991	24070		1.93	2.0E-26	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11493	24551	38226	2.96	2.0E-26	AI801412.1	EST_HUMAN	to89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element;contains element MER20 MER20 repetitive element ;
11704	24701		2.06	2.0E-26	AF055066.1	NT	Homo sapiens MHC class 1 region
12389	25275		1.76	2.0E-26	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
12604	26088	31658	2.33	2.0E-26	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
139	13365	26398	8.96	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2105	15244	28365	1.42	1.0E-26	AL039363.2	EST_HUMAN	DKFZp434H1910_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5'
2751	15868		6.28	1.0E-26	AF261085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
6980	20208		2.89	1.0E-26	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
11131	24203		1.96	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566C2146 5'
12655	26178		2.77	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
13175	25763		1.16	1.0E-26	AW408742.1	EST_HUMAN	UI-HF-BM0-adw-d-10-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7757	20816		0.87	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9503	22769		5.02	9.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12143	25118		6.5	9.0E-27	BF445556.1	EST_HUMAN	naa03c07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.t1 OFR repetitive element ;
11	13249	26249	4.22	8.0E-27	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
571	13763		4.57	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1448	14601	27678	23.84	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1448	14601	27679	23.84	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2236	15369	28499	1.82	8.0E-27	AW864776.1	EST_HUMAN	PM2-SN0018-220300-002-e07 SN0018 Homo sapiens cDNA
3254	16428	29446	1.8	8.0E-27	P12236	SWISSPROT	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3434	16602	29621	0.75	8.0E-27	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5812	19002	32308	1.07	8.0E-27	AV732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 5'
7117	18543		2.65	8.0E-27	BE926560.1	EST_HUMAN	MR4-BT0398-250800-204-d06 BT0398 Homo sapiens cDNA
7192	20057	33467	2.49	8.0E-27	N84970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
9410	22484	36048	1.63	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
9410	22484	36049	1.63	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
701	13884		1.77	7.0E-27	Z70664.1	NT	Human endogenous retroviral element HC2
5201	18322		2.19	7.0E-27	AW629172.1	EST_HUMAN	hi51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN. ;
9058	22137		0.97	7.0E-27	D86984.1	NT	Human mRNA for KIAA0231 gene, partial cds
10988	24067		3.7	7.0E-27	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
10964	24045	37679	3.21	6.0E-27	M26697.1	NT	Human nucleolar protein (B23) mRNA, complete cds
12094	25074	38781	1.55	6.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
7954	21004		0.73	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10442	23477	37081	3.21	5.0E-27	BF666614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
10442	23477	37082	3.21	5.0E-27	BF666614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
6883	20035	33444	1.65	4.0E-27	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8125	21207		0.98	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8172	21254		1.31	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9945	22984	36577	0.61	4.0E-27	AW880859.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11903	24891	38592	2.62	4.0E-27	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
13213	26080	31655	1.17	4.0E-27	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2099	15239	28361	7.1	3.0E-27	X60658.1	NT	R.rattus RYA3 mRNA for a potential ligand-binding protein
4386	17529	30510	1.55	3.0E-27	BE071924.1	EST_HUMAN	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
5462	18662	31641	6.81	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
9505	22771	36342	3.49	3.0E-27	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
42	13280	26286	9.28	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1944	15087		24.24	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
3178	16353		13.34	2.0E-27	AW629172.1	EST_HUMAN	hi51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN. ;
3296	16470	29489	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3296	16470	29490	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6814	19967	33373	0.79	2.0E-27	H02655.1	EST_HUMAN	yj36e01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to SP:HMGC_MOUSE Q02591 HOMEOBOX PROTEIN ;
8282	21364	34883	1.17	2.0E-27	AI866347.1	EST_HUMAN	wi28g07.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426268 3'
9469	22526		2.6	2.0E-27	AA551527.1	EST_HUMAN	nh08h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.t3 L1 repetitive element ;
9995	23033	36625	0.83	2.0E-27	X60658.1	NT	R.rattus RYA3 mRNA for a potential ligand-binding protein
10241	23276	36868	1.45	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
10241	23276	36869	1.45	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
11197	24266	37901	3.61	2.0E-27	AU121685.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
11777	15087		6.43	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
12107	25087	38791	1.64	2.0E-27	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternativcly spliced
449	13645		2.34	1.0E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1021	14192	27251	4.97	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6674	19833	33222	6.51	1.0E-27	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA

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7010	20146	33566	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
7010	20146	33567	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8809	21888	35430	1.16	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9186	22264		1.69	1.0E-27	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
9923	22963	36551	2.65	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
12005	24990	38694	3.05	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds
144	13368		2.26	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314 SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313 ;
321	13535	26567	2.17	9.0E-28	AU126260.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
10601	23636	37243	0.47	9.0E-28	AA174078.1	EST_HUMAN	zp18g12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
12224	25173		3.04	9.0E-28	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12565	26003		13.39	8.0E-28	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0556 PROTEIN. ;contains element MER22 repetitive element ;
1208	14370	27430	11.5	7.0E-28	AU142750.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
11463	24522	38192	1.65	7.0E-28	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12181	25141		5.04	7.0E-28	AV735348.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
9119	22198		1.28	6.0E-28	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
12866	25577		5.92	6.0E-28	AA504562.1	EST_HUMAN	aa60e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element;contains element PTR5 repetitive element ;
328	13542		2.75	5.0E-28	AI921003.1	EST_HUMAN	wo18c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element ;
4116	17270	30269	38.94	5.0E-28	R79762.1	EST_HUMAN	yi89f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
2689	15809	28926	1.46	4.0E-28	AW195066.1	EST_HUMAN	xn33c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
3177	16352	29358	1.34	4.0E-28	BE409100.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
7483	20558	34030	3.55	4.0E-28	AI198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
11105	24177		4.19	4.0E-28	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
11255	24324		14.89	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
11278	20558	34030	4.34	4.0E-28	AI198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12622	25418		1.7	4.0E-28	AW854244.1	EST_HUMAN	RC3-CT0254-240400-210-f12 CT0254 Homo sapiens cDNA
12773	26069		1.62	4.0E-28	AW862350.1	EST_HUMAN	RC0-CT0379-070100-031-h01 CT0379 Homo sapiens cDNA

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1312	14468		2.29	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5227	18349		0.94	3.0E-28	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9027	22106	35647	2.28	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-f09 HT0713 Homo sapiens cDNA
11176	24245	37878	2.09	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
12653	25433		3.77	3.0E-28	AI831991.1	EST_HUMAN	wj98f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element;contains element HGR repetitive element ;
12803	25536		3.29	3.0E-28	BE082801.1	EST_HUMAN	RC2-BT0642-210200-013-f03 BT0642 Homo sapiens cDNA
12865	25576	31993	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12865	25576	31994	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
91	13326	26354	12.79	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1191	14353	27411	9.24	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2546	15671	28795	2.16	2.0E-28	AI348634.1	EST_HUMAN	qo35b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element ;
3446	16614	29632	0.81	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6437	19604	32968	1.48	2.0E-28	BF224402.1	EST_HUMAN	hr76c03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element ;
6460	19627		3	2.0E-28	BF212905.1	EST_HUMAN	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8234	21316	34837	0.53	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9783	22823		2.23	2.0E-28	AW972305.1	EST_HUMAN	EST384394 MAGE resequences, MAGL Homo sapiens cDNA
11913	24900	38603	2.52	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12631	25424		1.74	2.0E-28	H06376.1	EST_HUMAN	yl79c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:44300 5'
1508	14661	27744	2.85	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2294	15426	28560	3.91	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
4691	17826		0.95	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
8044	21127		1.95	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
8208	21290		3.03	1.0E-28	8922793	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
9478	22535	36099	4.75	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
10080	23118	36720	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
10080	23118	36721	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12186	25145		7.66	1.0E-28	AA054182.1	EST_HUMAN	zf51c01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
13013	25881		4.56	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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13135	26122	31543	1.8	9.0E-29	AW663987.1	EST_HUMAN	hi76g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12752	25498		2.57	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1632	14784	27870	1.98	7.0E-29	AW966447.1	EST_HUMAN	EST378521 MAGE resequences, MAGI Homo sapiens cDNA
13197	25779		9.03	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
608	13797	26817	9.39	6.0E-29	AI936748.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element ;
12495	25342		5.19	6.0E-29	BE940436.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
12587	25395		2.1	6.0E-29	BF568097.1	EST_HUMAN	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
5113	18241		2.39	5.0E-29	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8929	22008		8.35	5.0E-29	AW887541.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
12795	25531		1.49	5.0E-29	BE612449.1	EST_HUMAN	601451827F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855726 5'
3304	16478		2.28	4.0E-29	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
6133	19312		7.06	4.0E-29	BE164930.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
8272	21354	34870	0.64	4.0E-29	AI678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.t2 MER29 repetitive element ;
8272	21354	34871	0.64	4.0E-29	AI678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.t2 MER29 repetitive element ;
8944	22023	35563	3.59	4.0E-29	J04988.1	NT	Human 90 kD heat shock protein gene, complete cds
4536	17674	30658	1.31	3.0E-29	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
4855	17988	30976	1.1	3.0E-29	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
6053	19235	32560	0.83	3.0E-29	BE314018.1	EST_HUMAN	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
8931	22010	35548	3.23	3.0E-29	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
9500	22556	36119	1.22	3.0E-29	AW303317.1	EST_HUMAN	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element;contains MER19.t2 MER19 repetitive element ;
9731	22796		1.49	3.0E-29	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10164	23201		0.61	3.0E-29	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
11546	24602	38278	2.26	3.0E-29	AA403053.1	EST_HUMAN	zt62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 G1335769 GAG-POL POLYPROTEIN. ;
12385	25272		1.38	3.0E-29	D63882.1	NT	Human HsLIM15 mRNA for HsLim15, complete cds
13092	26132		1.62	3.0E-29	D63882.1	NT	Human HsLIM15 mRNA for HsLim15, complete cds
505	13699	26727	0.98	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
505	13699	26728	0.98	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1563	14716	27794	7.8	2.0E-29	AI963604.1	EST_HUMAN	wr65d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1563	14716	27795	7.8	2.0E-29	AI963604.1	EST_HUMAN	wr65d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1782	14931	28024	2.31	2.0E-29	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
1782	14931	28025	2.31	2.0E-29	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
4394	17537	30516	2.55	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5946	19132	32446	0.78	2.0E-29	AI082459.1	EST_HUMAN	os71e04.x1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.t2 L1 repetitive element ;
6309	19481	32835	1.49	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7732	19481	32835	1.28	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
8164	21246	34766	1.16	2.0E-29	BE867157.1	EST_HUMAN	601442206F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846648 5'
8777	21856	35398	0.61	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
8777	21856	35399	0.61	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
9708	22757	36327	2.76	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9708	22757	36328	2.76	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37084	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37085	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11767	24760		1.67	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnaJ (SPF31), mRNA
8992	22071	35611	8.27	1.0E-29	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
10850	23883	37503	2.81	1.0E-29	X60658.1	NT	R.rattus RYA3 mRNA for a potential ligand-binding protein
6712	19870	33261	3.53	9.0E-30	AA781215.1	EST_HUMAN	nz20c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element ;
12266	25200		4.55	9.0E-30	11422745	NT	Homo sapiens zinc/iron regulated transporter-like (ZIRTL), mRNA
6449	19616		10.5	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8465	21546	35076	2.26	8.0E-30	AA383873.1	EST_HUMAN	EST97317 Thymus I Homo sapiens cDNA 5' end similar to EST containing O family repeat
8882	21961	35495	2.79	8.0E-30	AI557072.1	EST_HUMAN	PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'
1545	14697		1.07	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1814	14963	28056	1.57	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3259	16433	29450	3.15	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
4881	16433	29450	1.02	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
10760	23793	37412	0.76	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13161	18485		1.75	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4121	17275	30274	43.22	5.0E-30	AI399992.1	EST_HUMAN	tg92g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
5353	25928		5.79	5.0E-30	U87931.1	NT	Human aconitate hydratase (ACO2) gene, exon 7
11126	24198		2.12	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11423	24484	38148	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11423	24484	38149	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2210	15344	28470	2.38	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
2210	15344	28471	2.38	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
9106	22185	35729	1.56	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA
1175	14338		4.56	3.0E-30	AI338551.1	EST_HUMAN	qq93c05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element ;
3853	17013	30013	1.15	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
8138	21220		0.53	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8683	21763		0.45	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10649	23683	37294	0.74	3.0E-30	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
11482	24541	38211	1.52	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
692	13875	26908	1.42	2.0E-30	AW857315.1	EST_HUMAN	CM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1108	14273		2.53	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1509	14662	27745	5.5	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2779	15895	29005	9.93	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2986	16162	29179	6.83	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3889	17048	30048	1.95	2.0E-30	AW206581.1	EST_HUMAN	UI-H-BI1-afo-c-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4900	18030	31018	2.02	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4900	18030	31019	2.02	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
8734	21814	35349	4.69	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5'
8836	21915	35452	1.71	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8836	21915	35453	1.71	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
10201	23238	36828	3.78	2.0E-30	AW971568.1	EST_HUMAN	EST383657 MAGE resequences, MAGL Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10287	23322	36924	6.31	2.0E-30	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
297	13514	26548	10.87	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5'
551	13744	26769	1.62	1.0E-30	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.t3 MER1 MER1 repetitive element ;
734	13916	26956	5.15	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2286	15418	28550	11.56	1.0E-30	AA664377.1	EST_HUMAN	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
2533	15658	28782	2.15	1.0E-30	BF347728.1	EST_HUMAN	602022560F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157991 5'
3120	16296	29310	0.91	1.0E-30	AA315045.1	EST_HUMAN	EST186868 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end
7901	20953	34460	1.96	1.0E-30	BF183230.1	EST_HUMAN	601809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
8176	21258	34780	0.49	1.0E-30	BE061586.1	EST_HUMAN	MR0-BT0249-091299-101-g01 BT0249 Homo sapiens cDNA
12786	26117		1.57	1.0E-30	AA299211.1	EST_HUMAN	EST11698 Uterus Homo sapiens cDNA 5' end
12937	26025		5.31	1.0E-30	H55593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3862	17022	30020	0.8	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3862	17022	30021	0.8	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8519	21600	35135	0.88	9.0E-31	R18214.1	EST_HUMAN	yf99b08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8519	21600	35136	0.88	9.0E-31	R18214.1	EST_HUMAN	yf99b08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8825	21904		1.99	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
8827	21906	35445	0.65	9.0E-31	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
13193	25776	31934	1.29	9.0E-31	6755441	NT	Mus musculus syndecan 4 (Sdc4), mRNA
1102	14267	27325	2.52	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2484	15611		7.93	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
729	13911		1.59	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2733	15850	28962	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2733	15850	28963	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8595	21676	35212	1.02	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8595	21676	35213	1.02	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9466	22523		1.03	7.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
3769	16930		3.42	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8347	21428		1.39	6.0E-31	AF055066.1	NT	Homo sapiens MHC class 1 region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8526	21607	35146	0.75	6.0E-31	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
10976	24055	37689	1.43	6.0E-31	AU119105.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
12327	25236	32108	3.7	6.0E-31	AW372868.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
12459	25947		2.54	6.0E-31	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	13420	26450	3.39	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
197	13420	26451	3.39	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8640	21720		1.29	5.0E-31	BF056540.1	EST_HUMAN	7k06f04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT. ;contains L1.t1 L1 repetitive element ;
609	13798		3.02	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
1642	14794	27878	1.14	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
1861	15007		2.09	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2849	15963		1.57	4.0E-31	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10754	23787	37402	0.46	4.0E-31	AF084464.1	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
12787	25526		1.55	4.0E-31	11430273	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
12924	25609		2	4.0E-31	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
2660	15782	28897	1.75	3.0E-31	6005871	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
7494	20569	34041	8.04	3.0E-31	4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI) (NDUFB8) mRNA
7663	20730	34206	1.23	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8355	21436		1.51	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
9779	22819	36397	2.59	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10822	23855	37477	0.65	3.0E-31	AA421242.1	EST_HUMAN	zu06d04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
10867	23952	37582	2.03	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
11421	24482		3.47	3.0E-31	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1967	15110	28211	1.58	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-f03 LT0051 Homo sapiens cDNA
2288	15420	28552	1.05	2.0E-31	AI393383.1	EST_HUMAN	tg44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2416	15545	28674	2.22	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
2511	15637	28758	4.63	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.t2 THR repetitive element ;
5389	18591	31563	0.76	2.0E-31	AW444496.1	EST_HUMAN	UI-H-BI3-akb-f-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'

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5829	19020	32326	3.43	2.0E-31	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
9277	22353		1.53	2.0E-31	AA877764.1	EST_HUMAN	nr06f04.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9408	22482	36046	3.46	2.0E-31	7661535	NT	Homo sapiens B9 protein (B9), mRNA
10110	23148	36748	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
10110	23148	36749	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
10280	23315	36914	2.75	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
10280	23315	36915	2.75	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12430	25305		3.49	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12578	26202		2.59	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
17	13255	26256	9.91	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1696	14848	27932	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1696	14848	27933	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1696	14848	27934	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
5407	18609	31681	3.97	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA
6261	19435	32781	2.57	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
7441	20518	33990	0.84	1.0E-31	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
8005	21055	34567	1.35	1.0E-31	BE972818.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
10441	23476	37080	0.5	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11156	24227	37857	2.35	1.0E-31	AI086434.1	EST_HUMAN	qf21h03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN. ;
6776	19931	33327	2.19	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
7530	20603	34077	0.66	9.0E-32	L31770.1	NT	Bos taurus vacuolar H+-ATPase subunit mRNA, complete cds
7766	20825		0.91	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2139	15275	28397	5.1	8.0E-32	AI056770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5599	18794	31843	0.77	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA
12406	25285		2.36	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin V(K)I gene, part with 5' breakpoint between orphon and neighbouring non-amplified region
7523	20596		1.32	6.0E-32	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12869	26181		2.5	6.0E-32	AA864653.1	EST_HUMAN	oh37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.t3 L1 repetitive element ;
1059	14225	27282	10.42	5.0E-32	AF116627.1	NT	Homo sapiens PRO1181 mRNA, complete cds
954	14127		1.64	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7779	20835	34326	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7779	20835	34327	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8554	21635		0.93	4.0E-32	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
468	13663	26699	2.64	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1484	14637	27721	15.82	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAKC07 5'
2973	16149	29168	0.75	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2973	16149	29169	0.75	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9594	22649	36221	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
9594	22649	36222	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
11166	24237	37868	3.43	3.0E-32	AA777621.1	EST_HUMAN	zi95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.t3 THR repetitive element ;
12433	25307		7.95	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12843	16149	29168	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
12843	16149	29169	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
13020	25671		6.47	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6382	19551	32907	0.89	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6608	19768	33156	5.55	2.0E-32	Z38133.1	NT	H.sapiens mRNA for myosin
6608	19768	33157	5.55	2.0E-32	Z38133.1	NT	H.sapiens mRNA for myosin
8473	21554	35085	3.34	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8473	21554	35086	3.34	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
13154	25750	31923	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
13154	25750	31924	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
3163	16338		1.25	1.0E-32	BE743299.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
7200	20065	33476	6.64	1.0E-32	11439789	NT	Homo sapiens chromosome 11open reading frame 9 (C11ORF9), mRNA
8795	21874	35413	4.56	1.0E-32	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3570	16735		4.8	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11. ;
6550	19712		3.17	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8988	22067	35607	1.81	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
11038	24117		4.55	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
62	13300	26320	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
62	13300	26321	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2228	15362	28491	3.04	7.0E-33	AI590115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element ;
2714	15832		7.95	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
3314	16487		15	7.0E-33	AW971307.1	EST_HUMAN	EST383396 MAGE resequences, MAGL Homo sapiens cDNA
9147	22226		0.87	7.0E-33	X54890.1	NT	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
11067	24142	37777	1.88	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
11526	24582	38258	1.59	7.0E-33	AW971568.1	EST_HUMAN	EST383657 MAGE resequences, MAGL Homo sapiens cDNA
12413	26292	32082	9.74	7.0E-33	AA601416.1	EST_HUMAN	no16h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.t1 L1 repetitive element ;
3830	16990		0.93	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6192	19368	32717	0.91	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
6192	19368	32718	0.91	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8778	21857	35400	1.86	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8899	21978	35517	3.12	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
10214	23250	36839	2.03	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
10214	23250	36840	2.03	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1818	14967		1.9	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-a02 FT0169 Homo sapiens cDNA
1931	15074		1.32	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1947	15090	28190	1.63	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1947	15090	28191	1.63	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2346	15477		2.92	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4169	17319	30312	0.66	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
10454	23489	37097	0.82	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10454	23489	37098	0.82	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12212	25165		1.45	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1152	14316		2.25	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2194	15329	28454	3.37	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2491	15618		1.16	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element;contains MER28.b2 MER28 repetitive element ;
2610	15734	28850	4.78	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4606	17743	30722	2.38	4.0E-33	AW293349.1	EST_HUMAN	UI-H-BI2-ahl-c-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5519	18717	31731	24.75	4.0E-33	AA053053.1	EST_HUMAN	zl71a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6522	19687	33060	0.79	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6522	19687	33061	0.79	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1113	14278		5.62	3.0E-33	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
1114	14278		5.83	3.0E-33	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2522	16064		1.16	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLCBCF09 3'
10655	23689	37298	0.87	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE. ;
18	13256		1.67	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
107	13256		5.53	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
4539	17677		4.53	2.0E-33	BE159039.1	EST_HUMAN	MR0-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
5100	18228	31199	8.64	2.0E-33	AA626683.1	EST_HUMAN	ab51g11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5204	18325	31294	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5204	18325	31295	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6553	19715	33091	1.39	2.0E-33	AI277492.1	EST_HUMAN	ql96d01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
9301	22377		2.15	2.0E-33	AI052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
9	13247		1.61	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7565	20637	34113	0.86	1.0E-33	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10227	26229		1.4	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11602	24655	38340	1.56	1.0E-33	AW996818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
11962	24947	38652	2.44	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12768	25511		1.25	1.0E-33	AW904491.1	EST_HUMAN	RC5-NN1055-260400-021-G03 NN1055 Homo sapiens cDNA
12929	13247		5.7	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12960	25626	31979	2.19	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
13179	25766		4.77	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
2240	15373	28501	0.98	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
4620	17757	30739	1.93	8.0E-34	BE062570.1	EST_HUMAN	QV2-BT0258-071299-019-g07 BT0258 Homo sapiens cDNA
7974	21024	34537	0.67	8.0E-34	BE069882.1	EST_HUMAN	MR4-BT0399-200100-001-h03 BT0399 Homo sapiens cDNA
1476	14629	27714	2.5	7.0E-34	T70845.1	EST_HUMAN	yd15e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
10204	14629	27714	0.54	7.0E-34	T70845.1	EST_HUMAN	yd15e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
12482	25334		3.85	7.0E-34	H12866.1	EST_HUMAN	yj14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
483	13677	26711	1.74	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
483	13677	26712	1.74	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
5247	18368	31335	1.58	6.0E-34	AW998611.1	EST_HUMAN	PM0-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
12290	25215	32099	2.22	6.0E-34	U03686.1	NT	Mus musculus DAB/2J hair-specific (hacl-1) gene
1929	15072		3.15	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5173	18295	31257	5.24	5.0E-34	U30883.1	NT	Human splicing factor SRp55-1 (SRp-55) mRNA, complete cds
9067	22146	35693	1.17	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10890	23974	37605	2.02	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11532	24588		1.93	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2054	15195	28309	2.09	4.0E-34	AI804667.1	EST_HUMAN	tt94c06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2249194 3'
3241	16415	29430	0.9	4.0E-34	5803166	NT	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
5981	19166	32486	0.62	4.0E-34	AA861773.1	EST_HUMAN	ak35c01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407936 3'
9238	22315	35857	0.83	4.0E-34	BF209778.1	EST_HUMAN	601874950F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
6361	19531	32890	0.66	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11420	24481		2.96	3.0E-34	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
9152	22230	35774	0.75	2.0E-34	AI678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.t2 MER29 repetitive element ;
9152	22230	35775	0.75	2.0E-34	AI678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.t2 MER29 repetitive element ;
11431	24492	38156	8.54	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)

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11431	24492	38157	8.54	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1534	14687	27767	10.13	1.0E-34	P12236	SWISSPROT	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
1738	14887		7.18	1.0E-34	AU136024.1	EST_HUMAN	AU136024 PLACE1 Homo sapiens cDNA clone PLACE1003383 5'
3764	16925	29927	2.51	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4181	17331	30323	0.79	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4181	17331	30324	0.79	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4602	17739		8.26	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA
6266	19440	32787	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
6266	19440	32788	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
9527	22592	36163	0.64	1.0E-34	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
9898	22938	36523	8.07	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1563_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564A1563 5'
11459	24518	38186	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11459	24518	38187	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11473	24532	38202	2.92	1.0E-34	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12680	26125		2.44	1.0E-34	AA807097.1	EST_HUMAN	oc31c11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
12950	25660		5.84	1.0E-34	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3735	16896	29900	1.3	9.0E-35	AW663302.1	EST_HUMAN	hh77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
232	13453		7.21	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1776	14925	28019	3.63	8.0E-35	BF589937.1	EST_HUMAN	naa33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912 O75912 DIACYLGLYCEROL KINASE IOTA. ;
1776	14925	28020	3.63	8.0E-35	BF589937.1	EST_HUMAN	naa33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912 O75912 DIACYLGLYCEROL KINASE IOTA. ;
4989	18118	31097	2.61	8.0E-35	BF183195.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
10929	24011	37645	1.53	8.0E-35	BE378480.1	EST_HUMAN	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
12404	25283		5.89	8.0E-35	BF589282.1	EST_HUMAN	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
6813	19773	33164	1.61	7.0E-35	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
1445	14598	27675	1.06	6.0E-35	AA757115.1	EST_HUMAN	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
2025	15166	28271	4.63	6.0E-35	6005975	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
4164	17314	30309	0.8	6.0E-35	AW297191.1	EST_HUMAN	UI-H-BW0-ajd-d-09-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
8081	21163	34680	4.03	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8906	21985	35524	0.57	6.0E-35	X94232.1	NT	H.sapiens mRNA for novel T-cell activation protein

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8906	21985	35525	0.57	6.0E-35	X94232.1	NT	H.sapiens mRNA for novel T-cell activation protein
9867	22907	36492	0.61	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0366 gene, partial cds
10107	23145	36743	2.97	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
148	13373	26406	0.61	5.0E-35	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
1746	14895	27989	2.25	5.0E-35	X63392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
2844	15958	29067	0.99	5.0E-35	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3074	16250	29271	2.87	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4529	17667	30653	1.72	5.0E-35	AF023268.1	NT	Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
8378	21459		4.25	5.0E-35	BE890992.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8405	21486	35015	2.17	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
8405	21486	35016	2.17	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
11451	24511		2.54	5.0E-35	AA001786.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1465	14619	27703	20.46	4.0E-35	BE257907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1862	15008	28114	11.21	4.0E-35	H91193.1	EST_HUMAN	yu98a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
7358	20437		1.67	4.0E-35	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
8715	21795	35332	8.05	4.0E-35	AL046596.1	EST_HUMAN	DKFZp434L148_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
12098	25078	38786	2.5	4.0E-35	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
1610	14763	27843	33.92	3.0E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2408	15539		2.64	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5456	18656	31634	23.43	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2. ;
5456	18656	31635	23.43	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2. ;
9689	22738		1.45	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10378	23413	37022	1.5	3.0E-35	AW003083.1	EST_HUMAN	wr03a05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
111	16005	26372	1.25	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
1215	14376	27436	1.89	2.0E-35	T11909.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
2292	15424	28558	4.56	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gab2, complete cds
2748	15865	28976	1.13	2.0E-35	AW665005.1	EST_HUMAN	hl86a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979166 3' similar to SW:TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12 ;
3386	16556	29570	1.08	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3386	16556	29571	1.08	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3647	16810		0.77	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4019	17176	30184	0.85	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4019	17176	30185	0.85	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4792	17927		3.01	2.0E-35	H49239.1	EST_HUMAN	yq19a12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
5700	18894	32186	1.93	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA
7253	20336	33785	0.6	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7253	20336	33786	0.6	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
11036	24115	37749	2.93	2.0E-35	X59417.1	NT	H.sapiens PROS-27 mRNA
12157	16556	29570	1.22	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12157	16556	29571	1.22	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12342	25247	32111	1.33	2.0E-35	BE904978.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12342	25247	32112	1.33	2.0E-35	BE904978.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12931	25614		7.22	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
13056	16005	26372	1.74	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
47	13286	26295	5.76	1.0E-35	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
47	13286	26296	5.76	1.0E-35	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
771	13952	27000	35.82	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
771	13952	27001	35.82	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
932	14107		1.28	1.0E-35	T87947.1	EST_HUMAN	yd93a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;
2607	15730	28847	1.89	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2826	15940	29050	1.34	1.0E-35	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2826	15940	29051	1.34	1.0E-35	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
3212	16386	29397	1.87	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
3232	16406	29418	1.67	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEF06 3'
3232	16406	29419	1.67	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEF06 3'
4542	17680	30661	4.82	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4542	17680	30662	4.82	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5627	18821	31896	1.48	1.0E-35	11526236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7135	18561	31475	0.74	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cDNA
7135	18561	31476	0.74	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cDNA
7652	20720	34196	0.99	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
7819	20874	34373	0.91	1.0E-35	11418002	NT	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
9742	25861	36383	2.46	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
9742	25861	36384	2.46	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10805	23838	37462	0.72	1.0E-35	BF589594.1	EST_HUMAN	naa06d06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341 O31341 BETA-GALACTOSIDASE ;
10805	23838	37463	0.72	1.0E-35	BF589594.1	EST_HUMAN	naa06d06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341 O31341 BETA-GALACTOSIDASE ;
12055	25036	38743	1.49	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12055	25036	38744	1.49	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12062	25043		2.04	1.0E-35	AI525119.1	EST_HUMAN	prommа-7.D01.r bvtumor Homo sapiens cDNA 5'
12188	26077		6.35	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12405	25284		1.26	1.0E-35	11418110	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
12806	25539		2.49	1.0E-35	BE792832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
6131	19310	32650	0.67	8.0E-36	X78479.1	NT	B.bovis BBSc mRNA for scinderin
9430	22504	36070	0.76	8.0E-36	AA348480.1	EST_HUMAN	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
2997	16173	29192	1.53	7.0E-36	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
3188	16363		5.25	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
5273	18392	31360	1.09	7.0E-36	Q27409	SWISSPROT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)
5273	18392	31361	1.09	7.0E-36	Q27409	SWISSPROT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)
7832	20887	34389	6.31	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
7832	20887	34390	6.31	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
12570	25388	32040	27.38	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2060	15201	28315	1.92	6.0E-36	7706622	NT	Homo sapiens ninjurin 2 (NINJ2), mRNA
2490	15617		5.59	6.0E-36	AB035346.1	NT	Homo sapiens TCL6 gene, exon 12
3729	16890	29894	0.59	6.0E-36	BF515101.1	EST_HUMAN	UI-H-BW1-anv-c-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5446	18646	31624	7.17	6.0E-36	AI435169.1	EST_HUMAN	th93b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7258	20341	33792	3.03	6.0E-36	AW780143.1	EST_HUMAN	ho06h02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52292 IMPORTIN ALPHA-2 SUBUNIT ;
8853	21932	35471	4.62	6.0E-36	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
10430	23465		0.63	6.0E-36	C16927.1	EST_HUMAN	C16927 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-535C11 5'
11841	24830	38521	3.49	6.0E-36	AI380499.1	EST_HUMAN	tf95c09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2 MER9 repetitive element ;
140	13366	26399	15.16	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
2809	15923	29033	21.08	5.0E-36	BE388436.1	EST_HUMAN	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3700	16861	29863	3.24	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4909	18039	31028	1.31	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4909	18039	31029	1.31	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
7966	21016	34528	0.59	5.0E-36	11079227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
12155	13366	26399	6.11	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
12458	25322	32095	2.36	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1252	14411	27473	1.57	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1677	14829	27913	1.36	4.0E-36	BE382574.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
2297	15429		4.14	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3435	16603	29622	1.1	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3435	16603	29623	1.1	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4877	18008	30992	0.69	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5833	19024		0.96	4.0E-36	R64023.1	EST_HUMAN	yi19f05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139713 5'
6180	19366	32704	2.49	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), trancript variant 3, mRNA
7831	20886	34388	1.78	4.0E-36	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
8752	21831	35369	1.45	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8752	21831	35370	1.45	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11235	24304	37941	3.13	4.0E-36	AA400370.1	EST_HUMAN	zu69c10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
12475	25328		1.91	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
12520	25951		4.27	4.0E-36	AV753629.1	EST_HUMAN	AV753629 TP Homo sapiens cDNA clone TPGABH01 5'
714	13896	26934	2.93	3.0E-36	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2373	15504	28630	1.19	3.0E-36	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4624	17761	30743	7.5	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
11368	24429	38086	1.84	3.0E-36	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3238	16412	29427	2.5	2.0E-36	BE259267.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5074	18202	31174	10.78	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5603	18798	31848	2.68	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
5970	19156	32471	3.75	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBJ28 5' end
6706	19864	33254	13.94	2.0E-36	T69629.1	EST_HUMAN	yc44a07.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
9588	22643	36212	0.94	2.0E-36	BF512794.1	EST_HUMAN	UI-H-BW1-amu-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9749	22687	36258	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9749	22687	36259	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
908	14083	27148	1.74	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2212	15346	28474	1.71	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2212	15346	28475	1.71	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2275	15408	28538	1.83	1.0E-36	BF673761.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
3425	16594		3.33	1.0E-36	AF156962.1	NT	Homo sapiens human endogenous retrovirus W proC6-19 protease (pro) gene, partial cds
5847	19037	32344	0.64	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G022 5'
6020	19203	32523	1.23	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6312	19484		4.27	1.0E-36	AI867714.1	EST_HUMAN	wb37c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element;
6519	19684	33055	1.9	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6519	19684	33056	1.9	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6820	19973	33381	0.72	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
8147	21229	34747	4.06	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8147	21229	34748	4.06	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8243	21325	34841	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745670
8243	21325	34842	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745670
8373	21454	34977	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8373	21454	34978	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
9229	22307	35850	3.33	1.0E-36	AW103658.1	EST_HUMAN	xe82b07.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2614357 3'
10320	23355	36964	3.83	1.0E-36	BF364169.1	EST_HUMAN	QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA
10534	23569	37176	0.64	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10534	23569	37177	0.64	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
11190	24259	37895	2.55	1.0E-36	AW897636.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11662	24741	38432	3.55	1.0E-36	AW504143.1	EST_HUMAN	UI-HF-BN0-ale-c-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
12048	25029		10.8	1.0E-36	11545901	NT	Homo sapiens PP3227 protein (PP3227), mRNA
12340	25245		2.93	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12835	25556		5.76	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
13131	25737		2.76	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7539	20612	34087	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
7539	20612	34088	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
12619	25417		3.57	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
3436	16604	29624	1.4	8.0E-37	4757979	NT	Homo sapiens chimerin (chimaerin) 2 (CHN2) mRNA
5363	18566		1.7	8.0E-37	BE698077.1	EST_HUMAN	CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA
5949	19135	32448	3.48	8.0E-37	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
5949	19135	32449	3.48	8.0E-37	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
5998	19183	32505	7.08	8.0E-37	AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
8068	21150	34670	6.2	8.0E-37	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1313	14469		4.92	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
5228	18350	31320	3.04	7.0E-37	AW968823.1	EST_HUMAN	EST380899 MAGE resequences, MAGJ Homo sapiens cDNA
10994	24073	37706	8.66	7.0E-37	AI817700.1	EST_HUMAN	wk25b11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.t2 PTR5 repetitive element ;
11134	24206	37831	1.89	7.0E-37	AI536702.1	EST_HUMAN	tm87g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element ;
8634	21714	35251	0.59	6.0E-37	AF169689.1	NT	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12864	25575		2.3	6.0E-37	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
12984	25641		4.5	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6218	19393	32741	4.3	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6218	19393	32742	4.3	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8956	22035	35576	1.03	5.0E-37	AV750211.1	EST_HUMAN	AV750211 NPC Homo sapiens cDNA clone NPCBGH09 5'
11160	24231		4.02	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
12335	25242		3.63	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3

WO 01/57272 PCT/US01/00663

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2495	15622	28741	2.97	4.0E-37	AA702794.1	EST_HUMAN	zi90b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6416	19585	32947	0.68	4.0E-37	AW794502.1	EST_HUMAN	RC6-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9556	22621	36192	0.56	4.0E-37	AA843806.1	EST_HUMAN	ak09c02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2074	15214	28332	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2074	15214	28333	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2581	15706		1.54	3.0E-37	AW961150.1	EST_HUMAN	EST373222 MAGE resequences, MAGF Homo sapiens cDNA
3030	16206		4.02	3.0E-37	AW961150.1	EST_HUMAN	EST373222 MAGE resequences, MAGF Homo sapiens cDNA
5985	19170	32492	0.7	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547G067 5'
7728	20790	34279	0.72	3.0E-37	AI749952.1	EST_HUMAN	at34c05.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT. ;
392	13629	26666	0.89	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
392	13629	26667	0.89	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1105	14270	27328	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1105	14270	27329	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
2021	15162	28267	1.32	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3999	17156	30162	6.71	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4360	17503	30485	0.6	2.0E-37	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
5504	18703		0.9	2.0E-37	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
6676	19835	33224	0.6	2.0E-37	11990617	NT	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
6798	19953	33353	3.72	2.0E-37	AA346720.1	EST_HUMAN	EST62931 Fetal heart II Homo sapiens cDNA 5' end
8185	21267	34790	0.47	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8185	21267	34791	0.47	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8227	21309	34829	2.32	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
11856	24844	38541	10.07	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12797	25770		1.44	2.0E-37	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
13184	25770		4.19	2.0E-37	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2154	15290	28417	6.95	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3267	16441		1.03	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
5055	18183	31158	2.34	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6127	19306		0.89	1.0E-37	7305360	NT	Mus musculus otogelin (Otog), mRNA
8409	21490	35019	1.12	1.0E-37	BE546032.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
8933	22012	35551	3.59	1.0E-37	AA171406.1	EST_HUMAN	zp21b02.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1.t2 L1 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10937	24019	37652	2.19	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
12671	25447		1.94	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA
5898	19086	32398	1.72	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
1249	14408	27470	1.96	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2567	15692	28817	1.21	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153992 5'
12735	14408	27470	1.37	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
13210	26049		1.44	8.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2254	15387	28515	1.7	7.0E-38	AW972825.1	EST_HUMAN	EST384920 MAGE resequences, MAGL Homo sapiens cDNA
3107	16283	29299	1.98	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3859348 5'
5706	18899	32192	0.98	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5706	18899	32193	0.98	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7482	20557	34029	0.59	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
12189	25147		4.27	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12704	25468	32025	6.66	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13160	25913	31881	1.79	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
745	13926	26967	0.9	5.0E-38	AW971819.1	EST_HUMAN	EST383908 MAGE resequences, MAGL Homo sapiens cDNA
2525	15650	28774	4.57	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIIR gene (partial), exon 8
3796	16957	29961	0.94	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
3971	16957	29961	0.77	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
5288	15650	28774	0.98	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIIR gene (partial), exon 8
7172	20305	33748	1.63	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
121	13351	26380	4.28	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
121	13351	26381	4.28	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1183	14346	27403	1.15	3.0E-38	11436947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2167	15302		4.42	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3787	16948		1.49	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA
3958	17116	30119	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3958	17116	30120	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4736	17871		0.61	3.0E-38	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6893	25836	33463	5.89	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7393	20471	33937	0.58	3.0E-38	AW302461.1	EST_HUMAN	xw04d01.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2827009 3'
7763	20822	34313	6.53	3.0E-38	BF373664.1	EST_HUMAN	CM3-FT0181-140700-241-f07 FT0181 Homo sapiens cDNA
8851	21930	35469	2.11	3.0E-38	H85494.1	EST_HUMAN	yv88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
8851	21930	35470	2.11	3.0E-38	H85494.1	EST_HUMAN	yv88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10177	23214		1.84	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11598	24651		1.88	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12990	14346	27403	1.23	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
61	13290	26303	1.96	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1411	14565	27639	3.66	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA
1678	14830	27914	13.95	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1678	14830	27915	13.95	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
3622	16786		0.92	2.0E-38	AF070670.1	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4704	17839	30824	18.99	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5252	18339	31312	0.68	2.0E-38	AA437181.1	EST_HUMAN	zv61d09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758129 5' similar to TR:G817957 G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
5836	19026	32331	0.75	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
5836	19026	32332	0.75	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7897	20949	34457	1.47	2.0E-38	AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8680	21760		4.47	2.0E-38	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9096	22175	35719	0.49	2.0E-38	F06450.1	EST_HUMAN	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
9165	22243	35786	1.26	2.0E-38	AF069755.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9422	22496		1.36	2.0E-38	BE222256.1	EST_HUMAN	hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710 GAG POLYPROTEIN. ;
10665	23699	37309	1.67	2.0E-38	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11781	24771	38467	4.86	2.0E-38	BE712790.1	EST_HUMAN	QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA
11939	24925	38626	2.86	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11939	24925	38627	2.86	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12244	25186		6.21	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAXH07 5'
12246	25187		1.26	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12546	25370		3.36	2.0E-38	M55630.1	NT	Human topoisomerase I pseudogene 2
12559	25381	32073	4.81	2.0E-38	H55641.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
12632	25425		2.87	2.0E-38	S74906.1	NT	E1 beta=pyruvate dehydrogenase beta {promoter} [human, placenta, Genomic, 1280 nt]
13174	25762		1.35	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1117	14282		1.96	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element ;
2055	15196	28310	2.62	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2077	15217	28336	1.33	1.0E-38	7661969	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2564	15689	28815	1.69	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4271	17416	30405	0.93	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4439	17579	30558	0.6	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4444	17584	30563	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4444	17584	30564	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4719	17854	30837	1.08	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5268	18387	31355	1.89	1.0E-38	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6151	19327	32672	4.59	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
6151	19327	32673	4.59	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
7563	20635	34110	2.55	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9354	22429	35987	0.58	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9610	22665	36236	6.31	1.0E-38	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
12403	25877		4.79	1.0E-38	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12116	25096	38801	1.64	9.0E-39	AA112438.1	EST_HUMAN	zm27f07.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:526885 5'
55	13294	26309	4.93	8.0E-39	4502312	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1425	14579	27652	1.3	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1876	15020		1.8	8.0E-39	AI823404.1	EST_HUMAN	wh53f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890 POL PROTEIN ;
2160	15296	28421	7.08	7.0E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
11047	24124	37758	2.4	6.0E-39	BF331829.1	EST_HUMAN	QV1-BT0631-040900-357-f02 BT0631 Homo sapiens cDNA
13064	25697		2.24	6.0E-39	BE670394.1	EST_HUMAN	7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828 ;
1032	14201	27259	1.64	5.0E-39	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3050	16226	29247	9.33	5.0E-39	AI750154.1	EST_HUMAN	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.t1 LTR7 repetitive element ;
12720	25479		1.53	5.0E-39	11420289	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA

WO 01/57272 PCT/US01/00663

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
564	13756	26782	4.39	4.0E-39	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
3663	16826	29835	0.9	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5950	19136	32450	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
5950	19136	32451	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
8267	21349	34864	1.02	4.0E-39	AA682949.1	EST_HUMAN	ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element ;
9530	22595	36165	0.46	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
9530	22595	36166	0.46	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12744	25494		6.36	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12884	25586		2.56	4.0E-39	BE836452.1	EST_HUMAN	QV0-FN0063-260600-278-c06 FN0063 Homo sapiens cDNA
48	13287	26297	11.96	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	26298	11.96	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	26299	11.96	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12236	25180	38348	6.59	3.0E-39	AI084557.1	EST_HUMAN	ox63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12236	25180	38349	6.59	3.0E-39	AI084557.1	EST_HUMAN	ox63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12284	25212		5.72	3.0E-39	H37903.1	EST_HUMAN	yp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
920	14095		7.78	2.0E-39	BE409203.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
935	14110		11.55	2.0E-39	AI525119.1	EST_HUMAN	prom rna-7.D01.r bvtumor Homo sapiens cDNA 5'
1057	14223		3.9	2.0E-39	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
1560	14713		33.59	2.0E-39	AW372318.1	EST_HUMAN	PM0-BT0340-211299-003-d02 BT0340 Homo sapiens cDNA
2030	15171	28279	4.48	2.0E-39	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;
2692	15812	28928	1.89	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4523	17662	30649	1.74	2.0E-39	BF370207.1	EST_HUMAN	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
5608	18803	31868	4.45	2.0E-39	AA508880.1	EST_HUMAN	ng86f03.s1 NCI_CGAP_Pr8 Homo sapiens cDNA clone IMAGE:941693
7526	20599	34073	2.08	2.0E-39	AA080867.1	EST_HUMAN	zn06f02.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
7702	20767	34251	0.68	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
7702	20767	34252	0.68	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8505	21586	35120	0.63	2.0E-39	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9826	22866		0.79	2.0E-39	AI686660.1	EST_HUMAN	tu35e03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253052 3'
11716	24756	38452	2.13	2.0E-39	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
1543	14695	27774	2.83	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1543	14695	27775	2.83	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1561	14714	27791	5.96	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
1763	14912	28007	1.14	1.0E-39	H55224.1	EST_HUMAN	CHR220163 Chromosome 22 exon Homo sapiens cDNA clone C22_205 5'
4782	17917	30903	9.32	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4782	17917	30904	9.32	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4824	17957	30943	9.13	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5474	18673	31686	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5474	18673	31687	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5747	18939	32239	1.2	1.0E-39	T80876.1	EST_HUMAN	yd26g06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains Alu repetitive element;contains LTR1 repetitive element ;
5781	18973	32278	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5781	18973	32279	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6965	20193		1.95	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7521	20594	34069	2.15	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8762	21841	35382	1.04	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
11165	24236	37867	1.4	1.0E-39	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
569	13761	26785	2	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1263	14420	27484	16.02	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1263	14420	27485	16.02	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1480	14633	27718	15.75	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3885	17044	30043	1.18	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4081	18467	30242	3.99	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4466	17606	30584	5.63	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3106	16282	29298	1.04	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
4033	17189		3.43	8.0E-40	BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
7894	20946	34452	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7894	20946	34453	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11136	24208	37834	2.63	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2788	15904	29011	9.91	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
2788	15904	29012	9.91	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
6060	19242		1.85	6.0E-40	BE504766.1	EST_HUMAN	hz40g01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3210480 3'
6275	19449		1.38	6.0E-40	7661999	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7075	20128	33544	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7075	20128	33545	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10182	23219	36811	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
10182	23219	36812	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2670	15791	28907	2.75	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1925	15068	28173	3.81	4.0E-40	AI686005.1	EST_HUMAN	tt91b01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN. ;
2175	15310		6.81	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4508	17647	30635	7.2	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8070	21152	34672	0.64	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8181	21263	34785	6.98	4.0E-40	AA742809.1	EST_HUMAN	nv34e10.r1 NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
9255	22332	35881	5.84	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
9255	22332	35882	5.84	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10955	24036	37671	1.95	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4250	17396	30385	0.9	3.0E-40	AI925949.1	EST_HUMAN	wh12f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
4993	18122		0.83	3.0E-40	AA055118.1	EST_HUMAN	zf16h09.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377153 3'
6592	19752	33137	0.66	3.0E-40	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6777	19932	33328	7.06	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8575	21656	35197	3.66	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9169	22247	35790	1.27	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9412	22486	36050	1.6	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10899	23983	37615	1.49	3.0E-40	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
11544	24600	38276	9.12	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
335	13548		3.91	2.0E-40	AI223036.1	EST_HUMAN	qg52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
817	13996		5.58	2.0E-40	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1872	15016		2.33	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1988	15130	28233	2.8	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1988	15130	28234	2.8	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2133	15269	28389	1.39	2.0E-40	AI968562.1	EST_HUMAN	wt90a11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN. ;
2238	15371	28500	2.21	2.0E-40	5453592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
2754	15871		1.66	2.0E-40	BE275932.1	EST_HUMAN	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3196	16371	28978	5.27	2.0E-40	5453592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
5021	18150	31128	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5021	18150	31129	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
908	14081		1.2	1.0E-40	AA225989.1	EST_HUMAN	nc09a09.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007608
2686	15806	28922	1.82	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
2750	15867		3.88	1.0E-40	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17. ;
3370	16542		2.14	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4733	17868	30851	3.69	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6385	19554	32912	0.68	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6385	19554	32913	0.68	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7236	20320	33763	1.83	1.0E-40	AA573201.1	EST_HUMAN	nj42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7236	20320	33764	1.83	1.0E-40	AA573201.1	EST_HUMAN	nj42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7381	20459	33922	0.82	1.0E-40	P26808	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]
11157	24228	37858	6.41	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
11993	24978	38683	1.49	1.0E-40	AA614255.1	EST_HUMAN	np09h03.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1115861 similar to TR:G1136406 G1136406 KIAA0173 PROTEIN. ;
11993	24978	38684	1.49	1.0E-40	AA614255.1	EST_HUMAN	np09h03.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1115861 similar to TR:G1136406 G1136406 KIAA0173 PROTEIN. ;
12079	25059		1.86	1.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12687	26032		6.94	1.0E-40	BF334112.1	EST_HUMAN	MR2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA
3906	17065	30064	0.59	9.0E-41	W01596.1	EST_HUMAN	za36a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294602 5'
8106	21188	34708	1.6	8.0E-41	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
851	16024	27089	2.52	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
851	16024	27090	2.52	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5379	18581	31450	0.9	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6132	19311	32651	2.71	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6483	19650	33012	1.04	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7133	18559	31473	0.96	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11718	24758	38453	2.06	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
11931	24917	38620	1.41	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
13182	26028		8.58	7.0E-41	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
291	13508	26543	1.13	6.0E-41	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2179	15314	28443	3.09	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
8158	21240	34760	1.31	6.0E-41	BF513783.1	EST_HUMAN	UI-H-BW1-amp-b-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
13156	25952		1.25	6.0E-41	AW873637.1	EST_HUMAN	ho64f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to contains MER32.b3 MER32 repetitive element ;
1845	14991	28092	1.37	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79626 3'
4223	17371		1.17	5.0E-41	4885635	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6678	19837		2.34	5.0E-41	BE067042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
402	13599		1.69	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1122	14287	27342	2.37	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1442	14595	27670	14.6	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE. ;contains LTR5.b1 LTR5 repetitive element ;
1442	14595	27671	14.6	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE. ;contains LTR5.b1 LTR5 repetitive element ;
1454	14607	27687	3.34	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1665	14817	27900	7.72	4.0E-41	AI500406.1	EST_HUMAN	tm96c04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element ;
2953	16130	29144	5.02	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2953	16130	29145	5.02	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4262	17407	30393	2.13	4.0E-41	X92685.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
6638	19797		1.8	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
9895	22935	36519	5.06	4.0E-41	BF304683.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11969	24954		7.38	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAACC07 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit *Database* Source	Top Hit Descriptor
12900	25917		1.3	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
13110	25725	31942	1.61	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
970	14143	27203	1.8	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4455	17595	30575	4.03	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5609	18804	31869	11.76	3.0E-41	X87689.1	NT	H.sapiens mRNA for putative p64 CLCP protein
6511	19676	33046	1.23	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7967	21017	34529	0.71	3.0E-41	R54765.1	EST_HUMAN	yj75d08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154575 5'
12119	25099	38804	1.36	3.0E-41	AW994941.1	EST_HUMAN	QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA
12119	25099	38805	1.36	3.0E-41	AW994941.1	EST_HUMAN	QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA
12196	25153		1.98	3.0E-41	AA609768.1	EST_HUMAN	ef17f10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'
12783	25525		1.43	3.0E-41	BF125922.1	EST_HUMAN	601762940F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026081 5'
1871	14744	27827	31.25	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2013	15153	28258	2.17	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2293	15425	28559	1.26	2.0E-41	D86962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2341	15472	28606	5.52	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2889	14744	27827	11.99	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3406	16576	29591	0.69	2.0E-41	AA449549.1	EST_HUMAN	zx08b04.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785839 5'
3941	17100	30097	0.69	2.0E-41	5032106	NT	Homo sapiens son of seventeless (Drosophila) homolog 1 (SOS1) mRNA
4744	17879	30862	1.23	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4744	17879	30863	1.23	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
5656	18850	32132	0.6	2.0E-41	AA584575.1	EST_HUMAN	no12c07.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:X52851_rna1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
6763	19919	33314	0.98	2.0E-41	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
7850	20905	34409	9.27	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
8259	21341	34858	1.36	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8259	21341	34859	1.36	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8288	21370	34891	1.42	2.0E-41	AA328265.1	EST_HUMAN	EST31723 Embryo, 12 week I Homo sapiens cDNA 5' end
9175	22253	35796	1.65	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
9617	22672	36241	0.66	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9617	22672	36242	0.56	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11775	24767	38463	2.87	2.0E-41	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13148	25747		1.2	2.0E-41	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
3276	16450	29470	1.05	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database . Source	Top Hit Descriptor
3276	16450	29471	1.05	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4689	17824	30811	9.46	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
9618	22673	36243	1.57	1.0E-41	AI217868.1	EST_HUMAN	qf75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
12334	25241		1.67	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8717	21797		1.19	9.0E-42	BE179191.1	EST_HUMAN	RC0-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
9375	22450	36011	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9375	22450	36012	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
475	13670	26702	5.34	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2176	15311	28439	8.63	8.0E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12375	26035		30.09	8.0E-42	AA493896.1	EST_HUMAN	nh07c02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA ;
12396	25904		2.91	8.0E-42	AW088062.1	EST_HUMAN	xc97a04.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.t2 OFR repetitive element ;
955	14128		2.23	7.0E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8666	21746		0.5	7.0E-42	R10963.1	EST_HUMAN	yf38g04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129174 5'
9445	22561	36124	1.32	7.0E-42	AI204358.1	EST_HUMAN	qf58g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
1903	15046	28155	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
1903	15046	28156	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
2363	15494		3.6	6.0E-42	AW238656.1	EST_HUMAN	xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.t1 L1 repetitive element ;
5584	18779	31824	1.65	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5834	18779	31824	1.5	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
138	13364		6.34	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
451	13647	26683	1.56	5.0E-42	BE217913.1	EST_HUMAN	hv31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
499	13694		3.05	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
500	13695		1.14	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6825	19978	33385	0.94	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6825	19978	33386	0.94	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6941	20264	33691	2.57	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7351	20430	33892	1.55	5.0E-42	AF071569.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8978	22057	35599	2.88	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10832	23865	37487	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10832	23865	37488	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
11246	24315	37955	1.77	5.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
772	13953	27002	5.6	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
772	13953	27003	5.6	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
1091	14256	27312	1.82	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4311	17454	30442	1.39	4.0E-42	X59417.1	NT	H.sapiens PROS-27 mRNA
4343	17486	30469	1.1	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4364	17507	30488	4.67	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4706	17841	30825	17.64	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5285	18404	31372	0.93	4.0E-42	7661635	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
10701	23734	37339	0.57	4.0E-42	AW371201.1	EST_HUMAN	CM0-BT0282-171299-127-b03 BT0282 Homo sapiens cDNA
10884	23968	37597	2.32	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
10884	23968	37598	2.32	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11240	24309	37946	1.43	4.0E-42	AI435225.1	EST_HUMAN	ti11d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
11698	24695	38387	1.69	4.0E-42	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3862086 5'
1512	14665	27750	3.79	2.0E-42	BF376834.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2466	15593	28718	1.6	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCCBB08 5'
2483	15610		4.24	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2496	15623	28742	3.6	2.0E-42	AW250059.1	EST_HUMAN	2819293.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
5875	19065	32372	11.82	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGE resequences, MAGC Homo sapiens cDNA
5875	19065	32373	11.82	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGE resequences, MAGC Homo sapiens cDNA
6892	20044	33452	0.9	2.0E-42	AI052586.1	EST_HUMAN	ow83d05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1653417 3'
10046	23084	36685	1.28	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10260	23295	36892	0.64	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
10260	23295	36893	0.64	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
12037	25019	38723	1.53	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
752	13932	26977	1.75	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1067	14233	27292	2.2	1.0E-42	AW295809.1	EST_HUMAN	UI-H-BI1-afh-e-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1125	14290	27345	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1125	14290	27346	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1271	16033	27498	11.99	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds

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1271	16033	27499	11.99	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1735	14884	27977	1.15	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2087	15227	28349	1.18	1.0E-42	AF110296.1	NT	Homo sapiens PDNP1 gene, exon 17
2609	15733	28849	1.42	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
3029	16205	29228	9.15	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3799	16960	29964	3.31	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3895	17054	30054	1.11	1.0E-42	5031610	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
4036	17192	30202	0.99	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4361	17504	30486	3.47	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4716	17851	30834	0.61	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA
4867	18000	30984	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4867	18000	30985	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4901	18031	31020	6.13	1.0E-42	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
11440	24501	38169	1.39	1.0E-42	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
10291	23326	36929	6.16	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
669	13855	26883	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
669	13855	26884	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
718	13900	26938	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
718	13900	26939	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
718	13900	26940	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5816	19006	32312	0.72	8.0E-43	H13952.1	EST_HUMAN	yj08e11.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3731	16892	29896	7.48	7.0E-43	AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
8968	22047		3.98	7.0E-43	AI936748.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element ;
1374	14529		11.62	6.0E-43	AA491890.1	EST_HUMAN	ne72d08.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2657	15780		4.03	6.0E-43	AV708201.1	EST_HUMAN	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
4963	18092	31068	252.27	6.0E-43	AI421540.1	EST_HUMAN	tf26c04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097318 3' similar to SW:BRR2_YEAST P32639 PRE-MRNA SPLICING HELICASE BRR2 ;
6441	19608	32971	2.53	6.0E-43	9955973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7048	20101	33518	1.8	6.0E-43	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.t3 MER1 MER1 repetitive element ;
10056	23094	36696	1.77	6.0E-43	AA195154.1	EST_HUMAN	zr35e06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G529641 G529641 DB1, COMPLETE CDS. ;contains element PTR7 repetitive element ;
11363	24424		2.45	6.0E-43	AL119158.1	EST_HUMAN	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
145	13370		1.82	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
515	13709	26736	3.4	5.0E-43	AA382780.1	EST_HUMAN	EST96033 Testis I Homo sapiens cDNA 5' end
2908	16086	29100	1.59	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'
6435	20096	33512	0.9	5.0E-43	AI613509.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
7043	20096	33512	0.69	5.0E-43	AI613509.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
8381	21462	34985	0.64	5.0E-43	AA442271.1	EST_HUMAN	zv54a03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
8381	21462	34986	0.64	5.0E-43	AA442271.1	EST_HUMAN	zv54a03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9080	22159		0.73	5.0E-43	H74277.1	EST_HUMAN	yu49g12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:229510 5'
9564	22706	36272	4.09	5.0E-43	AA465288.1	EST_HUMAN	aa33d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
10609	23643	37251	2.6	5.0E-43	AI733244.1	EST_HUMAN	oo52c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591 PV14 GENE. ;
10651	23685	37295	1.02	5.0E-43	AL049110.1	EST_HUMAN	DKFZp434D0119_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119
11001	24080	37715	4.53	5.0E-43	AW863007.1	EST_HUMAN	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
11213	24282	37921	2.24	5.0E-43	W29011.1	EST_HUMAN	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
995	15987	27227	4.4	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5373	18576	31444	1.09	4.0E-43	AI056338.1	EST_HUMAN	oy47h03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1669013 3'
6499	19665	33028	0.68	4.0E-43	6996009	NT	Homo sapiens glycyl-tRNA synthetase (GARS), mRNA
7280	20363		1.6	4.0E-43	11416793	NT	Homo sapiens protocadherin beta 6 (PCDHB6), mRNA
8371	21452	34975	5.18	4.0E-43	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ;
8371	21452	34976	5.18	4.0E-43	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ;
10521	23556	37164	1.02	4.0E-43	6005967	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
12311	25227		2.7	4.0E-43	R20950.1	EST_HUMAN	yg06b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ;
13030	25898		1.33	4.0E-43	AI436093.1	EST_HUMAN	th92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:O02710 O02710 GAG POLYPROTEIN. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1240	14399		3.46	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1730	14880	27971	2.52	3.0E-43	X97869.1	NT	H.sapiens gene encoding La autoantigen
2120	16055	28377	1.1	3.0E-43	R83422.1	EST_HUMAN	yp82f01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193945 5' similar to contains MSR1 repetitive element ;
3662	16825	29834	1.22	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein {rearranged translocation} [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4405	17548	30532	0.9	3.0E-43	AA548154.1	EST_HUMAN	nk55d06.s1 NCI_CGAP_Pr7 Homo sapiens cDNA clone IMAGE:1017419
6014	19198	32515	0.94	3.0E-43	D34613.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6487	19654	33016	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6487	19654	33017	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6867	20019	33428	5.09	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8357	21438		4.39	3.0E-43	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.t2 THR repetitive element ;
9020	22099	35639	1	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
10068	23106	36709	0.68	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC63648), mRNA
12026	25010	38712	1.42	3.0E-43	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
188	13410		7.24	2.0E-43	AI190764.1	EST_HUMAN	qd61c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.t3 PTR7 PTR7 repetitive element ;
6604	19764	33152	1.2	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element ;
6604	19764	33153	1.2	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element ;
7426	20503	33973	1.29	2.0E-43	AW207390.1	EST_HUMAN	UI-H-BI1-afi-a-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8503	21584		3.16	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11476	24535		4.75	2.0E-43	T03007.1	EST_HUMAN	FB1G5 Fetal brain, Stratagene Homo sapiens cDNA clone FB1G5 3'end similar to LINE-1
1681	14833	27917	2.95	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1681	14833	27918	2.95	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1742	14891	27985	4.12	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2766	15902	29009	4.73	1.0E-43	BF348283.1	EST_HUMAN	602022313F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157666 5'
5526	18723	31740	0.88	1.0E-43	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6744	19900	33291	6.84	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6744	19900	33292	6.84	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7106	18533	31488	1.19	1.0E-43	R19751.1	EST_HUMAN	yg40e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34732 5' similar to SP:BD38_MOUSE P28656 BRAIN PROTEIN DN38 ;
8117	21199	34720	0.6	1.0E-43	AF175265.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
8256	21338		2.17	1.0E-43	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
9037	22116	35659	28.54	1.0E-43	AW963676.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
10498	23533	37143	0.66	1.0E-43	AW953229.1	EST_HUMAN	EST365299 MAGE resequences, MAGB Homo sapiens cDNA
11206	24275	37912	5.81	1.0E-43	AI984961.1	EST_HUMAN	wr87h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
11647	24726	38418	3.05	1.0E-43	11424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
12248	25189		2.29	1.0E-43	AL137964.1	EST_HUMAN	DKFZp761D1015_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5'
12550	25373	32071	3.16	1.0E-43	AI675416.1	EST_HUMAN	wb99b04.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2313775 3'
12805	25538	32013	3.21	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
913	14088	27153	5.32	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
913	14088	27154	5.32	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
8736	21815	35350	2.86	8.0E-44	X94354.1	NT	H.sapiens DNA for Cone cGMP-PDE gene
10545	23580	37189	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
10545	23580	37190	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11436	24497	38164	2.87	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
11987	24972	38677	1.76	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
12501	25345	32065	2.89	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12544	25735	31946	2.17	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12945	25938	31760	1.85	8.0E-44	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
13126	25735	31946	2.29	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
676	13862		1.13	7.0E-44	R06035.1	EST_HUMAN	ye89e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2307	15439	28573	1.19	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3031	16207	29229	4.44	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3031	16207	29230	4.44	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3965	17123	30126	2.71	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4356	17499	30479	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4356	17499	30480	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8379	21460	34983	2.39	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
6229	19404	32754	0.67	6.0E-44	Z20946.1	EST_HUMAN	HSAAADEYU P, Human foetal Brain Whole tissue Homo sapiens cDNA
314	13530		4.25	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
342	13553		2.42	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8072	21154	34673	4.12	5.0E-44	AI568523.1	EST_HUMAN	tn40d02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.t1 OFR OFR repetitive element ;
9584	22726		1.39	5.0E-44	AU124571.1	EST_HUMAN	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
3501	16668	29678	4.27	4.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
5128	18253		0.89	4.0E-44	AI435225.1	EST_HUMAN	ti11d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
7639	20708	34187	0.87	4.0E-44	BE883178.1	EST_HUMAN	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
8466	21547	35077	0.86	4.0E-44	L21948.1	NT	Human fibrillin (FBN1) locus polymorphism
9079	22158		0.71	4.0E-44	BE176618.1	EST_HUMAN	RC3-HT0585-010400-023-d08 HT0585 Homo sapiens cDNA
11513	24570	38247	5.64	4.0E-44	U90878.1	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
1827	14975		1.5	3.0E-44	6912477	NT	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
3167	16342	29350	5.11	3.0E-44	AA169851.1	EST_HUMAN	zp18b05.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
7970	21020	34533	0.65	3.0E-44	BE884820.1	EST_HUMAN	601510547F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
9719	22784	36355	0.63	3.0E-44	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1074	14240	27296	1.43	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1074	14240	27297	1.43	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1234	14393	27455	3.61	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1234	14393	27456	3.61	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1340	14496	27568	6.82	2.0E-44	AF133588.1	NT	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1400	14554	27628	1.5	2.0E-44	BE465325.1	EST_HUMAN	hw14g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN. ;
2219	15353	28484	3.07	2.0E-44	AF070651.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2605	15728		1.26	2.0E-44	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
2642	15765	28879	0.94	2.0E-44	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
2676	15798		2.3	2.0E-44	5901933	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3559	16724	29740	1.34	2.0E-44	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4692	17827	30813	1.75	2.0E-44	AW864379.1	EST_HUMAN	PM4-SN0016-120500-003-e04 SN0016 Homo sapiens cDNA
6220	19395	32744	1.75	2.0E-44	11449901	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
6996	18515	31507	2.18	2.0E-44	AF038968.1	NT	Homo sapiens general transcription factor 2-I (GTF2I) mRNA, alternatively spliced product, complete cds
7572	20644	34121	3.8	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7572	20644	34122	3.8	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8623	21703	35238	0.7	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8623	21703	35239	0.7	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8819	21898	35437	1.8	2.0E-44	BE389058.1	EST_HUMAN	601286914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613586 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12152	25122		4.59	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
12730	26094		1.56	2.0E-44	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
53	13292	26306	5.24	1.0E-44	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
53	13292	26307	5.24	1.0E-44	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
594	13784	26804	1.63	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
1224	14384		1.96	1.0E-44	AW994803.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
1605	14758		8.06	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2299	15431	28563	6.17	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.t3 THR repetitive element ;
2299	15431	28564	6.17	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.t3 THR repetitive element ;
2818	15932	29043	1.74	1.0E-44	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3819	16979		3	1.0E-44	AA455869.1	EST_HUMAN	aa01c09.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5221	18343	31314	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5221	18343	31315	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8460	21541	35070	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA
8460	21541	35071	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA
8848	21927	35466	0.96	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9227	22305	35848	0.56	1.0E-44	AI337183.1	EST_HUMAN	qx88g07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009628 3'
11264	24333		4.13	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
11820	24809	38505	3.47	1.0E-44	10092664	NT	Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA
11890	24878	38574	3.21	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
11890	24878	38575	3.21	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4701	17836	30821	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4701	17836	30822	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6787	19942	33340	1.41	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2591	15716	28834	3.9	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5193	18315	31283	9.63	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8298	21380	34902	1.03	8.0E-45	AA377985.1	EST_HUMAN	EST90893 Synovial sarcoma Homo sapiens cDNA 5' end
1583	14735		2.36	6.0E-45	AI675425.1	EST_HUMAN	wb99c06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.t1 L1 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4087	17242		3.77	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
12911	26154		1.89	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
915	14090		1.71	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2058	15199	28313	4.42	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-f01 CN0044 Homo sapiens cDNA
3281	16455	29477	2.87	5.0E-45	AI523766.1	EST_HUMAN	tg94f07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1. ;
5629	18823	31897	8.95	5.0E-45	AA397781.1	EST_HUMAN	zt72d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
6143	19321	32664	1.09	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6143	19321	32665	1.09	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6190	19366	32714	0.92	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6190	19366	32715	0.92	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6318	19490	32847	0.87	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6318	19490	32848	0.87	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8471	21552	35082	1.12	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9241	22318	35861	1.45	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11997	24982	38688	2.5	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1167	14330	27385	6.3	4.0E-45	X95826.1	NT	H.sapiens ART4 gene
2365	15496	28622	2.15	4.0E-45	BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
9157	22235		0.81	4.0E-45	AA226220.1	EST_HUMAN	no26e07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element ;
12166	26089	31659	1.36	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
3411	16580		0.93	3.0E-45	T71480.1	EST_HUMAN	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
4199	16580		1.03	3.0E-45	T71480.1	EST_HUMAN	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6366	19536	32895	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
6366	19536	32896	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
8645	21725		1.76	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
8991	22070	35610	4.31	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10515	23550	37159	7.52	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10515	23550	37160	7.52	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
13040	26078		3.45	3.0E-45	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2572	15697		3.12	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3097	16273	29287	0.92	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6651	19810	33198	5.45	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7786	20842	34334	1.1	2.0E-45	BE782184.1	EST_HUMAN	601467793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8610	21690	35228	0.91	2.0E-45	AW834834.1	EST_HUMAN	RC0-LT0001-150200-032-d11 LT0001 Homo sapiens cDNA
9784	22824	36402	0.51	2.0E-45	AI636786.1	EST_HUMAN	ts56a01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232552 3'
11042	25867	37754	12.66	2.0E-45	BE934350.1	EST_HUMAN	MR0-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA
11450	24510	38177	2.71	2.0E-45	AA458770.1	EST_HUMAN	aa87f12.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to TR:G1144569 G1144569 R-SLY1. ;
11794	24784	38481	3.35	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
11794	24784	38482	3.35	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
13087	25710		2.73	2.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
126	13617		1.22	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
422	13617		1.99	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
485	13679	26714	1.02	1.0E-45	4506412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1201	14363	27423	1.66	1.0E-45	7657290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3172	16347	29354	10.41	1.0E-45	U32169.1	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3581	16746	29764	0.85	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3664	16827	29836	0.69	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4599	17736	30716	6.4	1.0E-45	BE396633.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
4848	17981		1.05	1.0E-45	H57443.1	EST_HUMAN	yr05b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:204363 5'
5081	18209	31181	1.56	1.0E-45	11545796	NT	Homo sapiens niban protein (NIBAN), mRNA
8220	21302	34822	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8220	21302	34823	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8806	21885	35425	0.9	1.0E-45	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9321	22397	35950	3.92	1.0E-45	BE887843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9722	22787	36358	0.99	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
12369	25263	32117	3.5	1.0E-45	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12562	25384		19.43	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12568	25387		6.42	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
13047	25686	31963	4.02	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8423	21504	35037	2.71	9.0E-46	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
8835	21914		6.82	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10697	23730	37335	6.89	9.0E-46	AW246964.1	EST_HUMAN	2822449.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2513	15639	28760	7.67	8.0E-46	AI433261.1	EST_HUMAN	tl32f08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2 TUBULIN BETA-1 CHAIN (HUMAN);
2513	15639	28761	7.67	8.0E-46	AI433261.1	EST_HUMAN	tl32f08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2 TUBULIN BETA-1 CHAIN (HUMAN);
8244	21326		2.72	8.0E-46	BE167244.1	EST_HUMAN	RC5-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA
4703	17838		4.79	7.0E-46	BE386165.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4928	18058		1.33	7.0E-46	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
6167	19343	32689	4	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
6623	19783	33171	1.8	7.0E-46	BF105845.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
12706	25469		2.6	7.0E-46	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2812	15926	29037	6.87	6.0E-46	AI884381.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2 MER19 repetitive element ;
2812	15926	29038	6.87	6.0E-46	AI884381.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2 MER19 repetitive element ;
6257	19431	32778	11.57	6.0E-46	AI635448.1	EST_HUMAN	ts58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE. ;
7366	20445	33907	0.99	6.0E-46	AW513244.1	EST_HUMAN	xo42e04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
7541	20614	34091	0.67	6.0E-46	BF509740.1	EST_HUMAN	UI-H-BI4-apg-b-06-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087298 3'
11673	23901		2.14	6.0E-46	BE784971.1	EST_HUMAN	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880995 5'
209	13432		5.31	5.0E-46	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3617	16781	29796	1.17	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3617	16781	29797	1.17	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6874	20026	33436	1.52	5.0E-46	BF590442.1	EST_HUMAN	naa38f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202 O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
7080	20174	33596	3.69	5.0E-46	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
7244	20327	33772	0.75	5.0E-46	AW582253.1	EST_HUMAN	QV4-ST0212-120100-075-f09 ST0212 Homo sapiens cDNA
7544	20616	34093	0.59	5.0E-46	BE549744.1	EST_HUMAN	7b38b05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
658	13844		3.95	4.0E-46	AA601143.1	EST_HUMAN	no54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1740	14889	27981	2.99	4.0E-46	AW770544.1	EST_HUMAN	hl86c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1740	14889	27982	2.99	4.0E-46	AW770544.1	EST_HUMAN	hl86c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
2798	15913	29021	7.4	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
5553	18750	31786	2.1	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5553	18750	31787	2.1	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12851	25565	31989	1.36	4.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2359	15490	28620	0.94	3.0E-46	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
4513	17652	30640	1.21	3.0E-46	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA
4898	18028	31015	1.11	3.0E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
4898	18028	31016	1.11	3.0E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
8949	22028	35569	12.45	3.0E-46	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
9206	22284	35824	0.61	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
9206	22284	35825	0.61	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
11873	24851	38556	1.78	3.0E-46	D31765.1	NT	Human mRNA for KIAA0061 gene, partial cds
860	14037	27099	12.65	2.0E-46	AA468646.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
1593	14746		3.78	2.0E-46	AA678246.1	EST_HUMAN	zi27a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'
1671	14823	27906	5.63	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
5089	18217	31188	1.26	2.0E-46	AA399286.1	EST_HUMAN	zt59e02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN. ;
7653	20721	34197	7.1	2.0E-46	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
8260	21342		1.29	2.0E-46	BE869151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
11524	24580		1.82	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
12294	26040		1.4	2.0E-46	BF028854.1	EST_HUMAN	601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3997326 5'
12555	25931		1.57	2.0E-46	H48391.1	EST_HUMAN	yr32d01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206977 5'
12596	25401		3.31	2.0E-46	AA001786.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
12934	25923	31864	4.26	2.0E-46	AW277214.1	EST_HUMAN	xq78h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1261	14418	27483	4.31	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2356	15487	28619	4.88	1.0E-46	AW978516.1	EST_HUMAN	EST390625 MAGE resequences, MAGP Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2473	15600	28725	3.53	1.0E-46	H97330.1	EST_HUMAN	EST48b095 WATM1 Homo sapiens cDNA clone 48b095
3321	16494	29511	2.12	1.0E-46	AA631912.1	EST_HUMAN	np78b02.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-1l mRNA. (HUMAN);
4995	18124		3.13	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5817	19007	32313	5.89	1.0E-46	BF194707.1	EST_HUMAN	7o92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6098	25818	32609	5.34	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6098	25818	32610	5.34	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6746	19902	33295	0.64	1.0E-46	BF196247.1	EST_HUMAN	7n48e07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element MER22 repetitive element ;
11102	19007	32313	3.72	1.0E-46	BF194707.1	EST_HUMAN	7o92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
11410	24471	38136	1.61	1.0E-46	AJ245621.1	NT	Homo sapiens CTL2 gene
12323	25233	32105	1.39	1.0E-46	BF531102.1	EST_HUMAN	602072264F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215398 5'
12323	25233	32106	1.39	1.0E-46	BF531102.1	EST_HUMAN	602072264F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215398 5'
13176	25764		1.99	1.0E-46	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
787	13966		3.7	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
5047	18175	31152	3.05	9.0E-47	AW770928.1	EST_HUMAN	hl93e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703 HYPOTHETICAL 12.4 KD PROTEIN. ;
6506	19672	33039	0.86	9.0E-47	11425439	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
11388	24449	38110	1.4	9.0E-47	11432209	NT	Homo sapiens similar to aldo-keto reductase family 1, member B1 (aldose reductase) (H. sapiens) (LOC63093), mRNA
12874	26027	31675	1.64	9.0E-47	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1851	14997	28100	32.2	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
1851	14997	28101	32.2	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2781	15897	29007	1.5	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3089	16265	29283	2.04	8.0E-47	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3715	16876	29881	0.77	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
3715	16876	29882	0.77	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
12962	25922		1.99	7.0E-47	AV683284.1	EST_HUMAN	AV683284 GKC Homo sapiens cDNA clone GKCASH11 5'
2613	15737	28851	3.04	6.0E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8890	21969	35505	0.52	6.0E-47	U77054.1	EST_HUMAN	HSU77054 Human Homo sapiens cDNA clone N7
9476	22533	36097	6.83	6.0E-47	AI695189.1	EST_HUMAN	tz98h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296659 3'
9913	22953	36538	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
9913	22953	36539	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6707	19865	33255	5.73	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
11035	24114		5.58	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
1432	14585	27660	7.03	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6971	20199	33625	0.82	4.0E-47	BE938896.1	EST_HUMAN	MR4-TN0108-280800-201-d04 TN0108 Homo sapiens cDNA
8677	21757	35292	2.22	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8677	21757	35293	2.22	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8818	21897	35436	0.83	4.0E-47	AW993777.1	EST_HUMAN	RC3-BN0034-220300-015-f05 BN0034 Homo sapiens cDNA
11936	24922		1.98	4.0E-47	AW515509.1	EST_HUMAN	xx66b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1];
558	13751	26778	2.09	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
558	13751	26779	2.09	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
841	14019	27075	3.99	3.0E-47	N57483.1	EST_HUMAN	yy54b04.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:277327 3'
968	14141	27202	10.04	3.0E-47	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3376	16548	29562	0.97	3.0E-47	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4073	17229		6.61	3.0E-47	U93181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
4482	17522	30603	1.14	3.0E-47	M12959.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6136	19315	32654	4.68	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adx-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6136	19315	32655	4.68	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adx-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6694	19852		1.71	3.0E-47	AI222413.1	EST_HUMAN	qh04e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7540	20613	34089	0.88	3.0E-47	AI819755.1	EST_HUMAN	wj11h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
7540	20613	34090	0.88	3.0E-47	AI819755.1	EST_HUMAN	wj11h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9033	22112	35654	0.77	3.0E-47	AW963796.1	EST_HUMAN	EST375869 MAGE resequences, MAGH Homo sapiens cDNA
9033	22112	35655	0.77	3.0E-47	AW963796.1	EST_HUMAN	EST375869 MAGE resequences, MAGH Homo sapiens cDNA
152	13377	26409	1.21	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
990	14162	27221	2.45	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
990	14162	27222	2.45	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1598	14751		0.95	2.0E-47	AI969279.1	EST_HUMAN	wq96b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2479851 3'
1623	14775	27859	1.61	2.0E-47	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1712	14863	27952	4.49	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3'
4467	17607	30585	1.61	2.0E-47	4504866	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4503	17643	30628	1.67	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
4503	17643	30629	1.67	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
4628	17764	30746	2.14	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4933	18063	31046	1.25	2.0E-47	AW965168.1	EST_HUMAN	EST377239 MAGE resequences, MAGI Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5245	18366		0.71	2.0E-47	AI041126.1	EST_HUMAN	ov61h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641845 3'
5904	19093	32407	0.8	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6097	19278	32607	1.32	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6097	19278	32608	1.32	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7876	25854		1.34	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8151	21233	34753	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8151	21233	34754	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8915	21994	35533	1.76	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9690	22739	36308	1.27	2.0E-47	11526136	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
12357	26073	31653	3.36	2.0E-47	R42423.1	EST_HUMAN	yf92e08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:29966 3' similar to contains OFR repetitive element ;
12394	26076		1.87	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1437	14590	27663	5.42	1.0E-47	AI333429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3926	17085	30080	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3926	17085	30081	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5187	18309	31275	2.4	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
7189	20054	33464	10.76	1.0E-47	AI880886.1	EST_HUMAN	at19e06.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995 RAS-RELATED PROTEIN RAP-1A (HUMAN);
9069	22148		4.24	1.0E-47	AW664648.1	EST_HUMAN	hi84a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10564	23599	37205	2.26	1.0E-47	L30115.1	NT	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
1643	14795	27879	3.84	9.0E-48	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3646	16809	29823	0.73	9.0E-48	BF359947.1	EST_HUMAN	CM2-MT0100-310700-290-f05 MT0100 Homo sapiens cDNA
5797	18987	32290	1.1	9.0E-48	BE888196.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
5797	18987	32291	1.1	9.0E-48	BE888196.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
6226	19401	32751	0.57	9.0E-48	AI833168.1	EST_HUMAN	at75h09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:O60844 O60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN. ;
6355	19525	32882	0.71	9.0E-48	AU123240.1	EST_HUMAN	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
11378	24439	38098	3.06	9.0E-48	BE393813.1	EST_HUMAN	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
1279	14435		1.75	8.0E-48	4501900	NT	Homo sapiens aminoacylase 1 (ACY1), mRNA
1280	14436		1.65	8.0E-48	4501900	NT	Homo sapiens aminoacylase 1 (ACY1), mRNA
3205	16380	29390	5.72	8.0E-48	AW768477.1	EST_HUMAN	hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3205	16380	29391	5.72	8.0E-48	AW768477.1	EST_HUMAN	hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
4041	17197	30208	0.66	8.0E-48	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
503	13698		2.58	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
504	13698		18.69	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1527	14680	27761	1.96	7.0E-48	6912719	NT	Homo sapiens tousled-like kinase 1 (TLK1), mRNA
1667	14819	27902	5.39	7.0E-48	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6685	19843	33233	24.01	7.0E-48	11416831	NT	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
12125	25105	38809	2.98	7.0E-48	R19623.1	EST_HUMAN	yg37b02.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34747 5'
3687	16850	29858	0.88	6.0E-48	AI761111.1	EST_HUMAN	wi69h03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
6183	19359	32707	0.84	6.0E-48	AB006955.1	NT	Homo sapiens mRNA for AIE-75, complete cds
6924	20239	33674	0.93	6.0E-48	11420995	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7628	25849	34172	0.78	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
7628	25849	34173	0.78	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9323	22399	35953	1.57	6.0E-48	AF026816.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9741	22806	36382	1.87	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9890	22930	36514	2.84	6.0E-48	AA189080.1	EST_HUMAN	zq45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
3384	18465	29569	1.48	5.0E-48	4826891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
8774	21853	35395	1.04	5.0E-48	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2829	15943	29053	1.02	4.0E-48	R45715.1	EST_HUMAN	Ha140-f Adult heart, Clontech Homo sapiens cDNA clone a140-f
11200	24269	37905	3.11	4.0E-48	AI620420.1	EST_HUMAN	tu47a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2254154 3'
12050	25031	38737	1.75	4.0E-48	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
1416	14570	27643	1.91	3.0E-48	AV690964.1	EST_HUMAN	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
2032	15173	28282	31.61	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2032	15173	28283	31.61	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3505	16672	29682	0.93	3.0E-48	AF172453.1	NT	Homo sapiens opioid growth factor receptor mRNA, complete cds
3721	16882	29888	0.9	3.0E-48	AW664531.1	EST_HUMAN	hi14b12.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
4362	17505		0.63	3.0E-48	AA009541.1	EST_HUMAN	zl04g03.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429844 5'
6015	19199	32516	2.08	3.0E-48	BE084571.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
7159	20292	33735	1.07	3.0E-48	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
8585	21666		3.73	3.0E-48	AA659930.1	EST_HUMAN	nv03f05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1 PTR5 repetitive element ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11114	24186	37818	8.1	3.0E-48	BF514170.1	EST_HUMAN	UI-H-BW1-anl-a-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
5	13244	26245	0.66	2.0E-48	AA465007.1	EST_HUMAN	zx80c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'
46	13285	26294	1.7	2.0E-48	AA631940.1	EST_HUMAN	fmfc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
4654	17790	30774	0.99	2.0E-48	BE246065.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
5935	19121	32433	0.64	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
5935	19121	32434	0.64	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
7688	20753	34236	3.99	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7688	20753	34237	3.99	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7703	20768	34253	3.54	2.0E-48	11496238	NT	Homo sapiens *v-rel avian reticuloendotheliosis viral oncogene homolog A* (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8550	21631	35168	1.13	2.0E-48	AV743451.1	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'
12109	25089		1.36	2.0E-48	AW291799.1	EST_HUMAN	UI-H-BI2-agl-b-11-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724453 3'
12320	13244	26245	2.98	2.0E-48	AA465007.1	EST_HUMAN	zx80c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'
12674	25990	31771	1.25	2.0E-48	BE737154.1	EST_HUMAN	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
57	13295	26311	2.33	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
896	14072	27137	4.67	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1101	14266	27323	1.52	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1101	14266	27324	1.52	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1324	14481	27548	4.01	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1968	15111	28212	13.8	1.0E-48	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C102
3577	16742	29759	0.94	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5240	18362	31330	1.1	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6417	19586	32948	1.24	1.0E-48	AI889077.1	EST_HUMAN	td17c01.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941 ;
6417	19586	32949	1.24	1.0E-48	AI889077.1	EST_HUMAN	td17c01.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941 ;
6628	19788		0.87	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
6727	19883	33274	0.59	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6727	19883	33275	0.59	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
7407	20485	33954	2.21	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
9031	22110	35651	0.65	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
9031	22110	35652	0.65	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9414	22488	36053	0.99	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9468	22525	36089	6.79	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9781	22821	36399	4.74	1.0E-48	BF304683.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10581	23616	37221	4.23	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10581	23616	37222	4.23	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
12282	26014		1.41	1.0E-48	W26785.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
2064	15204	28320	0.97	8.0E-49	AB026497.1	NT	Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds
6178	19354	32701	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6178	19354	32702	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8491	21572	35109	3.09	8.0E-49	U23850.1	NT	Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
10194	23231	36822	0.93	8.0E-49	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
11096	24169	37804	3.65	8.0E-49	AI623722.1	EST_HUMAN	ts38d12.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element;contains element PTR5 repetitive element ;
12097	25077	38785	2.08	8.0E-49	AA872183.1	EST_HUMAN	ob78e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337462 3'
142	13602	26637	1.21	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
142	13602	26638	1.21	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26637	1.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26638	1.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
406	13602	26637	2.25	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
406	13602	26638	2.25	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1248	14407	27469	4.37	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4772	17907	30890	0.9	7.0E-49	O60811	SWISSPROT	HYPOTHETICAL PROTEIN DJ845O24.3
5576	18771	31815	2.33	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923 O54923 RSEC15. ;
5586	18781	31826	1.3	7.0E-49	AL120937.1	EST_HUMAN	DKFZp762C033_s1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762C033 3'
5926	18771	31815	0.79	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923 O54923 RSEC15. ;
202	13425	26456	20.33	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
4231	17378	30367	0.64	6.0E-49	AL162091.1	EST_HUMAN	DKFZp761A138_s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138 3'
5954	19140	32456	0.64	6.0E-49	AW511225.1	EST_HUMAN	hd44e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636 O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II. ;
6572	19734	33113	1.27	6.0E-49	AU140742.1	EST_HUMAN	AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11557	24612	38291	3.39	6.0E-49	AW452218.1	EST_HUMAN	UI-H-BI3-alo-a-05-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11961	24946	38650	2.48	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
11961	24946	38651	2.48	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
12670	25897		10.54	6.0E-49	AA707567.1	EST_HUMAN	zj29c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
730	13912	26951	5.84	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
730	13912	26952	5.84	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1836	14983	28082	10.18	5.0E-49	AA172121.1	EST_HUMAN	zp29c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN. ;contains LTR7.t3 LTR7 LTR7 repetitive element ;
2808	15922	29032	7.1	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3346	16519	29533	7.59	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metallopanstimulin 1) (H. sapiens) (LOC63362), mRNA
538	13731	26754	28.39	4.0E-49	AW189533.1	EST_HUMAN	xl08b01.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:B0350.2B CE06703 ;
7395	20473	33939	0.96	4.0E-49	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7395	20473	33940	0.96	4.0E-49	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7422	20499	33970	0.68	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
7422	20499	33971	0.68	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
7992	21042	34554	0.69	4.0E-49	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
9065	22144	35690	0.47	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
9065	22144	35691	0.47	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
12514	26145		2.74	4.0E-49	AA210798.1	EST_HUMAN	zr90f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682977 5'
12615	25413		2.93	4.0E-49	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
574	13766	26789	0.91	3.0E-49	X68968.1	NT	H.sapiens mRNA for acetyl-CoA carboxylase
2713	15831		2.73	3.0E-49	AA016131.1	EST_HUMAN	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1 repetitive element ;
5098	18226	31198	2.68	3.0E-49	U46999.1	NT	Human type IV collagen (COL4A6) gene, exon 40
7577	20649	34127	9.83	3.0E-49	H39479.1	EST_HUMAN	EST25e12 WATM1 Homo sapiens cDNA clone 25e12
11582	24636	38316	1.41	3.0E-49	AA337561.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
678	13864		1.93	2.0E-49	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3294	16468	29487	1.15	2.0E-49	N26446.1	EST_HUMAN	yx23d06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262571 5'

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3659	16822	29832	0.86	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
6875	20027	33437	1.2	2.0E-49	AV717938.1	EST_HUMAN	AV717938 DCB Homo sapiens cDNA clone DCBALB01 5'
8291	21373		1.87	2.0E-49	M86033.1	EST_HUMAN	EST02558 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY50
12626	26008		2.69	2.0E-49	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
922	14097		9.1	1.0E-49	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1584	14736	27816	73.58	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1844	14990	28091	2.93	1.0E-49	BE255216.1	EST_HUMAN	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
5475	18674	31688	4.68	1.0E-49	BF131007.1	EST_HUMAN	601820053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
6202	19377	32728	0.85	1.0E-49	H18291.1	EST_HUMAN	yn48h04.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT ;
6208	19383	32733	1.09	1.0E-49	AW964640.1	EST_HUMAN	EST376713 MAGE resequences, MAGH Homo sapiens cDNA
7372	20451	33915	2.78	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7372	20451	33916	2.78	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7453	20530	34003	2.09	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7453	20530	34004	2.09	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
8874	21953		0.71	1.0E-49	9994184	NT	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
9193	22271	35809	1.48	1.0E-49	BE409340.1	EST_HUMAN	601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10331	23366	36975	1.23	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5'
11304	24369	38010	1.32	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDAWE04 5'
11590	24643	38325	2.91	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12148	25119		1.26	1.0E-49	BE169343.1	EST_HUMAN	MR0-HT0407-010200-006-f02 HT0407 Homo sapiens cDNA
12508	25349		1.82	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
5109	18237		0.92	9.0E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
6534	26215		0.63	9.0E-50	BE295758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
174	13398	26426	4.18	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
737	13919	26959	1.92	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
737	13919	26960	1.92	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1803	14952	28046	4.32	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2552	15677	28800	1.05	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2552	15677	28801	1.05	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2764	15879	28988	2.42	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
2891	15160		2.67	8.0E-50	D90334.1	NT	Homo sapiens hepatocyte growth factor(HGF) gene, exon 18

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634	13819	26843	1.07	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
6923	20238	33672	0.73	7.0E-50	BF091922.1	EST_HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
6923	20238	33673	0.73	7.0E-50	BF091922.1	EST_HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7457	20533	34008	0.74	7.0E-50	AA627822.1	EST_HUMAN	nq59e12.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN);
10993	24072	37705	23.18	7.0E-50	AI872137.1	EST_HUMAN	wm55g11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439908 3'
4462	17602		0.67	6.0E-50	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
8408	21489		3.28	6.0E-50	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element ;
11053	24130	37765	3.32	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
11053	24130	37766	3.32	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1835	14982	28080	1.34	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
1835	14982	28081	1.34	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
9294	22370		5.27	5.0E-50	AA557683.1	EST_HUMAN	nl45h10.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5 repetitive element ;
12090	25070	38777	1.78	5.0E-50	AA403053.1	EST_HUMAN	zt62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 G1335769 GAG-POL POLYPROTEIN. ;
940	14114		2.31	4.0E-50	AA601143.1	EST_HUMAN	no54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
3536	16701	29712	2.06	4.0E-50	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
6491	19657	33020	0.92	4.0E-50	11440683	NT	Homo sapiens cysteinyl-tRNA synthetase (CARS), mRNA
7383	20481	33924	1.02	4.0E-50	BE087536.1	EST_HUMAN	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA
1992	15134		9.4	3.0E-50	M18048.1	NT	Human endogenous retrovirus RTVL-H2
3371	16543	29557	0.92	3.0E-50	AA746142.1	EST_HUMAN	ob03f06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
3846	17006	30008	0.9	3.0E-50	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
6815	19968	33374	0.99	3.0E-50	11419317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
6815	19968	33375	0.99	3.0E-50	11419317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
6904	20219	33648	1.71	3.0E-50	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
7822	20877	34376	5	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7822	20877	34377	5	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds

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8782	21861	35404	0.66	3.0E-50	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10023	23061	36657	1.08	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
10032	23070	36670	1.03	3.0E-50	11418514	NT	Homo sapiens t-complex 10 (a murine tcp homolog) (TCP10), mRNA
10737	23770	37380	1.04	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
11364	24425	38080	1.51	3.0E-50	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11752	23938	37564	8.19	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
13217	25792	31922	1.35	3.0E-50	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
799	13978		7.94	2.0E-50	AF055086.1	NT	Homo sapiens MHC class 1 region
1104	14269	27327	6.16	2.0E-50	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
1474	14627	27713	33.77	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
4376	17519	30499	0.75	2.0E-50	D86424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
5329	18442	31412	1.37	2.0E-50	AB018319.1	NT	Homo sapiens mRNA for KIAA0776 protein, partial cds
7007	20143	33562	0.61	2.0E-50	AU124065.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001609 5'
8511	21592	35126	1.03	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8511	21592	35127	1.03	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8650	21730	35268	7.21	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8650	21730	35269	7.21	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
10088	23126	36728	1.6	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
10088	23126	36729	1.6	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
11960	24945		1.39	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
474	13669	26701	2.17	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2438	15566		10.11	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
10396	23431	37038	1.65	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6104	19284	32617	1.04	9.0E-51	AW611225.1	EST_HUMAN	hd44e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636 O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II. ;
6354	19524	32881	0.58	9.0E-51	AA744837.1	EST_HUMAN	ny67h03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283381 3'
8872	21951	35487	0.7	9.0E-51	AI791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9525	22590	36161	1.29	9.0E-51	AA043738.1	EST_HUMAN	zk51c09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486352 5'
9700	22749	36317	0.68	9.0E-51	AI791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9700	22749	36318	0.68	9.0E-51	AI791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
11764	23950	37579	1.97	9.0E-51	H89078.1	EST_HUMAN	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11764	23950	37580	1.97	9.0E-51	H89078.1	EST_HUMAN	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
12069	25050	38768	1.84	9.0E-51	AA885514.1	EST_HUMAN	am10h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1466451 3' similar to SW:CAYP_CANFA P10463 CALCYPHOSINE ;
4559	17697	30677	1.11	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4559	17697	30678	1.11	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4690	17825	30812	5.38	8.0E-51	AA610842.1	EST_HUMAN	np98e09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7321	20403	33865	0.71	8.0E-51	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
7830	20885	34387	2.11	8.0E-51	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
9664	22626		1.06	8.0E-51	AU138590.1	EST_HUMAN	AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'
3354	16526	29541	1.27	7.0E-51	AW889219.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
3447	16515	29633	0.82	7.0E-51	AW274720.1	EST_HUMAN	xn34e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
4282	17427	30416	1.37	7.0E-51	AL079623.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4282	17427	30417	1.37	7.0E-51	AL079623.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4375	17518	30498	1.18	7.0E-51	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
4471	17611	30589	1.44	7.0E-51	AW295603.1	EST_HUMAN	UI-H-BW0-aip-b-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
11985	24970	38674	1.36	7.0E-51	AF161449.1	NT	Homo sapiens HSPC331 mRNA, partial cds
1557	14710	27790	0.94	6.0E-51	6678763	NT	Homo sapiens putative DNA binding protein (M96), mRNA
2036	15177	28287	5.93	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3562	16727	29743	14.65	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4426	17566	30547	0.66	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4426	17566	30548	0.66	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6113	19293	32628	1.48	6.0E-51	X01788.1	NT	Human haptoglobin related (Hpr) gene exon 3
6124	19303	32642	8.16	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6124	19303	32643	8.16	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6900	20215	33645	0.93	6.0E-51	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7032	20168	33690	0.82	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA
7104	18531	31486	2.15	6.0E-51	11429665	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
9337	22413	35965	0.69	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9337	22413	35966	0.69	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9885	22925	36509	2.05	6.0E-51	7661535	NT	Homo sapiens B9 protein (B9), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9964	23003	36598	0.79	6.0E-51	U50093.1	NT	Human ankyrin (ANK1) gene, exon 2
11534	24590	38265	1.84	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
814	13993	27047	6.22	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
826	14004	27061	1.71	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1016	16028	27247	2.39	5.0E-51	AL133204.1	NT	Novel human gene mapping to chomosome X
1638	14790	27875	1.14	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2658	15781	28894	10.36	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
4055	17211	30221	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4055	17211	30222	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5183	18305	31269	1.04	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11558	24613	38292	3.8	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
137	13363	26397	14.26	3.0E-51	AI587348.1	EST_HUMAN	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1203	14365	27425	48.14	3.0E-51	AI587348.1	EST_HUMAN	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1976	15119	28220	1.38	3.0E-51	AA211296.1	EST_HUMAN	zq87g01.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:649008 3'
4446	17586	30567	1.85	3.0E-51	AL159142.1	NT	Novel human gene mapping to chomosome 22
7753	20813	34304	2.3	3.0E-51	R15914.1	EST_HUMAN	ya47c08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:63233 5' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);contains LTR5 repetitive element ;
9040	22119		3.85	3.0E-51	M29063.1	NT	Human hnRNP C2 protein mRNA
9268	26227		0.61	3.0E-51	AW583777.1	EST_HUMAN	ia04d06.y1 Human Pancreatic Islets Homo sapiens cDNA 5'
12867	25578		6.56	3.0E-51	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
377	13585	26619	1.98	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
706	13889	26921	0.89	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
706	13889	26922	0.89	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1723	14873	27965	16.75	2.0E-51	AA233352.1	EST_HUMAN	zr30a05.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233226 G233226 RTVL-H PROTEIN. ;contains LTR7.t3 LTR7 repetitive element ;
3827	16987	29990	3.05	2.0E-51	AI492415.1	EST_HUMAN	ti27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4616	17753	30734	1.21	2.0E-51	AW137826.1	EST_HUMAN	UI-H-BI1-adj-d-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
5326	18439	31408	0.66	2.0E-51	AI381520.1	EST_HUMAN	te76c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092622 3' similar to TR:P93107 P93107 PF20. ;

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6139	19317	32658	3.54	2.0E-51	BE782015.1	EST_HUMAN	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7462	20537		0.73	2.0E-51	AF219927.1	NT	Homo sapiens diacylglycerol kinase iota (DGKI) gene, exon 23
7615	20685	34161	1.29	2.0E-51	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
8896	21975	35512	1.61	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
8896	21975	35513	1.61	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9235	22312	35854	1.03	2.0E-51	11037064	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9712	22777	36347	1.76	2.0E-51	AI917078.1	EST_HUMAN	ts74a07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
9803	22843	36420	4.86	2.0E-51	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9818	22858	36438	0.69	2.0E-51	AB007926.1	NT	Homo sapiens mRNA for KIAA0457 protein, partial cds
10648	23682	37293	1.58	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
10690	23723	37329	1.07	2.0E-51	AA378559.1	EST_HUMAN	EST91296 Synovial sarcoma Homo sapiens cDNA 5' end
11610	18752	31789	5.82	2.0E-51	AI732851.1	EST_HUMAN	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
11610	18752	31790	5.82	2.0E-51	AI732851.1	EST_HUMAN	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
12860	25571	31992	1.62	2.0E-51	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA
117	13348	26375	10.94	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1523	14676		37.16	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCC12 5'
4918	18048	31036	0.82	1.0E-51	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
5505	18704	31720	3.7	1.0E-51	T18862.1	EST_HUMAN	b12056t Testis 1 Homo sapiens cDNA clone b12056
7827	20882	34384	1.03	1.0E-51	AI572532.1	EST_HUMAN	te39g02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
8087	21169	34684	0.51	1.0E-51	BF434359.1	EST_HUMAN	7o96b02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644091 3' similar to TR:P87892 P87892 PROTEASE ;
12076	26232		1.97	1.0E-51	AV760590.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSCBB02 5'
12610	25409		9.43	9.0E-52	AA777621.1	EST_HUMAN	zi95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.t3 THR repetitive element ;
158	13381	26412	11.42	8.0E-52	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;
1526	14679	27760	2.39	8.0E-52	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
1686	14838	27922	2.85	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA

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1688	14838	27923	2.85	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27922	6.75	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27923	6.75	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7686	20751	34232	0.76	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
7686	20751	34233	0.76	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
9215	22293	35836	1.86	7.0E-52	W56471.1	EST_HUMAN	zc59a06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element;
1214	14375		0.63	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271299-049-d07 BT0537 Homo sapiens cDNA
1729	14879	27970	7.1	6.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5845	19035	32341	1.05	6.0E-52	AI208794.1	EST_HUMAN	qg44f04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11484	24543	38214	2.36	6.0E-52	BE048172.1	EST_HUMAN	tz46h04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;
4562	17700	30682	2.27	5.0E-52	Z78898.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7
9592	22647	36218	0.48	5.0E-52	11437365	NT	Homo sapiens FSHD region gene 1 (FRG1), mRNA
1695	14847	27931	1.66	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1829	14977	28072	1.63	4.0E-52	4758843	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
4037	17193	30203	0.77	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4862	17995	30980	0.81	4.0E-52	AI766814.1	EST_HUMAN	wi89b02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400459 3'
5401	18603	31574	1.3	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5401	18603	31575	1.3	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
8228	21310	34830	1.19	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5'
8731	21811	35347	5.5	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12429	25304		3.44	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12987	25642		12.79	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13141	25741		1.3	4.0E-52	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
4204	17353		11.41	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
576	13768	26790	1.82	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
576	13768	26791	1.82	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2071	15211	28328	1.18	2.0E-52	AB033075.1	NT	Homo sapiens mRNA for KIAA1249 protein, partial cds

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2568	15693	28818	1.5	2.0E-52	BE207575.1	EST_HUMAN	bb66b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2796	15911		11.46	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5092	18220	31190	3.41	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5126	18251	31216	1.4	2.0E-52	AI141802.1	EST_HUMAN	qa56e05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5126	18251	31217	1.4	2.0E-52	AI141802.1	EST_HUMAN	qa56e05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5821	19011	32317	3.24	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA
6497	19663	33026	1.98	2.0E-52	11141868	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
6853	20006	33415	0.96	2.0E-52	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7081	20175	33597	0.76	2.0E-52	AI792146.1	EST_HUMAN	os45d12.y5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'
7996	21046	34558	0.69	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
7996	21046	34559	0.69	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8854	21933		8.71	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
9136	22215	35759	0.96	2.0E-52	AA778795.1	EST_HUMAN	zj45g05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9680	22642		1	2.0E-52	4758789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10321	23356	36965	4.6	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10321	23356	36966	4.6	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11481	24540	38209	3.14	2.0E-52	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
11481	24540	38210	3.14	2.0E-52	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
11491	24550	38225	2.52	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
11634	24714		1.46	2.0E-52	W70260.1	EST_HUMAN	zd49g12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5'
11918	24904		3.25	2.0E-52	11417990	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
12234	26194	31541	5.9	2.0E-52	AW236297.1	EST_HUMAN	xn72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element;contains element LTR2 repetitive element ;
12658	25437		5.72	2.0E-52	AI808985.1	EST_HUMAN	wf67d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859 Q16859 CARBOXYLESTERASE ;
546	13739	26764	1.89	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1402	14656	27630	18.76	1.0E-52	4504026	NT	Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA
2600	15724		1.86	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3126	16302	29315	2.6	1.0E-52	S61070.1	NT	pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5448	18548	31626	4.43	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6523	19688	33062	2.33	1.0E-52	U38964.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
7588	20859	34135	2.07	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8014	21064	34576	0.59	1.0E-52	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8660	21740		1.18	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9390	22465	36029	0.77	1.0E-52	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10804	23837		0.68	1.0E-52	AW020370.1	EST_HUMAN	df08g05.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10814	23847		1.06	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11004	24083	37720	2.12	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
11075	24150		1.72	1.0E-52	11426321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
12135	25115	38819	1.31	1.0E-52	11421401	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
12135	25115	38820	1.31	1.0E-52	11421401	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
3891	17050	30049	0.69	9.0E-53	4506064	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4511	17650	30638	3.3	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12480	25332		6.65	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5'
12958	26046		7.06	7.0E-53	AI421782.1	EST_HUMAN	tf44f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2099077 3' similar to contains THR.t1 THR repetitive element ;
4214	17363	30351	4.46	5.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
5293	18411	31377	0.92	5.0E-53	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12528	25360		1.93	5.0E-53	AW813563.1	EST_HUMAN	RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
50	13289	26301	2.07	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
50	13289	26302	2.07	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
9616	22671		0.67	4.0E-53	AI613037.1	EST_HUMAN	ty06h04.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2278327 3'
9958	22997		0.94	4.0E-53	F13080.1	EST_HUMAN	HSC3ID041 normalized infant brain cDNA Homo sapiens cDNA clone c-3id04
11489	24548	38221	2.99	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
11489	24548	38222	2.99	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2726	15844	28965	2.34	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3825	16985	29988	1.18	3.0E-53	AW050836.1	EST_HUMAN	wz22c07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2558796 3'
4713	17848	30831	0.75	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA
5541	18738	31755	0.97	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5743	18936	32236	1.01	3.0E-53	11526297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6323	19495	32851	1.46	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7247	20330	33776	0.76	3.0E-53	Y10388.3	NT	H.sapiens graf gene
7247	20330	33777	0.76	3.0E-53	Y10388.3	NT	H.sapiens graf gene
8499	21580	35116	10.97	3.0E-53	S72043.1	NT	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]
9060	22139	35683	0.85	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9257	22334		9.77	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
12361	25259		1.18	3.0E-53	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
470	13665		11.25	2.0E-53	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
2068	15209	28325	3.29	2.0E-53	7705394	NT	Homo sapiens hyaluronic acid receptor (HAR), mRNA
2404	15535	28662	6.26	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2601	15725		12.68	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
3280	16464	29483	0.79	2.0E-53	7705687	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
3317	16490	29508	1.29	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4170	17320	30313	2.59	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5542	18739	31756	2.46	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
5542	18739	31757	2.46	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
8055	21138	34658	1.01	2.0E-53	AW975598.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sapiens cDNA
8196	21278		0.48	2.0E-53	AA095852.1	EST_HUMAN	I5429.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9608	22663		3.47	2.0E-53	AW245676.1	EST_HUMAN	2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5'
10862	23895	37517	0.69	2.0E-53	BE550195.1	EST_HUMAN	7b50b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231627 3' similar to TR:Q04009 Q04009 MYOSIN HEAVY CHAIN. ;
1477	14630	27715	2.2	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
3496	16663	29675	2.99	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5078	18206	31178	1.06	1.0E-53	BE296386.1	EST_HUMAN	601176725F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531919 5'
6831	19984	33392	1.5	1.0E-53	BF364201.1	EST_HUMAN	CM4-NN1029-150800-543-e02 NN1029 Homo sapiens cDNA
7397	20475	33942	0.87	1.0E-53	BE012071.1	EST_HUMAN	RC5-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
8120	21202	34723	0.6	1.0E-53	AA249072.1	EST_HUMAN	I9571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9280	22366	35915	4.73	1.0E-53	X79536.1	NT	H.sapiens mRNA for hnRNPcore protein A1
12228	25176	38345	1.47	1.0E-53	AW245422.1	EST_HUMAN	2822943.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822943 3'
3324	16497	29515	0.61	9.0E-54	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5417	25803	31593	5.86	9.0E-54	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
212	13435	26465	1.29	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1882	15026	28133	2.08	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6057	19239	32564	23.39	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
395	13632	26669	1.35	7.0E-54	AA812537.1	EST_HUMAN	ai79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.t3 MER30 repetitive element ;
1877	15021	28128	2.23	7.0E-54	Y16645.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2278	15410	28541	7.63	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element ;
10333	23368	36978	2.1	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
11365	24426	38081	1.4	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11365	24426	38082	1.4	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11570	24625		3.42	7.0E-54	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
25	13263	26265	0.84	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
396	13633	26670	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
396	13633	26671	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3355	16527	29542	0.72	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4111	17265	30265	22.75	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4584	17721	30704	1.09	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4968	18097	31073	2.15	6.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4996	18125		2.04	6.0E-54	Y09846.1	NT	H.sapiens shc pseudogene, p66 isoform
5115	18125		3.31	6.0E-54	Y09846.1	NT	H.sapiens shc pseudogene, p66 isoform
11741	23927	37552	1.52	6.0E-54	AW813567.1	EST_HUMAN	RC3-ST0197-151099-011-f08 ST0197 Homo sapiens cDNA
2218	15352	28483	1.94	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
187	13409		56.19	4.0E-54	AF110103.1	NT	Tupaia belangeri beta-actin mRNA, partial cds
978	14151	27211	14.58	4.0E-54	AA306764.1	EST_HUMAN	EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1848	14994	28096	3.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1848	14994	28097	3.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3274	16448		1.85	4.0E-54	AI935086.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
96	13331	26358	8.12	3.0E-54	AA313487.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
1604	14757		0.96	3.0E-54	AW515742.1	EST_HUMAN	hd87g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2916542 3'
2635	15758	28872	1.19	3.0E-54	AL110383.1	EST_HUMAN	DKFZp434E0731_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6024	19207	32527	1.36	3.0E-54	4502434	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7548	20620	34096	1.34	3.0E-54	AA844061.1	EST_HUMAN	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
7548	20620	34097	1.34	3.0E-54	AA844061.1	EST_HUMAN	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
11277	24344		1.77	3.0E-54	11434806	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA
11341	24404	38053	4.01	3.0E-54	BF345600.1	EST_HUMAN	602019408F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155121 5'
11650	24729	38421	2.86	3.0E-54	AA393362.1	EST_HUMAN	zi70f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315 G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
12336	25243	32110	1.32	3.0E-54	AW954559.1	EST_HUMAN	EST366629 MAGE resequences, MAGC Homo sapiens cDNA
12379	26149		3.16	3.0E-54	AW748965.1	EST_HUMAN	RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA
659	13845	26871	17.67	2.0E-54	5031900	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1396	14550	27625	1.54	2.0E-54	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2604	15727	28846	1.25	2.0E-54	AW163175.1	EST_HUMAN	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
2666	15787	28903	2.25	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2960	16137	29155	1.95	2.0E-54	AW057524.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
3392	16562	29577	0.6	2.0E-54	AJ278314.1	NT	Homo sapiens mRNA for phospholipase C-beta-1b (PLCB1 gene)
3638	16802		6.1	2.0E-54	AA532925.1	EST_HUMAN	nj45g09.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
4321	17464		1.74	2.0E-54	4502642	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4563	17701		7.1	2.0E-54	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
5591	18786	31833	2.66	2.0E-54	4759069	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5720	18913	32209	1.21	2.0E-54	BE047864.1	EST_HUMAN	tz43c11.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
5882	19071	32379	3.99	2.0E-54	11426657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
5982	19167	32487	11.29	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
5982	19167	32488	11.29	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6796	19951	33351	1.63	2.0E-54	AF008915.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
6950	20263	33701	0.68	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
6950	20263	33702	0.68	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
7273	20356	33810	8.33	2.0E-54	11426544	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
9829	22869	36451	3.96	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
10213	23249	36838	1.14	2.0E-54	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10326	23361	36971	0.76	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10326	23361	36972	0.76	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10841	23874	37494	0.46	2.0E-54	AB007931.1	NT	Homo sapiens mRNA for KIAA0462 protein, partial cds
11275	19951	33351	1.46	2.0E-54	AF008915.1	NT	Homo sapiens EVI6 homolog mRNA, complete cds
12027	25011		1.72	2.0E-54	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
12893	25591	31970	4.36	2.0E-54	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4587	17724		1.65	1.0E-54	BF315418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
8927	22006	35545	0.5	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
10459	23494	37105	0.52	1.0E-54	AA412409.1	EST_HUMAN	zu10e09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
10459	23494	37106	0.52	1.0E-54	AA412409.1	EST_HUMAN	zu10e09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
13086	25709		2.33	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zrv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
10568	23603	37208	1.02	9.0E-55	BE081469.1	EST_HUMAN	QV2-BT0635-160400-143-h12 BT0635 Homo sapiens cDNA
1344	14500		1.59	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1348	14503		2.77	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11471	24530		1.83	8.0E-55	AW409714.1	EST_HUMAN	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5'
9004	22083		0.48	7.0E-55	AW103839.1	EST_HUMAN	xd76c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603622 3' similar to TR:O60365 O60365 FOS39554_1. ;
9383	22458	36021	1.28	7.0E-55	AA889581.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
9416	22490	36055	1.71	7.0E-55	AU139909.1	EST_HUMAN	AU139909 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'
11485	24544	38215	8.08	7.0E-55	AI561056.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2210249 3'
11485	24544	38216	8.08	7.0E-55	AI561056.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2210249 3'
12726	25911	31860	1.18	7.0E-55	BE670608.1	EST_HUMAN	7e37c01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284640 3'
13050	26063		6.37	7.0E-55	H23396.1	EST_HUMAN	ym57g07.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'
11804	24794	38492	1.96	6.0E-55	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1810	14959	28051	1.21	5.0E-55	AA704971.1	EST_HUMAN	zj95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
1810	14959	28052	1.21	5.0E-55	AA704971.1	EST_HUMAN	zj95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
4894	18024	31010	1.51	5.0E-55	AW206021.1	EST_HUMAN	UI-H-BI1-afy-g-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'
6670	19829	33217	1.49	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6670	19829	33218	1.49	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6805	25833	33360	1.08	5.0E-55	4505952	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
6805	25833	33361	1.08	5.0E-55	4505952	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
7182	20314	33757	1.03	5.0E-55	7382477	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 5, mRNA
7446	20523	33996	0.72	5.0E-55	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9244	22321	35865	2.3	5.0E-55	4506302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
9520	22585		0.91	5.0E-55	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
10243	23278	36872	1.53	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10243	23278	36873	1.53	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10427	23462	37069	1.13	5.0E-55	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
11502	24560	38236	1.3	5.0E-55	11421649	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
11502	24560	38237	1.3	5.0E-55	11421649	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
12421	25298		1.73	5.0E-55	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
56	16004	26310	2.24	4.0E-55	AW957994.1	EST_HUMAN	EST370064 MAGE resequences, MAGE Homo sapiens cDNA
689	13873	26906	32.17	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1472	14626	27710	2.15	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1472	14626	27711	2.15	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1544	14696		1.72	4.0E-55	BF061411.1	EST_HUMAN	7j52b10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.t3 L1 repetitive element ;
2081	15221	28341	2.19	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2081	15221	28342	2.19	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2151	15287	28412	8.36	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2151	15287	28413	8.36	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2384	15515	28644	3.02	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
8539	21620		9.85	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11505	24563		2.31	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12337	25244		1.82	4.0E-55	BF303941.1	EST_HUMAN	601886575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
6731	19887	33279	0.68	3.0E-55	AA077156.1	EST_HUMAN	7B09A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B09A09
12273	25205		4.18	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
13103	25719		3.53	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
388	13594	26830	1.69	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
565	13757		1.08	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
666	13852	26880	3.98	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products
3023	16199	29222	0.69	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4897	18027	31014	3.51	2.0E-55	BE719986.1	EST_HUMAN	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7673	25851	34217	0.85	2.0E-55	AW501988.1	EST_HUMAN	UI-HF-BN0-aks-f-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
9265	22342	35892	0.48	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
9265	22342	35893	0.48	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9361	22436		4.33	2.0E-55	AI002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element ;
9442	22516		0.67	2.0E-55	BE007959.1	EST_HUMAN	QV0-BN0147-280400-213-g06 BN0147 Homo sapiens cDNA
11192	24261	37897	2.35	2.0E-55	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
13177	16199	29222	1.34	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
99	13334	26361	1.62	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
194	13417	26448	40.5	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
588	13779	26798	1.38	1.0E-55	AI026718.1	EST_HUMAN	ov85g09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644160 3'
1173	14336	27392	3.92	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
2006	15146	28251	2.33	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
2006	15146	28252	2.33	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
2401	15532		4.65	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2415	15997	28673	1.44	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2586	15711	28829	19.68	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2620	15743	28857	5.51	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2620	15743	28858	5.51	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2677	15797	28914	3.37	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
2850	15964	29073	1.22	1.0E-55	AB033045.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
3495	16662	29674	1.16	1.0E-55	W28169.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4097	17252	30253	4.28	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4409	17551	30536	1.1	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4853	17986		0.94	1.0E-55	N77261.1	EST_HUMAN	yv44g03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245620 5'
4949	18079	31054	1.15	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4949	18079	31055	1.15	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5614	18808	31876	0.65	1.0E-55	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6401	19570	32932	7.26	1.0E-55	11433046	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
6401	19570	32933	7.26	1.0E-55	11433046	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
8178	21260	34782	1.7	1.0E-55	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8178	21260	34783	1.7	1.0E-55	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8266	21348	34863	0.49	1.0E-55	11421649	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
8273	21355	34872	0.93	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8273	21355	34873	0.93	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11152	24223	37851	2.41	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11152	24223	37852	2.41	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11733	23919	37544	1.86	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11755	23941	37567	1.34	1.0E-55	T10045.1	EST_HUMAN	seq1575 b4HB3MA Cot8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft61 5' similar to similar to Chinese Hamster DHFR-coamplified protein mRNA
11789	24779	38476	2.67	1.0E-55	8922743	NT	Homo sapiens hypothetical protein FLJ10891 (FLJ10891), mRNA
11876	24864	38560	1.78	1.0E-55	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
7522	20595	34070	1.85	9.0E-56	BE379074.1	EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
11545	24601	38277	1.34	8.0E-56	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2793	15909	29017	7.08	7.0E-56	H19934.1	EST_HUMAN	yn62g03.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element ;
7818	20873	34371	1.93	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
7818	20873	34372	1.93	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1727	14877	27968	2.7	5.0E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
9362	22437	35995	0.71	5.0E-56	AW015507.1	EST_HUMAN	UI-H-BI0p-aau-a-05-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10599	23634		1.35	5.0E-56	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12513	26137	31550	2.47	5.0E-56	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
28	13266	26268	8.64	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
28	13266	26269	8.64	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2773	15888	28998	3.61	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2773	15888	28999	3.61	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2873	13732	26756	9.22	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrolic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6387	19556	32915	4.94	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6387	19556	32916	4.94	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10724	23757	37364	1.68	4.0E-56	AF043349.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
11163	24234	37863	7.73	4.0E-56	AI498066.1	EST_HUMAN	tm65g12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163046 3'
11163	24234	37864	7.73	4.0E-56	AI498066.1	EST_HUMAN	tm65g12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163046 3'
1372	14527	27601	2.69	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1804	14953	28047	1.84	3.0E-56	6912743	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
2217	15351	28482	1.6	3.0E-56	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3195	16370	29376	1.67	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3195	16370	29377	1.67	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3939	17098		2.81	3.0E-56	AF055066.1	NT	Homo sapiens MHC class 1 region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4507	17646	30634	0.67	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4544	17682	30664	4.42	3.0E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4695	17830	30816	2.4	3.0E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
5801	18991	32293	1.5	3.0E-56	4759163	NT	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5801	18991	32294	1.5	3.0E-56	4759163	NT	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
7014	20150	33571	5.5	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7476	20551	34023	2.07	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
7476	20551	34024	2.07	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
9016	22095	35635	6.11	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10018	23056	36852	0.9	3.0E-56	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10698	23731	37336	1.39	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10980	24059	37693	2.62	3.0E-56	AB042556.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
11594	24647	38330	4.64	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11594	24647	38331	4.64	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
12377	25268	32075	1.62	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12377	25268	32076	1.62	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
537	13730		11.95	2.0E-56	AA199818.1	EST_HUMAN	zq52a08.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645206 3'
751	16021	26975	1.18	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
751	16021	26976	1.18	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
3053	16229	29249	0.94	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3391	16561		0.84	2.0E-56	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3624	16788	29805	1.26	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
7239	20323	33767	1.39	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1003	14174		3.01	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3765	16926	29928	1.84	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
3765	16926	29929	1.84	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
5145	18268	31238	1.42	1.0E-56	AI905162.1	EST_HUMAN	QV-BT077-130199-079 BT077 Homo sapiens cDNA
10161	23198		0.69	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10264	23289	36886	1.52	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220999-001-E02 CT0163 Homo sapiens cDNA
642	13827		1.39	9.0E-57	AW880885.1	EST_HUMAN	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
11494	24552	38227	1.72	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11494	24552	38228	1.72	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11811	24801	38500	2.2	9.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
14	13252	26252	1.02	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
308	13524	26558	2.93	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
907	14082	27147	7.49	8.0E-57	AW264599.1	EST_HUMAN	xr05d10.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875 INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
1859	15005	28112	1.45	8.0E-57	AA496109.1	EST_HUMAN	zv51b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
5355	26034	31679	1.92	8.0E-57	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6529	19693	33066	0.81	8.0E-57	AB020705.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds
6593	19753	33138	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
6593	19753	33139	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7607	20677	34152	0.62	8.0E-57	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7927	20977	34486	1.54	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
7927	20977	34487	1.54	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11768	13252	26252	3.51	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12041	25022	38726	1.74	8.0E-57	11433356	NT	Homo sapiens ninein (LOC51199), mRNA
12102	25082	38789	1.53	8.0E-57	11431260	NT	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
12791	25528	32007	1.67	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12808	25528	32007	1.94	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1246	14405	27467	0.88	7.0E-57	AJ003100.1	NT	Homo sapiens GYS2 gene, exon 14
2698	15817	28932	0.97	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2698	15817	28933	0.97	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3344	16517	29532	0.81	7.0E-57	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3982	17139	30143	3.14	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
3982	17139	30144	3.14	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
13185	26071		3.99	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
3849	17009	30010	6.03	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
827	14005	27062	0.64	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1362	14516		12.47	3.0E-57	AA230279.1	EST_HUMAN	nc13f07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN P46783 40S RIBOSOMAL PROTEIN S10. ;
2464	15591	28716	1.12	3.0E-57	AA348335.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
2768	15883	28992	1.03	3.0E-57	BE676622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20263 ;

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2768	15883	28993	1.03	3.0E-57	BE676622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20263 ;
3652	16815	29827	1	3.0E-57	AF232708.1	NT	Homo sapiens cell-line taA201a chloride ion current inducer protein I(Cln) gene, complete cds
3788	16949		51.29	3.0E-57	AW853964.1	EST_HUMAN	RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA
6153	19329	32675	1.25	3.0E-57	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6251	19425	32771	3.25	3.0E-57	BE796537.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8338	21419	34945	3.92	3.0E-57	W28130.1	EST_HUMAN	42f6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8363	21444	34966	1.99	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8363	21444	34967	1.99	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8476	21557	35090	0.78	3.0E-57	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8624	21704	35240	0.62	3.0E-57	J05262.1	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
9059	22138	35682	5.14	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9451	22567	36132	0.69	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
9451	22567	36133	0.69	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
11148	24220	37847	2.34	3.0E-57	AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
12384	26157	31554	6.37	3.0E-57	W23871.1	EST_HUMAN	zb45d11.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12982	25640	31984	1.17	3.0E-57	AJ003649.1	EST_HUMAN	AJ003649 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl10-1L1
1530	14683	27762	2.89	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1530	14683	27763	2.89	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2790	15906	29014	5.5	2.0E-57	AA845419.1	EST_HUMAN	ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
3525	16690		1.4	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3641	16805	29818	0.72	2.0E-57	R07702.1	EST_HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3641	16805	29819	0.72	2.0E-57	R07702.1	EST_HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4304	17447	30433	0.71	2.0E-57	AA018299.1	EST_HUMAN	ze40c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4304	17447	30434	0.71	2.0E-57	AA018299.1	EST_HUMAN	ze40c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4632	17768	30749	7.42	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5785	18977		1.48	2.0E-57	AA016131.1	EST_HUMAN	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1 repetitive element ;
6158	19334		31.41	2.0E-57	BF115266.1	EST_HUMAN	7n80f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.t1 MER22 repetitive element ;
6288	19461	32813	6.34	2.0E-57	11431281	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
8832	21911	35449	1.03	2.0E-57	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
10051	23089	36691	1.06	2.0E-57	AF057722.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11548	24604	38281	1.55	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11548	24604	38282	1.55	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11592	24645	38327	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
11592	24645	38328	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
13214	26097	31664	2.69	2.0E-57	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
2305	15437	28569	1.89	1.0E-57	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
8891	21970		1.87	1.0E-57	BE043031.1	EST_HUMAN	ho32a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN ;
12545	25369		11.29	1.0E-57	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
5794	18985	32288	0.83	9.0E-58	AA297847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
12854	25567	31990	1.94	9.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
602	13791		1.68	8.0E-58	BE868715.1	EST_HUMAN	601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
671	13857	26886	4.24	8.0E-58	AI798375.1	EST_HUMAN	tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
671	13857	26887	4.24	8.0E-58	AI798375.1	EST_HUMAN	tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1904	15047	28157	2.4	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1904	15047	28158	2.4	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
3040	16216		2.76	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
7387	20465	33930	0.93	7.0E-58	BE561971.1	EST_HUMAN	601346704F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687577 5'
11095	24168		4.54	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
11170	24241	37873	2.61	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BN0-ali-g-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
11170	24241	37874	2.61	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BN0-ali-g-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2328	15460	28593	1.53	6.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2448	15576	28706	5.25	6.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2966	16142	29160	1.01	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2966	16142	29161	1.01	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
6299	19472	32827	0.98	6.0E-58	AF106911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10517	23552	37163	1.27	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12654	25434		1.22	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
311	13527	26560	3.06	5.0E-58	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
728	13910	26950	6.96	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1221	14382	27442	2.9	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1221	14382	27443	2.9	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1222	14382	27442	2	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1222	14382	27443	2	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3400	16570	29585	4.09	5.0E-58	AA988183.1	EST_HUMAN	or98e07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4373	17516	30496	0.93	5.0E-58	AI636745.1	EST_HUMAN	ts89e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA P19984 PROFILIN II ;
5746	18938		1.91	5.0E-58	11496282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6307	19479	32834	6.55	5.0E-58	H23072.1	EST_HUMAN	ym51h07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52071 5'
6524	19689	33063	0.79	5.0E-58	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6600	19760	33148	1.03	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
6917	20232	33665	0.6	5.0E-58	AF051334.1	NT	Homo sapiens nibrin (NBS) mRNA, complete cds
6917	20232	33666	0.6	5.0E-58	AF051334.1	NT	Homo sapiens nibrin (NBS) mRNA, complete cds
7255	20338	33788	0.71	5.0E-58	4885400	NT	Homo sapiens holocytochrome c synthase (cytochrome c heme-lyase) (HCCS) mRNA
8156	21238	34759	9.08	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
8548	21629	35167	0.68	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
10061	23099	36701	0.96	5.0E-58	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10328	23363	36973	1.8	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10612	23646	37254	0.65	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10612	23646	37255	0.65	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
12352	26065		4.5	5.0E-58	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12850	26102		1.47	5.0E-58	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
384	13592	26627	1.71	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
819	13998	27052	1.87	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1496	14649	27731	1.24	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2696	15816	28930	2.12	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3402	16572	29587	1.41	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3834	16994	29996	1	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
7995	21045	34557	0.68	4.0E-58	BE463857.1	EST_HUMAN	hy18a02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197642 3'
11624	24675	38366	7.44	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
345	13556		0.96	3.0E-58	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
1420	14574	27647	2.6	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3246	16420	29435	3.07	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3246	16420	29436	3.07	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6390	19559	32918	0.61	3.0E-58	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-f09 BT0702 Homo sapiens cDNA
6574	19736	33115	1.1	3.0E-58	F07056.1	EST_HUMAN	HSC1TG081 normalized infant brain cDNA Homo sapiens cDNA clone c-11g08
6778	19933	33329	2.49	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DCAAZG04 5'
963	14136	27197	12.47	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
1318	14474		7.88	2.0E-58	BE208532.1	EST_HUMAN	ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5451	18651	31630	0.94	2.0E-58	AW074831.1	EST_HUMAN	xa08a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567704 3'
5473	25805	31652	2.53	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5473	25805	31685	2.53	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6182	19358	32706	1.7	2.0E-58	BF513488.1	EST_HUMAN	UI-H-BW1-ams-g-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
6249	19423	32769	2.16	2.0E-58	AI124874.1	EST_HUMAN	em57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME\; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN ;
6283	19456	32806	0.83	2.0E-58	R92587.1	EST_HUMAN	yq08h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196379 5'
7066	20119	33533	0.83	2.0E-58	AI291407.1	EST_HUMAN	qm84c01.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895424 3'
7307	20389	33848	2.79	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7307	20389	33849	2.79	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
10979	24058	37692	16.01	2.0E-58	BF307745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
11207	24276	37913	1.58	2.0E-58	AW872641.1	EST_HUMAN	hm25f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
740	13922	26962	1.06	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3'end
1093	14258	27314	1.33	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1358	14513	27586	1.12	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1358	14513	27587	1.12	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1427	14581	27654	2.8	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1697	14849	27935	1.28	1.0E-58	BE466132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3196935 3'
2719	15837	28947	1.01	1.0E-58	AF217514.1	NT	Homo sapiens uncharacterized bone marrow protein BM038 mRNA, complete cds
2863	15977	29087	1.14	1.0E-58	4759169	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA
2892	15206	28322	1.01	1.0E-58	5174444	NT	Homo sapiens G protein-coupled receptor 69A (GPR69A) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3627	16791	29809	0.93	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3627	16791	29810	0.93	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3814	16974	29977	0.66	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
5085	18213	31186	7.13	1.0E-58	AI141063.1	EST_HUMAN	oz43h01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
5964	19150	32465	1.37	1.0E-58	BE061860.1	EST_HUMAN	RC1-BT0254-290100-015-e01 BT0254 Homo sapiens cDNA
7002	20138	33556	0.87	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
8305	21387		0.49	1.0E-58	AW973537.1	EST_HUMAN	EST385637 MAGE resequences, MAGM Homo sapiens cDNA
9070	22149	35695	0.62	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
9182	22260	35802	0.77	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH09 5'
9282	22358	35907	0.64	1.0E-58	AA412397.1	EST_HUMAN	zt99f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
9282	22358	35908	0.64	1.0E-58	AA412397.1	EST_HUMAN	zt99f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
10389	23424	37031	0.65	1.0E-58	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
12074	25055		2.1	1.0E-58	X63392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
12100	25080	38787	2.61	1.0E-58	D61405.1	NT	Human MSH3 gene, exon10
2303	15435	28567	53.38	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
6979	20207	33635	0.74	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis I Homo sapiens cDNA 5' end
6979	20207	33636	0.74	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis I Homo sapiens cDNA 5' end
8374	21455	34979	1.55	8.0E-59	AI761963.1	EST_HUMAN	wh50d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
182	16006		1.97	6.0E-59	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
8015	21066	34579	0.62	6.0E-59	AA962431.1	EST_HUMAN	om81a04.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1553550 3' similar to TR:Q13732 Q13732 SA GENE PRODUCT PRECURSOR. ;
8440	21521	35050	0.69	6.0E-59	AI750970.1	EST_HUMAN	cn06h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06h02 random
3197	16372	29379	7.75	5.0E-59	AI807484.1	EST_HUMAN	wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
4780	17915	30901	9.94	5.0E-59	X83497.1	NT	H.sapiens DNA for ZNF80-linked ERV9 long terminal repeat
7129	18555	31470	8.22	5.0E-59	AW162304.1	EST_HUMAN	au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element ;
9006	22085	35628	1.03	5.0E-59	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
9906	22946	36532	1.44	5.0E-59	AV762869.1	EST_HUMAN	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
11146	24218	37845	4.54	5.0E-59	11434908	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
816	13995	27050	1.9	4.0E-59	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
1266	14423	27489	0.61	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1266	14423	27490	0.61	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
4912	18042	31032	1.14	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4912	18042	31033	1.14	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5654	18848	32130	0.95	4.0E-59	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12498	25996		3.99	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	13248		6.74	3.0E-59	AW965524.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cDNA
234	13455	26481	3.88	3.0E-59	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1748	14897	27992	10.81	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1748	14897	27993	10.81	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2198	15333	28459	8.54	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2198	15333	28460	8.54	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3104	16280	29294	0.67	3.0E-59	T18865.1	EST_HUMAN	h02017t Testis 1 Homo sapiens cDNA clone h02017 5' end
3104	16280	29295	0.67	3.0E-59	T18865.1	EST_HUMAN	h02017t Testis 1 Homo sapiens cDNA clone h02017 5' end
3199	16374	29383	4.27	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3199	16374	29384	4.27	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3930	17089	30086	1.19	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4808	17942	30929	2.75	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4965	18094	31071	2.12	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
5162	18284		1.22	3.0E-59	M95961.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 2
6350	19520	32877	2.4	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7516	20589	34064	1.85	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
8116	21198	34718	1.11	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
8116	21198	34719	1.11	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
10250	23285	36880	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
10250	23285	36881	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12635	25428		11.11	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
6946	20259		0.59	2.0E-59	AA470073.1	EST_HUMAN	zt98d05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730377 3'
7216	20081	33494	0.59	2.0E-59	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
9837	22877		4.84	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
10745	23778		1.34	2.0E-59	BF365554.1	EST_HUMAN	RC0-NT0036-100700-032-a07 NT0036 Homo sapiens cDNA
11069	24144	37780	2.19	2.0E-59	AW410698.1	EST_HUMAN	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11069	24144	37781	2.19	2.0E-59	AW410698.1	EST_HUMAN	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
12373	25266	32118	4.28	2.0E-59	AI631809.1	EST_HUMAN	wa36c12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542 Q86542 RTVL-H PROTEIN. ;contains LTR7.b1 LTR7 repetitive element ;
12963	26019	31669	3.87	2.0E-59	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
167	13392		5.65	1.0E-59	BE296411.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
1569	14722	27803	1.04	1.0E-59	T92522.1	EST_HUMAN	ye25c09.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118768 5' similar to SP:S21348 S21348 HYPOTHETICAL PROTEIN 4 - ;
2683	15803		2.65	1.0E-59	AA748468.1	EST_HUMAN	oa56h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7735	20796	34285	1.14	1.0E-59	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
7895	20947	34454	1.3	1.0E-59	BE256814.1	EST_HUMAN	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
7895	20947	34455	1.3	1.0E-59	BE256814.1	EST_HUMAN	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
9585	22727	36296	0.98	1.0E-59	11419630	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
9804	22844	36421	0.58	1.0E-59	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9804	22844	36422	0.58	1.0E-59	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
11094	20796	34285	10.98	1.0E-59	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
783	13963	27013	1.45	8.0E-60	AW977845.1	EST_HUMAN	EST389849 MAGE resequences, MAGO Homo sapiens cDNA
1499	14652	27734	3.21	8.0E-60	4759159	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2241	15374	28502	4.76	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2241	15374	28503	4.76	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6103	19283	32616	1.16	8.0E-60	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6633	19792	33181	0.89	8.0E-60	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
7874	20928	34434	0.89	8.0E-60	11420841	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA
8152	21234	34755	3	8.0E-60	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9139	22218	35762	2.93	8.0E-60	11428949	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA
9671	22633	36202	0.78	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9671	22633	36203	0.78	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10799	23832	37455	0.62	8.0E-60	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11071	24146	37783	4.17	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
11071	24146	37784	4.17	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
773	13954	27004	11.11	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
774	13954	27004	25.11	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
838	14016	27071	1.47	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA

WO 01/57272 PCT/US01/00663

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2197	15332	28458	1.82	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2845	15959	29068	0.96	7.0E-60	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4295	17438	30425	2.4	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4698	17833	30818	0.91	7.0E-60	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
9607	22662	36235	4.21	7.0E-60	H58041.1	EST_HUMAN	yr12f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
11646	24725	38417	1.73	7.0E-60	H58041.1	EST_HUMAN	yr12f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
2248	15381	28509	1.16	6.0E-60	BE964974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
8632	21712		8.04	6.0E-60	H52456.1	EST_HUMAN	yq78h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains OFR repetitive element ;
86	13321	26348	1.06	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
86	13321	26349	1.06	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2308	15440	28574	1.83	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2308	15440	28575	1.83	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
3037	16213		1.45	4.0E-60	AA299037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7508	20582	34055	0.78	4.0E-60	BF196068.1	EST_HUMAN	hr81f05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE Q61085 GTP-RHO BINDING PROTEIN 1 ;
9326	22402		0.65	4.0E-60	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1907	15050	28161	4.98	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1907	15050	28162	4.98	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1918	15061		2.81	3.0E-60	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
4579	17716	30699	2.75	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
5494	18693	31709	0.59	3.0E-60	BF365143.1	EST_HUMAN	QV4-NN1149-250900-423-f01 NN1149 Homo sapiens cDNA
5757	18949	32251	2.21	3.0E-60	AW836196.1	EST_HUMAN	RC3-LT0023-200100-012-a01 LT0023 Homo sapiens cDNA
7093	18520	31513	1.07	3.0E-60	AI792814.1	EST_HUMAN	ol60h11.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE P52624 URIDINE PHOSPHORYLASE ;
8597	21678	35215	4.59	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8597	21678	35216	4.59	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8783	21862	35405	0.6	3.0E-60	AI040235.1	EST_HUMAN	ox56d09.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE Q05860 FORMIN ;
8940	22019	35560	3.84	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
13053	26058		1.55	3.0E-60	AA485286.1	EST_HUMAN	ab07h04.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.t1 LTR10 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
31	13269	26273	1.7	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1455	14608	27688	3.99	2.0E-60	Z11694.1	NT	H.sapiens 41kDa protein kinase related to rat ERK2
1759	14908	28001	2.2	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
3669	16832	29843	0.78	2.0E-60	4757867	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4025	17181	30190	0.73	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6430	19598	32964	0.85	2.0E-60	AI791952.1	EST_HUMAN	nn01f12.y5 NCI_CGAP_Cc9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR repetitive element ;
6621	19781	33169	1.26	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6855	20008	33418	1.08	2.0E-60	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
6989	18508	31524	2.15	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6989	18508	31525	2.15	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7259	20342	33793	8.18	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7259	20342	33794	8.18	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7810	20865		0.9	2.0E-60	BF512808.1	EST_HUMAN	UI-H-BW1-amu-c-02-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
8194	21276	34799	1.33	2.0E-60	X85597.1	EST_HUMAN	HS15BEST human adult testis Homo sapiens cDNA clone CAM_tEST15
9068	22147	35694	3.12	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
10183	23220	36813	1.83	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
10183	23220	36814	1.83	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
11759	23945	37572	1.7	2.0E-60	11434729	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5), mRNA
12672	25448		2.36	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12829	25985		1.47	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12848	25564		1.5	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
535	13728	26752	1.02	1.0E-60	BE178586.1	EST_HUMAN	PM3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA
4011	17168	30176	1.08	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
5070	18198	31172	2.57	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8134	21216	34737	1.39	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8955	22034		2.84	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 repetitive element ;
8982	22061	35601	1.35	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
12606	26079		1.49	1.0E-60	AJ252313.1	NT	Homo sapiens genomic hybrid Rhesus box
1123	14288	27343	8.4	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'

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8908	21987	35526	0.53	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8908	21987	35527	0.53	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
2735	15852	28965	1.41	8.0E-61	AW006478.1	EST_HUMAN	wt05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2735	15852	28966	1.41	8.0E-61	AW006478.1	EST_HUMAN	wt05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
3016	16192		2.63	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
8079	21161	34679	1.03	8.0E-61	AA583968.1	EST_HUMAN	nn59g06.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
130	13357	26389	0.79	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
130	13357	26390	0.79	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
276	13494	26524	3.06	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
834	14012	27068	6.49	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1352	14507	27579	12.72	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1659	14811	27896	1.04	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1679	14831	27916	2.91	6.0E-61	AA596033.1	EST_HUMAN	nn66h09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
3381	16553	29567	8.16	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
6155	19331	32677	2.96	6.0E-61	S79249.1	NT	Ig-beta/B29=CD79b {alternatively spliced} [human, B cells, mRNA Partial, 375 nt]
7497	20572	34045	1.49	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
7795	20851	34343	1.85	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-I (GTF2I) mRNA, complete cds
12564	14012	27068	1.66	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
13157	25752	31925	1.42	6.0E-61	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
226	13448	26476	2.54	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
226	13448	26477	2.54	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
370	13579	26612	0.7	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1713	14864	27953	2.84	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3101	16277	29291	2.19	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3268	16442	29462	1.82	5.0E-61	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4090	17245		2.22	5.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5118	13579	26612	0.75	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1798	14947	28039	1.94	4.0E-61	AU140307.1	EST_HUMAN	AU140307 PLACE2 Homo sapiens cDNA clone PLACE2000302 5'
5936	19122	32435	0.71	4.0E-61	7661637	NT	Homo sapiens DKFZP566B023 protein (DKFZP566B023), mRNA
12349	25252		9.47	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
8616	21696	35234	0.7	3.0E-61	AF150190.1	EST_HUMAN	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04
511	13705	26733	1.8	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1239	14398	27460	5.33	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA

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1239	14398	27461	5.33	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1699	14851	27938	1.36	2.0E-61	N53039.1	EST_HUMAN	yv53d11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
2706	15824		1.72	2.0E-61	N39397.1	EST_HUMAN	yy03f11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270189 5'
6556	19718	33094	0.88	2.0E-61	11426166	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
9217	22295	35839	1.67	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKC Homo sapiens cDNA clone GKCELG06 5'
9762	22700		0.98	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
10126	23164	36763	1.34	2.0E-61	AW500256.1	EST_HUMAN	UI-HF-BN0-akd-f-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
10456	23491	37101	2.84	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
11123	24195		4	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
13144	25744	31950	1.45	2.0E-61	AW995326.1	EST_HUMAN	QV0-BN0042-170300-162-f10 BN0042 Homo sapiens cDNA
448	13644		1.37	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
794	13973	27026	1.26	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1430	14584	27658	1.07	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1809	14958		1.02	1.0E-61	U32657.1	NT	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region
1906	15049	28160	4.43	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2270	15403	28531	1.54	1.0E-61	AW827281.1	EST_HUMAN	xn11b09.y1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element MSR1 repetitive element ;
2896	16075	29093	0.98	1.0E-61	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
3463	16630	29650	0.85	1.0E-61	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3826	16986	29989	1.16	1.0E-61	BE174455.1	EST_HUMAN	QV2-HT0577-140300-077-g06 HT0577 Homo sapiens cDNA
4374	17517	30497	1.05	1.0E-61	M68840.1	NT	Human monoamine oxidase A (MAOA) mRNA, complete cds
4561	17699	30680	0.95	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4561	17699	30681	0.95	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4981	18110	31086	9.55	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BW0-ajt-b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4981	18110	31087	9.55	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BW0-ajt-b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
5075	18203	31175	0.62	1.0E-61	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5509	18708	31723	0.71	1.0E-61	M76423.1	NT	H.sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5805	18996	32301	1.07	1.0E-61	7662303	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6004	19189	32508	1.32	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
7041	20094	33510	8.92	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
7240	20324	33768	0.77	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
7341	20421	33883	1.39	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA

WO 01/57272 PCT/US01/00663

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7341	20421	33884	1.39	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8326	21408	34935	2.69	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8508	21589	35123	3.34	1.0E-61	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9482	22539		2.78	1.0E-61	AW999726.1	EST_HUMAN	MR0-BN0070-040400-010-h01 BN0070 Homo sapiens cDNA
9557	22622	36193	0.58	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
10235	23270	36861	4.8	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10871	23956	37585	5.61	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11178	24247	37880	1.72	1.0E-61	AB044550.1	NT	Homo sapiens P/OKcl.19 mRNA for ubiquitin-conjyugating enzyme E2, complete cds
11325	24388	38033	1.44	1.0E-61	AB007830.1	NT	Homo sapiens mRNA for CSR2, complete cds
12242	26043		21.57	1.0E-61	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12286	26031	31677	4	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12286	26031	31678	4	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13026	25676	31959	10.94	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10565	23600	37206	1.06	9.0E-62	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
4673	17808	30798	0.85	8.0E-62	AA830420.1	EST_HUMAN	oc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN ;
1131	14296	27351	1.12	7.0E-62	AV714334.1	EST_HUMAN	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5'
3595	16759	29775	0.84	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
6038	19221	32544	0.97	7.0E-62	11427985	NT	Homo sapiens hypothetical protein (FLJ20261), mRNA
11632	24712	38403	4.05	7.0E-62	AI208681.1	EST_HUMAN	qg56a04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103 O15103 HYPOTHETICAL 27.3 KD PROTEIN. ;
3063	16239		1.55	6.0E-62	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3471	16638		5.37	6.0E-62	11418255	NT	Homo sapiens CGI-56 protein (CGI-56), mRNA
7803	20859	34351	3.47	6.0E-62	AI762801.1	EST_HUMAN	wi04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
7803	20859	34352	3.47	6.0E-62	AI762801.1	EST_HUMAN	wi04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
8277	21359		0.66	6.0E-62	AW501124.1	EST_HUMAN	UI-HF-BP0p-ait-d-09-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
8452	21533	35063	1.52	6.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
9554	22619	36189	3.67	6.0E-62	AW814393.1	EST_HUMAN	MR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA
429	13624	26664	1.46	5.0E-62	AI950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;contains element MER22 repetitive element ;
2478	15605	28729	5.16	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
2478	15605	28730	5.16	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2

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3506	16673	29683	2.55	5.0E-62	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4447	17587	30568	1.75	5.0E-62	AA431093.1	EST_HUMAN	zw78e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT P47245 NARDILYSIN ;
8746	21825	35362	0.74	5.0E-62	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
9717	22782	36353	12.91	5.0E-62	AW410687.1	EST_HUMAN	fh07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961616 5'
11543	24599	38274	2.38	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
11543	24599	38275	2.38	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
863	14040	27102	2.17	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
863	14040	27103	2.17	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
864	14040	27102	1.32	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
864	14040	27103	1.32	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2529	15654	28778	1.9	4.0E-62	AI827900.1	EST_HUMAN	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_rna1 HISTONE H2B.2 (HUMAN);
2529	15654	28779	1.9	4.0E-62	AI827900.1	EST_HUMAN	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_rna1 HISTONE H2B.2 (HUMAN);
3486	16654		9.09	4.0E-62	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
6046	19229	32553	1.71	4.0E-62	4506978	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
6426	19594	32960	2.81	4.0E-62	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7322	20404	33866	1.75	4.0E-62	11421041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
7812	20867	34361	2.21	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
7812	20867	34362	2.21	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
8364	21445	34968	1.12	4.0E-62	11429973	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
9047	22126	35670	6.42	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
11263	24332	37973	2.62	4.0E-62	Z78766.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
11263	24332	37974	2.62	4.0E-62	Z78766.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
11500	24558	38233	63.7	4.0E-62	S70584.1	NT	thyroid-stimulating hormone alpha subunit [human, Genomic, 268 nt, segment 3 of 4]
12269	25202	38360	1.18	4.0E-62	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12497	25989		1.65	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12946	25657	31955	1.66	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
13004	25653	31952	6.86	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13004	25653	31953	6.86	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13059	25693	31965	2.16	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
76	13312	26338	0.69	3.0E-62	4557794	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
3111	16287	29301	1.13	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3111	16287	29302	1.13	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3789	16950	29956	4.19	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
8737	21816	35351	3.74	3.0E-62	AI632733.1	EST_HUMAN	wa33f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299903 3' similar to contains THR.t2 THR repetitive element ;
1259	14417	27482	2.71	2.0E-62	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8974	22053	35595	5.59	2.0E-62	BF329911.1	EST_HUMAN	RC0-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
8974	22053	35596	5.59	2.0E-62	BF329911.1	EST_HUMAN	RC0-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10376	23411		3.71	2.0E-62	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11988	24973		8.83	2.0E-62	BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
1069	14235	27294	1.14	1.0E-62	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1575	14728	27809	18.41	1.0E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1842	14988	28088	1.64	1.0E-62	AA625207.1	EST_HUMAN	af70e11.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03453 ;
2981	16157	29176	1.22	1.0E-62	AL039044.1	EST_HUMAN	DKFZp566F104_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566F104 5'
4648	17784	30767	1.84	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
6418	19587	32950	2.02	1.0E-62	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7284	20367	33820	1.07	1.0E-62	AA490060.1	EST_HUMAN	ab05c02.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839906 3'
7295	20377	33834	2.69	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
7295	20377	33835	2.69	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
8957	22036	35577	0.54	1.0E-62	AA280050.1	EST_HUMAN	zs93e07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705060 5'
9258	22335	35885	1.65	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9258	22335	35886	1.65	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9302	22378	35928	1.92	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9302	22378	35929	1.92	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9757	22695	36263	3.03	1.0E-62	AA465170.1	EST_HUMAN	aa33d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11648	24727	38419	2.26	1.0E-62	Z78698.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14D8
12809	25540		4.63	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
13042	25684	31962	3.15	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
348	13559	26587	2.27	9.0E-63	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
2421	15550		2.17	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-558C10 5'
4152	17304	30297	8.77	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4152	17304	30298	8.77	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5358	18484	38824	4.69	9.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5582	18777	31822	1.44	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PkB kinase
7332	20413	33875	3.78	9.0E-63	11426985	NT	Homo sapiens nucleoporin 88kD (NUP88), mRNA
8009	21059	34571	1.77	9.0E-63	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8521	21602	35139	1.18	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
11296	24362	38003	1.3	9.0E-63	BF203406.1	EST_HUMAN	601865828F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4098487 5'
2420	15549	28677	3.05	8.0E-63	4557734	NT	Homo sapiens *monoamine* oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2446	15574	28703	2.58	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3550	16715	29727	4.26	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3550	16715	29728	4.26	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4381	17524	30505	4.36	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
952	14125		3.38	7.0E-63	AI872137.1	EST_HUMAN	wm55g11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439908 3'
5455	18655		70.59	6.0E-63	AA420803.1	EST_HUMAN	nc63f02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S RIBOSOMAL PROTEIN (HUMAN);
9075	22154	35698	0.62	5.0E-63	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3398	16568	29584	0.88	4.0E-63	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3910	17069	30066	1.06	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
3910	17069	30067	1.06	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6575	19737	33116	2.6	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
6575	19737	33117	2.6	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
11397	24458	38121	2.02	4.0E-63	AW134709.1	EST_HUMAN	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
11397	24458	38122	2.02	4.0E-63	AW134709.1	EST_HUMAN	UI-H-BI1-abq-a-02-0-UI.o1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1989	15131	28235	15.19	3.0E-63	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2840	15954	29061	1.49	3.0E-63	J00310.1	NT	Human Met-tRNA-I gene 1
2882	14425	27493	11.84	3.0E-63	6005963	NT	Homo sapiens zinc finger protein 144 (Mel-18) (ZNF144), mRNA
6603	19763	33151	33.93	3.0E-63	11545810	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9907	22947	36533	0.83	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
9907	22947	36534	0.83	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
196	13419	26449	1.69	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
203	13426	26457	1.65	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
510	13704		1.19	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
849	14027	27087	3.07	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1597	14750	27834	1.54	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1597	14750	27835	1.54	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1806	14955	28049	2.02	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
2146	15282	28407	1.05	2.0E-63	AI863961.1	EST_HUMAN	wj54b02.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406603 3' similar to gb:M57609 GLI3 PROTEIN (HUMAN);
3225	16399	29411	1.94	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3357	16529	29544	2.4	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
4014	17171	30179	3.19	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4988	18117	31096	1.28	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5376	25802	31447	0.95	2.0E-63	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
6005	19190	32509	2.41	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6005	19190	32510	2.41	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6315	19487	32842	1.07	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6315	19487	32843	1.07	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6841	19994	33403	1.43	2.0E-63	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6887	20039	33448	0.72	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6887	20039	33449	0.72	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7222	20086	33502	1.72	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7222	20086	33503	1.72	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7957	21007	34517	0.96	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8730	21810	35346	4.29	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9254	22331	35879	0.94	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9254	22331	35880	0.94	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
10143	23181	36776	1.2	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10985	24064	37699	10.73	2.0E-63	N78945.1	EST_HUMAN	zb18b05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);
11012	24091	37728	2.89	2.0E-63	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
11012	24091	37729	2.89	2.0E-63	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
12380	25929	31759	3.64	2.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
13101	25717	31940	1.19	2.0E-63	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
13172	25760	31930	1.37	2.0E-63	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
786	13965	27016	1.55	1.0E-63	7106446	NT	Mus musculus wingless-related MMTV integration site 3A (Wnt3a), mRNA
786	13965	27017	1.55	1.0E-63	7106446	NT	Mus musculus wingless-related MMTV integration site 3A (Wnt3a), mRNA
4461	17601	30579	3.31	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4461	17601	30580	3.31	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5468	18668	31647	1.73	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
5890	19078	32388	1.38	1.0E-63	AW582266.1	EST_HUMAN	QV0-ST0215-060100-083-b09 ST0215 Homo sapiens cDNA
6521	19686	33058	0.68	1.0E-63	AW451950.1	EST_HUMAN	UI-H-BI3-alt-h-02-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
6521	19686	33059	0.68	1.0E-63	AW451950.1	EST_HUMAN	UI-H-BI3-alt-h-02-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
8668	21748		2.97	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
13121	26047		8.88	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6089	19270	32598	0.61	9.0E-64	AW401433.1	EST_HUMAN	UI-HF-BK0-aad-b-09-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053153 5'
8051	21134	34654	5.57	9.0E-64	AI478186.1	EST_HUMAN	tm50b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1071	14237		3.45	8.0E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6268	19442	32791	3.51	8.0E-64	BE885755.1	EST_HUMAN	601508968F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
12187	25146		2.79	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12243	25185		3.68	8.0E-64	T60851.1	EST_HUMAN	yb98b02.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79179 5'
3618	16782		0.74	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4854	17987	30974	5.34	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4854	17987	30975	5.34	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
10239	23274	36865	2.62	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
1760	14909	28002	5.73	6.0E-64	AI651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1760	14909	28003	5.73	6.0E-64	AI651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);

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3192	16367	29372	3.91	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
3192	16367	29373	3.91	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
5739	18932	32230	2.95	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5739	18932	32231	2.95	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5758	18950	32252	5.32	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5767	18959	32260	0.68	6.0E-64	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
5951	19137	32452	0.74	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
5951	19137	32453	0.74	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
7384	20462	33925	2.54	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7384	20462	33926	2.54	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9528	22593	36164	7.39	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
9706	22755	36326	1.75	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
9919	22959	36546	2.16	6.0E-64	S76475.1	NT	trkC [human, brain, mRNA, 2715 nt]
11008	24087	37724	4.68	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11008	24087	37725	4.68	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11269	16367	29372	1.73	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
11269	16367	29373	1.73	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
12400	25280	32081	2.96	6.0E-64	11526198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
843	14021	27078	4.18	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
843	14021	27079	4.18	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1369	14524	27598	1.02	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1453	14608	27685	1.15	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1453	14608	27686	1.15	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1749	14898	27994	1.54	5.0E-64	U89358.1	NT	Human l(3)mbt protein homolog mRNA, complete cds
2887	14663	27746	4.43	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2887	14663	27747	4.43	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4068	17224	30231	7.25	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
8000	21050	34563	0.71	4.0E-64	BE794607.1	EST_HUMAN	601590382F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944397 5'
11051	24128	37763	2.34	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
11051	24128	37764	2.34	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2271	15404	28532	8.77	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-569E02 5'
3327	16500	29518	0.82	3.0E-64	BE794381.1	EST_HUMAN	601589566F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3529	16694	29704	1.83	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3529	16694	29705	1.83	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6206	19381	32731	1.31	3.0E-64	Z26273.1	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 28
6471	19638	32997	0.68	3.0E-64	AW500861.1	EST_HUMAN	UI-HF-BP0p-aix-c-05-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3073161 5'
6622	19782	33170	3.2	3.0E-64	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
8661	21741	35281	1.86	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8661	21741	35282	1.86	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8692	21772	35303	1.48	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
8692	21772	35304	1.48	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
9627	22682	36251	1.12	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9627	22682	36252	1.12	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9714	22779	36349	0.66	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGE resequences, MAGO Homo sapiens cDNA
9714	22779	36350	0.66	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGE resequences, MAGO Homo sapiens cDNA
11514	24571	38248	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11514	24571	38249	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11990	24975	38679	2.16	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1112	14277	27334	1.1	2.0E-64	AA609940.1	EST_HUMAN	af09d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1428	14582	27655	3.2	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2592	15717		1.28	2.0E-64	AI927030.1	EST_HUMAN	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element ;
2597	15721	28840	2.4	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2597	15721	28841	2.4	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3887	17046	30045	0.98	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequences, MAGE Homo sapiens cDNA
3887	17046	30046	0.98	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequences, MAGE Homo sapiens cDNA
6129	19308	32649	2.28	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6372	19541	32900	1.23	2.0E-64	AF113708.1	NT	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds
6614	19774	33165	5.04	2.0E-64	BF668537.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
6724	19881	33272	1.3	2.0E-64	AI078387.1	EST_HUMAN	oz29b03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3'
6840	19993	33402	2.96	2.0E-64	M77185.1	NT	H.sapiens dopamine receptor D5 pseudogene 1, partial cds
7990	21040	34552	0.67	2.0E-64	11431054	NT	Homo sapiens ataxin 2-binding protein 1 (A2BP1), mRNA
8868	21947	35480	1.08	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
8868	21947	35481	1.08	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9431	22505	36071	1.09	2.0E-64	AU132570.1	EST_HUMAN	AU132570 NT2RP4 Homo sapiens cDNA clone NT2RP4000109 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10184	23221	36815	0.5	2.0E-64	T06397.1	EST_HUMAN	EST04286 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDS88
10184	23221	36816	0.5	2.0E-64	T06397.1	EST_HUMAN	EST04286 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDS88
11000	24079	37714	2.21	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180556 5'
11306	24371	38012	4.28	2.0E-64	AI922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452211 3'
11306	24371	38013	4.28	2.0E-64	AI922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452211 3'
11509	24567	38244	1.46	2.0E-64	AW864773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
12804	25537		3.59	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
268	13487	26517	1.39	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1820	14969	28061	24.22	1.0E-64	AI929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN);contains element MSR1 repetitive element ;
3076	16252	29274	0.8	1.0E-64	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
3601	16765	29781	5.47	1.0E-64	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3675	16838	29848	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3675	16838	29849	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
4008	17165	30173	0.98	1.0E-64	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
10269	23304	36901	1.17	1.0E-64	AA042975.1	EST_HUMAN	zk53f08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486567 3'
12291	25216		4.56	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2350	15481	28613	1.87	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2350	15481	28614	1.87	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
11826	24815		19.08	9.0E-65	BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
11799	24789	38486	7.24	8.0E-65	AI929244.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21. ;
10358	23393	37004	2.16	7.0E-65	BE081653.1	EST_HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA
12095	25075	38782	2.88	7.0E-65	Z21378.1	EST_HUMAN	HSAAAEAWO TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test346 (b)
1081	14247	27304	0.81	6.0E-65	AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5'
1974	15117		20.04	6.0E-65	AA550929.1	EST_HUMAN	nj86d10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:999379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
6699	19857	33247	0.8	6.0E-65	AA503892.1	EST_HUMAN	nh37b07.s1 NCI_CGAP_Pr5 Homo sapiens cDNA clone IMAGE:954517
8945	22024	35564	2.45	6.0E-65	AW083252.1	EST_HUMAN	xc07b09.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S. ;contains L1.b2 L1 repetitive element ;
9213	22291	35833	4.63	6.0E-65	AA427678.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9213	22291	35834	4.63	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
9275	22351	35902	0.62	6.0E-65	AI085314.1	EST_HUMAN	qf18h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750425 3'
9275	22351	35903	0.62	6.0E-65	AI085314.1	EST_HUMAN	qf18h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750425 3'
11113	24185	37817	3.58	6.0E-65	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
11294	24360	38001	4.18	6.0E-65	BF340825.1	EST_HUMAN	602037721F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4185677 5'
11788	24778	38475	1.86	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
648	13833	26859	1.89	5.0E-65	AF064604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1384	14539	27613	1.92	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1384	14539	27614	1.92	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2223	15357	28487	1.07	5.0E-65	AB033768.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3328	16501	29519	1.79	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3328	16501	29520	1.79	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7008	20144	33563	1.38	5.0E-65	4504606	NT	Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA
10684	23718	37324	1.36	5.0E-65	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
198	13421	26452	1.3	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
764	13945	26991	1.23	4.0E-65	AI266468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
764	13945	26992	1.23	4.0E-65	AI266468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
1103	14268	27326	1.44	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1515	14668	27751	24.91	4.0E-65	4506638	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2413	15543	28670	1.02	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel16 Homo sapiens cDNA clone IMAGE:3171102 3'
2413	15543	28671	1.02	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel16 Homo sapiens cDNA clone IMAGE:3171102 3'
6284	19457	32807	4.96	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6284	19457	32808	4.96	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7233	20317	33760	0.66	4.0E-65	AY008372.1	NT	Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds
7266	20349	33801	5.04	4.0E-65	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7368	20447	33910	2.3	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7721	20785	34273	0.65	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7721	20785	34274	0.65	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7993	21043	34555	0.67	4.0E-65	U39656.1	NT	Human MAP kinase kinase 6 (MKK6) mRNA, complete cds
8025	21108	34624	0.83	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
8025	21108	34625	0.83	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
9346	22422	35975	0.88	4.0E-65	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10808	23841		2.12	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
11360	24422	38078	1.92	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12628	14268	27326	2.03	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
13201	13421	26452	1.26	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
100	13336	26364	0.65	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1260	15990		18.37	3.0E-65	X78932.1	NT	H.sapiens HZF9 mRNA for zinc finger protein
1589	14741	27822	4.52	3.0E-65	4504626	NT	Homo sapiens immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products
1868	16014	28122	1.31	3.0E-65	AI000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element ;
3350	16522	29538	1.24	3.0E-65	4504950	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3815	16975	29978	1.08	3.0E-65	AI000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element ;
4773	17908	30891	1.38	3.0E-65	6912385	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
10274	23309	36905	1.61	3.0E-65	BE787366.1	EST_HUMAN	601479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'
11672	23900	37523	8.41	3.0E-65	AA430006.1	EST_HUMAN	zw65a06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3490	16657	29670	7.53	2.0E-65	BF680294.1	EST_HUMAN	602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295966 5'
6666	19825		3.73	2.0E-65	BE263373.1	EST_HUMAN	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
7282	20365	33818	20.62	2.0E-65	BF576922.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
9046	22125	35668	1.2	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
9046	22125	35669	1.2	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
10892	23976	37608	1.46	2.0E-65	11419247	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
12241	25184		6.27	2.0E-65	AA307904.1	EST_HUMAN	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus
12748	26906		3.99	2.0E-65	BF246086.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
93	13328		0.69	1.0E-65	BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
552	13745	26770	1.43	1.0E-65	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
1889	16033	28141	3.31	1.0E-65	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2098	15238	28360	1.48	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3458	16625	29645	0.8	1.0E-65	BE466681.1	EST_HUMAN	hz24a09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3208888 3'
4105	17259	30259	2.07	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4105	17259	30260	2.07	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4323	17466	30451	2.53	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4323	17466	30452	2.53	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5143	18266	31235	1.57	1.0E-65	AW238282.1	EST_HUMAN	xp20c01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740896 3'
5143	18266	31236	1.57	1.0E-65	AW238282.1	EST_HUMAN	xp20c01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740896 3'
5400	18602	31572	0.86	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-f09 BT0702 Homo sapiens cDNA
5400	18602	31573	0.86	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-f09 BT0702 Homo sapiens cDNA
5594	18789	31837	0.58	1.0E-65	AI243738.1	EST_HUMAN	qh88h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR:Q07823 Q07823 MAC30 PROTEIN ;
8448	21529	35057	1.5	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
8448	21529	35058	1.5	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
8475	21556	35088	0.66	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8475	21556	35089	0.66	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8514	21595	35129	2.04	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
8514	21595	35130	2.04	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
9041	22120	35662	1.01	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
9222	22300	35843	1.33	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9222	22300	35844	1.33	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9231	22309		2.79	1.0E-65	11431994	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9309	22385	35937	0.55	1.0E-65	7662227	NT	Homo sapiens KIAA0656 gene product (KIAA0656), mRNA
9678	22640	36210	5.5	1.0E-65	AI191716.1	EST_HUMAN	qd56a02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC FINGER PROTEIN 8 (HUMAN);contains MER19.t1 MER19 repetitive element ;
10089	23127	36730	1.32	1.0E-65	AU153793.1	EST_HUMAN	AU153793 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
10509	23544	37155	0.65	1.0E-65	AA069559.1	EST_HUMAN	zf75a04.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 5'
10796	23829	37453	1.23	1.0E-65	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10885	23969	37599	1.91	1.0E-65	M26167.1	NT	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
11016	24095	37734	9.39	1.0E-65	4506660	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11395	24456	38118	1.9	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
11486	24545	38217	2.58	1.0E-65	AI621017.1	EST_HUMAN	ts76a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L15533_ma1 PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
12292	25217		2.38	1.0E-65	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12391	25276	32078	3.77	1.0E-65	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
73	13310	26334	0.9	9.0E-66	AL160311.1	NT	Novel human gene mapping to chomosome 22
73	13310	26335	0.9	9.0E-66	AL160311.1	NT	Novel human gene mapping to chomosome 22

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1385	14540	27615	1.53	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1385	14540	27616	1.53	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1513	14666		5.93	9.0E-66	M87299.1	NT	Human transposon-like element, partial
4007	17164	30171	0.66	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4007	17164	30172	0.66	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
11628	24708		1.6	7.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
4485	17625	30605	1.16	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595 ;
4485	17625	30606	1.16	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595 ;
4485	17625	30607	1.16	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595 ;
8629	21709		0.46	6.0E-66	BE178563.1	EST_HUMAN	PM2-HT0604-030300-001-b06 HT0604 Homo sapiens cDNA
11427	24488	38152	3.22	6.0E-66	X69181.1	NT	H.sapiens mRNA for ribosomal protein L31
1398	14552	27627	2.45	5.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
9494	22551	36113	8.4	5.0E-66	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
813	13992	27046	1.8	4.0E-66	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1775	14924	28018	0.97	4.0E-66	AW897798.1	EST_HUMAN	RC1-NN0063-100500-022-a02 NN0063 Homo sapiens cDNA
2355	15486	28618	5.3	4.0E-66	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2543	15668		3.15	4.0E-66	AJ223364.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4905	18035		5.02	4.0E-66	9635487	NT	Human endogenous retrovirus, complete genome
5668	18862	32147	3.57	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5861	19051	32358	0.87	4.0E-66	AW939119.1	EST_HUMAN	QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA
6995	18514	31506	4.91	4.0E-66	AW965473.1	EST_HUMAN	EST377546 MAGE resequences, MAGI Homo sapiens cDNA
7281	20364	33817	7.88	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
7807	18862	32147	0.83	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
8269	21351	34867	6.14	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
8327	21409	34936	0.7	4.0E-66	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
10896	23980	37612	1.49	4.0E-66	BF507493.1	EST_HUMAN	UI-H-BW1-amr-a-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
11660	24739	38430	1.63	4.0E-66	AB023215.1	NT	Homo sapiens mRNA for KIAA0998 protein, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1458	14611	27692	14.93	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1458	14611	27693	14.93	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
2039	15180	28290	1.04	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612 ;
2039	15180	28291	1.04	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612 ;
2039	15180	28292	1.04	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612 ;
2772	15887	28997	3.44	3.0E-66	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3186	16361	29367	7.29	3.0E-66	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5583	18778	31823	0.85	3.0E-66	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5695	18889	32180	0.65	3.0E-66	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5893	19081	32391	1.72	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5893	19081	32392	1.72	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
7585	20657	34134	1.74	3.0E-66	X92211.1	NT	H.sapiens germline immunoglobulin heavy chain, variable region, (15-1)
9725	22790	36361	0.59	3.0E-66	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
9920	22960	36547	0.52	3.0E-66	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10278	23313	36911	0.86	3.0E-66	7019480	NT	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
10741	23774	37380	0.95	3.0E-66	AF155659.1	NT	Homo sapiens molybdenum cofactor biosysthesis protein E (MCBPE) mRNA, complete cds
11800	24790	38487	4.55	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
52	13291	26304	1.48	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
52	13291	26305	1.48	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
435	13235	26235	0.87	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
435	13235	26236	0.87	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1873	15017	28126	2.02	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3039	16215	29236	1.07	2.0E-66	X65859.1	NT	H.sapiens pseudogene for the low affinity IL-8 receptor
3609	16773	29788	0.85	2.0E-66	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3861	17021	30019	0.78	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4176	17326	30317	0.69	2.0E-66	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4778	17913	30898	13.88	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4778	17913	30899	13.88	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
5937	19123	32436	0.82	2.0E-66	AW968854.1	EST_HUMAN	EST380930 MAGE resequences, MAGJ Homo sapiens cDNA
5937	19123	32437	0.82	2.0E-66	AW968854.1	EST_HUMAN	EST380930 MAGE resequences, MAGJ Homo sapiens cDNA
9048	22127	35671	3.57	2.0E-66	N45480.1	EST_HUMAN	yy59c02.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:277826 5'
12637	26147		2.84	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
1717	14867		1.14	1.0E-66	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909931 5'
2959	16136	29153	1.47	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2959	16136	29154	1.47	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4504	16136	29153	4.18	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4504	16136	29154	4.18	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5497	18696	31712	5.97	1.0E-66	BF673088.1	EST_HUMAN	602152996F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
5900	19089	32402	0.67	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
5900	19089	32403	0.67	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
7078	20131	33548	1.53	1.0E-66	BF328623.1	EST_HUMAN	RC5-BN0193-010900-034-G06 BN0193 Homo sapiens cDNA
8652	21732	35271	1.2	1.0E-66	AA668858.1	EST_HUMAN	aa80e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827262 3'
9626	22681	36250	0.64	1.0E-66	AA018828.1	EST_HUMAN	ze57e12.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363118 5'
10582	23617	37223	0.93	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10582	23617	37224	0.93	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
11185	24254	37889	2.24	1.0E-66	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
12398	25278		1.92	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
5034	18162		0.91	8.0E-67	M78158.1	EST_HUMAN	EST01750 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCPN31 similar to L1 repetitive element
391	13628	26665	1.63	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1413	14567	27641	2.66	7.0E-67	AA383416.1	EST_HUMAN	EST96812 Testis I Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1585	14737	27817	1.39	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1585	14737	27818	1.39	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2089	15229	28350	1.94	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2089	15229	28351	1.94	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2871	13628	26665	1.36	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6205	19380	32730	0.98	7.0E-67	10190695	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6400	19569	32930	1.67	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6400	19569	32931	1.67	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6863	20015	33425	1.12	7.0E-67	4885084	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
7809	20864	34358	0.99	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
7809	20864	34359	0.99	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8258	21340	34857	0.52	7.0E-67	4826895	NT	Homo sapiens phosphodiesterase I/nucleotide pyrophosphatase 3 (PDNP3) mRNA
8518	21599	35134	0.7	7.0E-67	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9132	22211	35756	0.68	7.0E-67	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
11565	24620		2.42	7.0E-67	11434579	NT	Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA
11973	24958	38660	2.02	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
12168	25131	38829	4.05	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12168	25131	38830	4.05	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12664	25441	32053	1.92	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13106	25721		1.74	7.0E-67	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA
573	13765	26788	1.09	6.0E-67	X68968.1	NT	H.sapiens mRNA for acetyl-CoA carboxylase
818	13997	27051	2.4	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmebrane receptor protein
1302	14458	27524	1.07	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
3237	16411	29426	1.39	6.0E-67	4506434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3524	16689	29698	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3524	16689	29699	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4243	17389	30375	0.92	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4243	17389	30376	0.92	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4827	17960	30947	2.22	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4827	17960	30948	2.22	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
13224	13765	26788	2.74	6.0E-67	X68968.1	NT	H.sapiens mRNA for acetyl-CoA carboxylase
3293	16467	29486	2.26	5.0E-67	AF009860.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11230	24299		2.17	5.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1359	14514	27588	1.13	4.0E-67	R90819.1	EST_HUMAN	yn02d11.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5'
8211	21293	34813	0.8	4.0E-67	AI733032.1	EST_HUMAN	oj26c05.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1493288 3' similar to SW:Z33A_HUMAN Q06730 ZINC FINGER PROTEIN 33A ;
8576	21657		1.48	4.0E-67	BF357321.1	EST_HUMAN	RC0-HT0934-150900-026-c03 HT0934 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11318	24381		1.76	4.0E-67	AA714294.1	EST_HUMAN	nw06a01.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385 PRO-POL-DUTPASE POLYPROTEIN ;
2874	13835	26862	2.03	3.0E-67	AA333768.1	EST_HUMAN	EST37903 Embryo, 9 week Homo sapiens cDNA 5' end
3542	16707	29718	2.05	3.0E-67	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
4816	17949	30934	2.96	3.0E-67	AW869159.1	EST_HUMAN	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
4845	17978		1.38	3.0E-67	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
8375	21456	34980	1.37	3.0E-67	BF196068.1	EST_HUMAN	hr81f05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE Q61085 GTP-RHO BINDING PROTEIN 1 ;
11537	24593		15.42	3.0E-67	AA927874.1	EST_HUMAN	om18b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
193	13416	26445	0.59	2.0E-67	BE348354.1	EST_HUMAN	hw16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9 CE09617 ;
868	14044	27109	5.29	2.0E-67	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
1129	14294		2.48	2.0E-67	AF167460.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
1933	15076	28179	1.23	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892 KIAA0798 PROTEIN. ;
1933	15076	28180	1.23	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892 KIAA0798 PROTEIN. ;
2458	15685	28713	1.18	2.0E-67	AF309561.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
2502	15629	28749	1.37	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3557	16722	29737	3.76	2.0E-67	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
4109	17263	30263	3.13	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6197	19372	32723	0.83	2.0E-67	AL049784.1	NT	Novel human gene mapping to chromosome 13
6252	19426	32772	4.95	2.0E-67	BF240758.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
6425	19593	32958	1.74	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6425	19593	32959	1.74	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6779	19934	33330	0.64	2.0E-67	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
8755	21834	35374	1.09	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
8755	21834	35375	1.09	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
9197	22275	35812	1.31	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9197	22275	35813	1.31	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9766	22763	36332	0.55	2.0E-67	AV731333.1	EST_HUMAN	AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
9910	22950	36536	0.99	2.0E-67	AW293624.1	EST_HUMAN	UI-H-BI2-ahn-e-10-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
10848	23881	37501	0.53	2.0E-67	AA928089.1	EST_HUMAN	on86b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563541 3'
11141	24213	37840	1.75	2.0E-67	BF685788.1	EST_HUMAN	602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11310	26230		2.55	2.0E-67	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11504	24562	38240	2.05	2.0E-67	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11743	23929	37555	2.44	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
12527	25988	31770	2.47	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
263	13482	26514	2.37	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
726	13908	26948	0.95	1.0E-67	AA702794.1	EST_HUMAN	zi90b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4833	17966	30954	0.73	1.0E-67	BF439247.1	EST_HUMAN	nab61f08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
11268	24337		1.47	1.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
12105	25085		3.44	9.0E-68	4506090	NT	Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA
2245	15378	28506	8.3	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3973	17130	30133	5.75	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN. ;
3973	17130	30134	5.75	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN. ;
8293	21375	34895	0.56	7.0E-68	AI810505.1	EST_HUMAN	wb89e03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2312860 3'
10666	23700	37310	6.43	6.0E-68	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
11417	24478	38143	1.31	6.0E-68	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
12868	25579		2.84	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
13165	25756	31927	1.45	6.0E-68	BF310675.1	EST_HUMAN	601894635F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5'
825	15986	27059	2	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
825	15986	27060	2	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	14020	27076	4.93	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	14020	27077	4.93	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3216	16390	29401	2.99	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4297	17440		0.64	5.0E-68	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
2594	15719	28836	1	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2594	15719	28837	1	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
5090	18218		7.11	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6085	19267	32596	0.69	4.0E-68	AF157063.1	NT	Homo sapiens sedlin (SEDL) gene, exon 4
6912	20227	33659	6.03	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6912	20227	33660	6.03	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7859	20913	34418	0.84	4.0E-68	7661683	NT	Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9240	22317	35859	5.59	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9240	22317	35860	5.59	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9380	22455	36018	3.17	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
11251	24320	37960	1.64	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11251	24320	37961	1.64	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11434	24495	38161	1.72	4.0E-68	AB040948.1	NT	Homo sapiens mRNA for KIAA1515 protein, partial cds
12728	25485	32026	1.17	4.0E-68	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
3751	16912	29915	3.54	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9656	21099		3.5	3.0E-68	AI342323.1	EST_HUMAN	qi38h02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR.t2 THR repetitive element ;
10720	23753	37359	1.35	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
13111	25902		2.83	3.0E-68	AW939485.1	EST_HUMAN	QV1-DT0072-010200-056-h06 DT0072 Homo sapiens cDNA
2925	18474		29.7	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4135	17288	30283	0.79	2.0E-68	BE675766.1	EST_HUMAN	7f15f02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:O80828 O80828 HYPOTHETICAL 88.8 KD PROTEIN. ;
4803	17938	30926	2.33	2.0E-68	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
7015	20151		9.21	2.0E-68	R45088.1	EST_HUMAN	yg38g04.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34896 3'
7209	20074	33486	3.81	2.0E-68	BF035316.1	EST_HUMAN	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
7527	20600	34074	0.68	2.0E-68	BF336745.1	EST_HUMAN	IL3-CT0534-180900-273-A01 CT0534 Homo sapiens cDNA
9150	22228	35772	0.56	2.0E-68	Q05859	SWISSPROT	FORMIN 4 (LIMB DEFORMITY PROTEIN)
11521	24577	38255	1.49	2.0E-68	BF330594.1	EST_HUMAN	QV0-BT0074-130999-014-g04 BT0074 Homo sapiens cDNA
12285	26170		1.59	2.0E-68	BE897376.1	EST_HUMAN	601437367F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5'
13192	25775		1.32	2.0E-68	AW016803.1	EST_HUMAN	UI-H-BI0-aam-b-05-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709824 3'
81	13316	26344	0.83	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
307	13523	26557	16.49	1.0E-68	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
2326	15458	28590	1.24	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2326	15458	28591	1.24	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
4117	17271	30270	0.9	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
5140	18263	31231	0.71	1.0E-68	AA897343.1	EST_HUMAN	al47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5437	18637	31616	1.92	1.0E-68	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
7853	20908	34412	0.76	1.0E-68	11436716	NT	Homo sapiens sentrin/SUMO-specific protease (SENP1), mRNA
10385	23420	37027	0.45	1.0E-68	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
11089	24163	37799	2.16	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11089	24163	37800	2.16	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11142	24214	37841	2.81	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSMT3) mRNA, complete cds
11468	24527	38200	1.7	1.0E-68	11433277	NT	Homo sapiens myosin IC (MYO1C), mRNA
11580	24634	38313	2.83	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11580	24634	38314	2.83	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11963	24948	38653	1.81	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
11963	24948	38654	1.81	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12849	13316	26344	2.53	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
13100	26092	31661	3.05	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13184	25755		1.88	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
22	13260	26260	2.42	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
22	13260	26261	2.42	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1053	14219	27275	0.99	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1053	14219	27276	0.99	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4246	17392	30380	0.6	9.0E-69	4757867	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4268	17411	30397	0.89	9.0E-69	4504010	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD) (GLCLR) mRNA
11128	24200		7.86	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3473	16640		1.28	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
6482	19649	33011	4.44	7.0E-69	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
8047	21130	34649	1.85	6.0E-69	AI192764.1	EST_HUMAN	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8047	21130	34650	1.85	6.0E-69	AI192764.1	EST_HUMAN	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
9174	22252	35795	1.05	5.0E-69	AA826039.1	EST_HUMAN	od60a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1372300 3'
533	13726		1.18	4.0E-69	AI873630.1	EST_HUMAN	wm26h11.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437125 3'
5881	25812	32378	1.53	4.0E-69	BE561063.1	EST_HUMAN	601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677641 5'
5966	19152	32467	4.62	4.0E-69	AI764973.1	EST_HUMAN	wh57b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137 O55137 ACYL-COA THIOESTERASE. ;
6764	19920	33315	3.17	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6764	19920	33316	3.17	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9115	22194	35739	0.55	4.0E-69	AU119634.1	EST_HUMAN	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5'
397	13634	26672	5.24	3.0E-69	BE258012.1	EST_HUMAN	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
627	13812	26834	2.78	3.0E-69	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1586	14738		1.12	3.0E-69	T80514.1	EST_HUMAN	yd08a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP:A48836 A48836 SPEGF III=EGF REPEAT-CONTAINING FIBROPELLIN-LIKE PROTEIN - SEA URCHIN ;
2449	15577		2.18	3.0E-69	6729910	NT	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
5357	18483	38823	1.37	3.0E-69	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
7529	20602	34076	0.76	3.0E-69	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7578	20650	34128	1.74	3.0E-69	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds
7724	20788	34277	8.4	3.0E-69	AF268075.1	NT	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
8567	21648	35190	1.33	3.0E-69	AW138646.1	EST_HUMAN	UI-H-BI1-acw-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
8967	22046		0.74	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
9613	22668	36238	1.74	3.0E-69	X13223.1	NT	H.sapiens mRNA for N-acetylglucosamide-(beta 1-4)-galactosyltransferase
9733	22798	36372	3.15	3.0E-69	X06233.1	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
10034	23072	36672	0.56	3.0E-69	5730036	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10877	23962	37590	2.74	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
11080	24155		7.68	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
12112	25092	38795	1.77	3.0E-69	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
12112	25092	38796	1.77	3.0E-69	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
12305	25223		3.1	3.0E-69	11419157	NT	Homo sapiens HGC6.2 protein (HGC6.2), mRNA
131	13612	26651	1.09	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphaIIb protein gene, partial cds
131	13612	26652	1.09	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphaIIb protein gene, partial cds
417	13612	26651	4.42	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphaIIb protein gene, partial cds
417	13612	26652	4.42	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphaIIb protein gene, partial cds
1934	15077	28181	1.79	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2906	16084		4.14	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
8751	21830	35368	0.95	2.0E-69	AA114270.1	EST_HUMAN	zm29g01.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:527088 5'
1680	14832		1	1.0E-69	BF330124.1	EST_HUMAN	RC0-BN0305-200600-031-f05 BN0305 Homo sapiens cDNA
1739	14888	27980	2.4	1.0E-69	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
5137	18260		0.63	1.0E-69	BE409094.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
6175	19351	32697	0.83	1.0E-69	BE902501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
6175	19351	32698	0.83	1.0E-69	BE902501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
6738	19894	33285	4.36	1.0E-69	AW393969.1	EST_HUMAN	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
6958	20271	33709	1.22	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6958	20271	33710	1.22	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6978	20294	33631	2.91	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6976	20294	33632	2.91	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7021	20157	33578	0.61	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3810614 5'
7021	20157	33579	0.61	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3810614 5'
10377	23412	37020	5.01	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10377	23412	37021	5.01	1.0E-69	BE245070.1	EST_HUMAN	602043782F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181325 5'
10625	23659	37268	0.9	1.0E-69	BF528429.1	EST_HUMAN	Homo sapiens keratin 8 (KRT8) mRNA
11112	24184		35.41	1.0E-69	4504918	NT	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12237	25181	38352	1.88	1.0E-69	BF125887.1	EST_HUMAN	wf64e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element;contains element MIR repetitive element ;
12673	25449		3.4	1.0E-69	AI809994.1	EST_HUMAN	nc13d12.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008023
2409	16031	28667	1.56	8.0E-70	AA230303.1	EST_HUMAN	Homo sapiens DGS-I mRNA, 3' end
4493	17633	30615	1.64	8.0E-70	L77566.1	NT	tm89f01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1856	15002	28108	2.42	7.0E-70	AI497807.1	EST_HUMAN	tm89f01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1856	15002	28109	2.42	7.0E-70	AI497807.1	EST_HUMAN	zt15h04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
1984	15127	28229	1.67	7.0E-70	AA282955.1	EST_HUMAN	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
2125	15261		5.13	7.0E-70	5031668	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
4340	17483	30465	4.29	7.0E-70	4757723	NT	Homo sapiens MIST mRNA, partial cds
5600	18795	31844	5.4	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5600	18795	31845	5.4	7.0E-70	AB032369.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
7064	20117	33531	1.9	7.0E-70	AJ000052.1	NT	Homo sapiens titin immunoglobulin domain protein (myotilin) (TTID), mRNA
7945	20995	34506	0.64	7.0E-70	11417306	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8628	21706	35242	2.55	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8626	21706	35243	2.55	7.0E-70	AB037715.1	NT	Human displacement protein (CCAAT) mRNA
8919	21998	35538	3.8	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
8919	21998	35539	3.8	7.0E-70	M74099.1	NT	Human PBX3 mRNA
9358	22433	35991	5.59	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9358	22433	35992	5.59	7.0E-70	X59841.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9635	21078	34590	2.88	7.0E-70	AF153715.1	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9660	21102	34617	1.7	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9660	21102	34618	1.7	7.0E-70	11525964	NT	

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9857	22897	36480	0.53	7.0E-70	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
10505	23540	37149	0.85	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10505	23540	37150	0.85	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11329	24392	38039	1.77	7.0E-70	11429685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
11329	24392	38040	1.77	7.0E-70	11429685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
11897	24885	38583	2.37	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11897	24885	38584	2.37	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
894	14070	27135	2.51	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2205	15339	28466	2.29	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4629	17765	30747	0.7	6.0E-70	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
2618	16066	28854	1.78	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2618	16066	28855	1.78	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
12247	25188		5	5.0E-70	BE166034.1	EST_HUMAN	MR3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA
6894	20045	33454	1.03	4.0E-70	T06037.1	EST_HUMAN	EST03926 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDN25
6933	20248	33682	1.84	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
6933	20248	33683	1.84	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
1619	14771	27853	1.71	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1619	14771	27854	1.71	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
5270	18389	31367	1.11	3.0E-70	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
5737	18930	32227	0.59	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5737	18930	32228	0.59	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6066	19248	32575	1	3.0E-70	AI831975.1	EST_HUMAN	wh90d03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2388005 3'
6503	19669	33033	1.69	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
6503	19669	33034	1.69	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
10314	23349	36955	0.62	3.0E-70	BE502973.1	EST_HUMAN	hz81h02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214419 3'
39	13277	26283	1.03	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
707	13890	26923	15.24	2.0E-70	N42161.1	EST_HUMAN	yy07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
707	13890	26924	15.24	2.0E-70	N42161.1	EST_HUMAN	yy07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
723	13905	26947	1.85	2.0E-70	AI246899.1	EST_HUMAN	qx51h01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1046	14212	27269	1.36	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1211	14372	27432	2.16	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1211	14372	27433	2.16	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1441	14594	27669	1.23	2.0E-70	BE467311.1	EST_HUMAN	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1688	14840	27924	1.07	2.0E-70	AA180093.1	EST_HUMAN	hz64c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212758 3'
1688	14840	27925	1.07	2.0E-70	AA180093.1	EST_HUMAN	zp45h05.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to SW:GAG_HTL1A
1781	14930	28023	4.92	2.0E-70	AL163202.2	NT	zp45h05.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
2394	15525	17082	9.42	2.0E-70	AA054010.1	EST_HUMAN	zp45h05.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
3923	17082	30078	0.71	2.0E-70	AL133207.2	NT	TR:G1041293 G1041293 D2085.5 ;
4160	17311	30307	5.88	2.0E-70	M69181.1	NT	zp45h05.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
5632	18826	31901	8.42	2.0E-70	X72662.1	NT	TR:G1041293 G1041293 D2085.5 ;
5632	18826	31902	8.42	2.0E-70	X72662.1	NT	TR:G1041293 G1041293 D2085.5 ;
6333	19504	32862	1.23	2.0E-70	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6771	19926	33321	2.65	2.0E-70	D12625.1	NT	Homo sapiens NALP1 mRNA, complete cds
6806	19960	33362	10.35	2.0E-70	AF123074.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
6806	19960	33363	10.35	2.0E-70	AF123074.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
7136	18582	31477	1.5	2.0E-70	11422642	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
8103	21185	34704	2.81	2.0E-70	M21741.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
8417	21498	35030	0.66	2.0E-70	11423599	NT	H.sapiens gene for schwannomin (CS8)
8860	21939		1.34	2.0E-70	H47869.1	EST_HUMAN	H.sapiens gene for schwannomin (CS8)
9370	22445	36007	1.14	2.0E-70	11526365	NT	Homo sapiens NALP1 mRNA, complete cds
10342	23377	36988	1.26	2.0E-70	AF123303.1	NT	Homo sapiens NALP1 mRNA, complete cds
11324	24387	38031	3.39	2.0E-70	8923420	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
11324	24387	38032	3.39	2.0E-70	8923420	NT	Homo sapiens dynactin p62 subunit (LOC51164), mRNA
11840	24926	38628	7.78	2.0E-70	4503520	NT	Homo sapiens dynactin p62 subunit (LOC51164), mRNA
12662	25439	32050	2.42	2.0E-70	11430460	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
							Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
							Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
							Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
							Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
							yp79g02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193682 5'
							storage disease type III) (AGL), mRNA
							Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
							Homo sapiens amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen
							Homo sapiens sialyltransferase 6 (N-acetyllactosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12662	25439	32051	2.42	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3480	16647		3.72	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
9480	22537		0.64	1.0E-70	W85795.1	EST_HUMAN	zh55g05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416024 5'
10003	23041		0.88	1.0E-70	AA442292.1	EST_HUMAN	zv54c03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
11175	24244	37877	7.61	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLBGB10 5'
6065	19247	32573	6.03	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 O14045 PHOSPHOTRANSFERASE. ;
6065	19247	32574	6.03	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 O14045 PHOSPHOTRANSFERASE. ;
7175	20308	33751	2.05	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
11813	20308	33751	3.47	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
9270	22346		2.88	8.0E-71	AA171451.1	EST_HUMAN	zp21d11.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL ;
10828	23861	37484	0.53	8.0E-71	AW273820.1	EST_HUMAN	xv24d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR:O54730 O54730 TRANSPLANTABILITY ASSOCIATED PROTEIN 1 ;
7533	20606	34081	7.86	7.0E-71	AA442230.1	EST_HUMAN	zv60h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
8877	21956	35491	1.34	7.0E-71	AA705457.1	EST_HUMAN	zj91a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
11614	24665	38353	2.2	7.0E-71	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2284	15416	28548	7.11	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4235	17382	30371	1.18	5.0E-71	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
6002	19187	32506	1.59	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6801	19956	33356	1.4	5.0E-71	11641408	NT	Homo sapiens keratin, hair, acidic, 7 (KRTHA7), mRNA
7060	20113	33528	0.94	5.0E-71	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7296	20378	33836	0.82	5.0E-71	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7679	20744	34225	1.79	5.0E-71	M38106.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
7884	20936	34442	0.8	5.0E-71	11526445	NT	Homo sapiens MAGUK protein p55T; Protein Associated with Lins 2 (LOC51678), mRNA
7912	20963	34471	20.85	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8720	21800	35335	0.56	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFRKB) mRNA
8720	21800	35336	0.56	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFRKB) mRNA
10115	23153		2.06	5.0E-71	X13467.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
10476	23511	37124	0.49	5.0E-71	U70968.1	NT	Human arrestin (SAG) gene exon 8

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10870	23955	37584	1.45	5.0E-71	5729900	NT	Homo sapiens IGF-II mRNA-binding protein 3 (KOC1), mRNA
10943	24025	37660	1.53	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
10943	24025	37661	1.53	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
11226	24295	37936	3.85	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11467	24526	38199	2.1	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC63325), mRNA
12558	25380		1.75	5.0E-71	11418039	NT	Homo sapiens RNA binding motif protein 9 (RBM9), mRNA
106	13342	26370	1.84	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
360	13571	26601	31.91	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
360	13571	26602	31.91	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2951	16128	29141	1.67	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4548	17686	30667	1.97	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5101	18229	31200	4.56	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
8223	21305		1.13	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone PLACE1002775 5'
10931	24013	37646	3.32	3.0E-71	AA557683.1	EST_HUMAN	nl45h10.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5 repetitive element ;
1258	14416	27481	4.54	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5435	18635	31614	7.23	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5435	18635	31615	7.23	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
7107	18534	31489	0.71	2.0E-71	AL042439.1	EST_HUMAN	DKFZp434D1721_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1721 5'
9207	22285	35826	0.5	2.0E-71	BF195585.1	EST_HUMAN	7n85c11.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571221 3' similar to TR:Q9Z165 Q9Z165 PUTATIVE FOUR REPEAT ION CHANNEL ;
10813	23846	37467	2.12	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10813	23846	37468	2.12	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10933	24015	37647	4.37	2.0E-71	BE018477.1	EST_HUMAN	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B ;
11860	24848	38545	1.46	2.0E-71	BF149173.1	EST_HUMAN	Tmul022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA similar to gi 6598881
11860	24848	38546	1.46	2.0E-71	BF149173.1	EST_HUMAN	Tmul022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA similar to gi 6598881
11882	24870	38567	2.05	2.0E-71	R55626.1	EST_HUMAN	yj77c11.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154772 5'
12318	25231		4.88	2.0E-71	T95489.1	EST_HUMAN	ye43e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
655	13841	26868	1.55	1.0E-71	AI077927.1	EST_HUMAN	oy15e03.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element ;
964	14137	27198	1.38	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1124	14289	27344	13.07	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1371	14526	27600	11.13	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pI4K230) mRNA, complete cds
2147	15283	28408	1.52	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2147	15283	28409	1.52	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2757	15874	28982	6.06	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3590	16754	29769	1.56	1.0E-71	AF119665.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3685	16848	29855	6.57	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3685	16848	29856	6.57	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3738	16899	29902	0.9	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3738	16899	29903	0.9	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3835	16995	29997	2.2	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 19
4593	17730	30712	2.13	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
6881	20033	33443	1.48	1.0E-71	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
7235	20319	33762	1.49	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
7464	20539	34013	12.52	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8340	21421	34946	0.82	1.0E-71	AF105267.1	NT	Homo sapiens glypican-6 (GPC6) mRNA, complete cds
8362	21443	34965	2.21	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8641	21721	35257	4.23	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
8641	21721	35258	4.23	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
9429	22503	36069	0.68	1.0E-71	S72393.1	NT	CSNK2A1=casein kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
10211	23247	36837	6.22	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
10273	23308		2.74	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10759	23792	37411	0.97	1.0E-71	11433142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
11024	24103		2.49	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
11121	24193	37824	3.31	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11413	24474	38138	3.2	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11413	24474	38139	3.2	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
12709	25471		10.17	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds

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420	13615	26654	0.77	9.0E-72	AI857636.1	EST_HUMAN	wk95g03.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN. ;contains Alu repetitive element;
420	13615	26655	0.77	9.0E-72	AI857636.1	EST_HUMAN	wk95g03.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN. ;contains Alu repetitive element;
6237	19412	32760	0.86	8.0E-72	BF035752.1	EST_HUMAN	601458747F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862451 5'
4228	17375	30361	1.75	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitocondrial protein, mRNA
4228	17375	30362	1.75	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitocondrial protein, mRNA
4228	17375	30363	1.75	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitocondrial protein, mRNA
7274	20357	33811	3	7.0E-72	S41694.1	NT	{pseudogene} PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
12857	25569		1.53	7.0E-72	F26269.1	EST_HUMAN	HSPD13670 HM3 Homo sapiens cDNA clone s4000051G02
8578	21659		5.7	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
64	13302	26324	1.19	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
64	13302	26325	1.19	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
65	13302	26324	3.1	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
65	13302	26325	3.1	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1162	14326		2.31	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7089	20183	33607	1.62	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8976	22055	35598	4.16	5.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR:Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ;contains element MSR1 repetitive element ;
10166	23203	36797	0.71	5.0E-72	AV724632.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAKB01 5'
11519	24575	38252	2.95	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
11519	24575	38253	2.95	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
11945	24931	38633	1.55	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
11945	24931	38634	1.55	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
12390	26136		2.46	5.0E-72	BE926645.1	EST_HUMAN	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
4943	18073		0.91	4.0E-72	11034844	NT	Homo sapiens hypothetical protein dJ1057B20.2 (DJ1057B20.2), mRNA
5581	18776	31821	0.68	4.0E-72	AF170025.1	NT	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds
6687	19845	33236	0.85	4.0E-72	T87947.1	EST_HUMAN	yd93a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;
7567	20639	34115	3.26	4.0E-72	5729867	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA

WO 01/57272 PCT/US01/00663

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9987	23026	36618	0.87	4.0E-72	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10312	23347	36953	0.57	4.0E-72	11434344	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10604	23638	37245	0.54	4.0E-72	AW836230.1	EST_HUMAN	RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
10604	23638	37246	0.54	4.0E-72	AW836230.1	EST_HUMAN	RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
10634	23668	37278	1.04	4.0E-72	AI248796.1	EST_HUMAN	qh67c02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to TR:Q14498 Q14498 SPLICING FACTOR. [1] ;contains Alu repetitive element;contains element L1 repetitive element ;
11563	24618	38298	1.57	4.0E-72	AA465388.1	EST_HUMAN	aa23f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
11563	24618	38299	1.57	4.0E-72	AA465388.1	EST_HUMAN	aa23f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
11818	24807	38503	6.28	4.0E-72	H79421.1	EST_HUMAN	yu28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
11938	24924	38624	2.19	4.0E-72	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11938	24924	38625	2.19	4.0E-72	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11976	24961	38663	1.67	4.0E-72	T81910.1	EST_HUMAN	yd29d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
12779	25521	32003	11.86	4.0E-72	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
21	13259	26259	0.7	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
926	14101		1.48	3.0E-72	AA723823.1	EST_HUMAN	ah63a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310290 3'
1180	14343	27398	6.32	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1180	14343	27399	6.32	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1220	14381	27440	3.98	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1220	14381	27441	3.98	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1548	14700	27779	1.16	3.0E-72	BE242161.1	EST_HUMAN	TCAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1252
3143	16319	29331	12.72	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3352	16524	29539	2.7	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3927	17086	30082	2.51	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene {alternatively spliced, splice junction} [human, precursor B-cell line REH, mRNA Partial, 211 nt]
4667	17802	30789	3.17	3.0E-72	11416196	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4889	18019	31003	1.25	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4889	18019	31004	1.25	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds

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5637	18831		1.12	3.0E-72	4759093	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6101	19281	32613	1.94	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6101	19281	32614	1.94	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6295	19468	32822	4.53	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6295	19468	32823	4.53	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6747	19903	33296	4.1	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
7758	20817	34307	2.01	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8369	21450	34973	5.42	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
10646	23680	37290	1.09	3.0E-72	X98289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
12678	25453	32018	2.18	3.0E-72	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
6079	19261	32590	1.38	2.0E-72	11426671	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
9297	22373	35923	0.64	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9297	22373	35924	0.64	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
10978	24057	37691	5.46	2.0E-72	AA789277.1	EST_HUMAN	aj28b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
12772	25515	31999	3.39	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
2137	15273	28394	8.14	1.0E-72	AA846225.1	EST_HUMAN	al83d02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3'
5887	19075	32384	3.54	1.0E-72	7657676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6689	19847	33237	1.22	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6689	19847	33238	1.22	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6769	25832	33319	1.29	1.0E-72	AV751818.1	EST_HUMAN	AV751818 NPD Homo sapiens cDNA clone NPDAIE11 5'
7815	20870	34366	3.5	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
7815	20870	34367	3.5	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9790	22830	36408	7.37	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
9790	22830	36409	7.37	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1488	14641	27723	1.17	9.0E-73	AW374968.1	EST_HUMAN	MR0-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA
6164	19340	32687	0.92	9.0E-73	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
11193	24262		24.49	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1063	14228	27285	0.73	8.0E-73	AW071755.1	EST_HUMAN	ws55c06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q59050 Q59050 HYPOTHETICAL PROTEIN MJ1656. ;
5698	18892	32184	0.98	8.0E-73	4505798	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6702	19860	33250	6.29	8.0E-73	11426469	NT	Homo sapiens lysozyme homolog (LOC57151), mRNA
8287	21369	34890	2.1	8.0E-73	AF113129.1	NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9553	22618	36188	4.35	8.0E-73	BE019900.1	EST_HUMAN	bb62a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
9941	22980	36570	1.76	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9941	22980	36571	1.76	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10134	23172	36770	0.51	8.0E-73	X91940.1	NT	H.sapiens mRNA for WNT-8B protein
10834	23867	37490	0.47	8.0E-73	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
12001	24986	38690	1.49	8.0E-73	AF084520.1	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 mRNA, complete cds
12598	25403	32044	1.2	8.0E-73	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12842	25560	31986	4.55	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
1157	14321	27376	1.61	7.0E-73	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3373	16545	29559	0.7	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5059	18187		1.29	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
162	13387		3.04	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7323	20405	33867	3.42	6.0E-73	BE166574.1	EST_HUMAN	QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA
5368	18571	31439	2.05	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM4A1), mRNA
1911	15054	28165	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1911	15054	28166	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
6837	19990	33398	0.73	3.0E-73	AA136403.1	EST_HUMAN	zn95e04.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:565950 3' similar to gb:Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8958	22037	35578	0.73	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071 5'
8958	22037	35579	0.73	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071 5'
10927	24010		1.45	3.0E-73	X99660.1	NT	H.sapiens SH3GLP2 pseudogene, 5' end
11261	24330	37970	1.41	3.0E-73	BE711238.1	EST_HUMAN	RC6-HT0678-290600-013-H10 HT0678 Homo sapiens cDNA
11261	24330	37971	1.41	3.0E-73	BE711238.1	EST_HUMAN	RC6-HT0678-290600-013-H10 HT0678 Homo sapiens cDNA
11910	24897		1.82	3.0E-73	AI004040.1	EST_HUMAN	ou11d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1625955 3'
13118	25730		3.04	3.0E-73	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
13122	25732		2.05	3.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
874	14050	27115	1.57	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
2000	15141		9.67	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2371	15502		1.49	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3249	16423	29440	2.03	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA

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3640	16804	29816	0.68	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3640	16804	29817	0.68	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4555	17693		1.31	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6567	19729	33106	0.59	2.0E-73	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6567	19729	33107	0.59	2.0E-73	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6610	19770	33160	5.46	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6839	19992	33400	1.87	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6839	19992	33401	1.87	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7984	21033	34546	1.01	2.0E-73	M94048.1	NT	Human peripheral myelin protein 22 mRNA, complete cds
9732	22797	36370	0.54	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
9732	22797	36371	0.54	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10637	23671	37261	1.31	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10715	23748	37355	1.38	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10715	23748	37356	1.38	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
11309	24374	38017	2.91	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11309	24374	38018	2.91	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11339	24402	38051	1.44	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12599	15141		4.32	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1824	14973	28068	3.52	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
6490	19656	33019	1.19	1.0E-73	BE151283.1	EST_HUMAN	CM1-HT0282-111199-042-h10 HT0282 Homo sapiens cDNA
9699	22748	36316	1.22	1.0E-73	AI147427.1	EST_HUMAN	qg61b07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839837 5' similar to contains element MER22 repetitive element ;
11736	23922	37547	3.74	1.0E-73	BE385477.1	EST_HUMAN	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
12045	25026	38731	1.34	9.0E-74	X77225.1	NT	H.sapiens mRNA for TFIIA
12045	25026	38732	1.34	9.0E-74	X77225.1	NT	H.sapiens mRNA for TFIIA
759	13940	26985	4.83	8.0E-74	4557426	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
6036	19219	32541	1.73	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
6036	19219	32542	1.73	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
2004	15144	28249	4.96	7.0E-74	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
3407	16577	29592	1.83	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9444	22560	36123	1.48	7.0E-74	BE967432.1	EST_HUMAN	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932997 5'
12841	25559	31985	4.73	7.0E-74	BE266305.1	EST_HUMAN	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'

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1146	14311	27368	3.65	6.0E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1656	14809	27893	1.03	6.0E-74	AW263177.1	EST_HUMAN	xn78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636 3'
2390	15521	28649	15.52	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2390	15521	28650	15.52	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2927	16104	29119	0.97	6.0E-74	AW014039.1	EST_HUMAN	UI-H-BI0-aah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2927	16104	29120	0.97	6.0E-74	AW014039.1	EST_HUMAN	UI-H-BI0-aah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3805	16965	29968	1.22	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3805	16965	29969	1.22	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5481	18680	31695	3.49	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
928	14103	27166	1.93	5.0E-74	AW020986.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2767	15882		4.98	5.0E-74	AW362756.1	EST_HUMAN	PM0-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
5523	18720	31736	1.92	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5910	19099	32413	12.5	5.0E-74	X69670.1	NT	H.sapiens mRNA for TPCR16 protein
5961	19147	32462	8.1	5.0E-74	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6030	19213	32533	2.94	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6030	19213	32534	2.94	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7035	20171	33593	3.69	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8226	21308	34828	2.33	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10973	24053	37686	1.67	5.0E-74	Y09420.1	NT	H.sapiens mRNA for HIP-I
10973	24053	37687	1.67	5.0E-74	Y09420.1	NT	H.sapiens mRNA for HIP-I
11090	24164	37801	1.36	5.0E-74	5729766	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
290	13507	26542	3.31	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
875	14051	27116	10.3	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
2018	15158	28262	3.07	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2018	15158	28263	3.07	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2134	15270	28390	9.96	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2134	15270	28391	9.96	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2201	15336	28463	1.32	4.0E-74	AB032994.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2498	15625	28745	1.16	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene

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3160	16335	29345	6.22	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3616	16780	29795	1.1	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4174	17324	30315	1.29	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4679	17814	30802	1.86	4.0E-74	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4735	17870	30854	1.07	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmebrane receptor protein
5133	18258	31224	1.03	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
5185	18307	31271	1.12	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
5185	18307	31272	1.12	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
8747	21826		3.53	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
8773	21852	36394	0.62	3.0E-74	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
9572	22714	36282	2.32	3.0E-74	M78984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCPF91
10546	23581	37191	2.16	3.0E-74	AA601493.1	EST_HUMAN	no17g05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
980	14153	27213	28.83	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
980	14153	27214	28.83	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1202	14364	27424	1.63	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1273	14430	27501	1.44	2.0E-74	AI950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;contains element MER22 repetitive element ;
1625	14777	27861	10.45	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1625	14777	27862	10.45	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2668	15789	28905	2.18	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.r tumor2 Homo sapiens cDNA 3'
5119	18245	31210	2.52	2.0E-74	AL355092.1	NT	Novel human gene mapping to chomosome 22
5119	18245	31211	2.52	2.0E-74	AL355092.1	NT	Novel human gene mapping to chomosome 22
5919	25813	32419	1.88	2.0E-74	BE711134.1	EST_HUMAN	RC6-HT0678-220500-011-C03 HT0678 Homo sapiens cDNA
6017	25816	32518	1.77	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6017	25816	32519	1.77	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6087	25816	32518	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6087	25816	32519	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7252	20335	33784	2.5	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
8126	21208	34728	1.8	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds

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9582	22724	36294	5.27	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12526	25359		2.87	2.0E-74	AA196181.1	EST_HUMAN	zp96a06.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
13169	26176		1.16	2.0E-74	BF002855.1	EST_HUMAN	7g50a08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309878 3'
54	13293	26308	1.5	1.0E-74	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
347	13558	26586	3.71	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
512	13706	26734	1.8	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
519	13712	26739	2.59	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
614	13803	26823	1.28	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
804	13984	27036	0.86	1.0E-74	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
1024	14195	27253	2.26	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2301	15433	28566	6.03	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3209	16383	29394	2.82	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3460	16627	29646	1.29	1.0E-74	AA258549.1	EST_HUMAN	zr60c01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667776 5'
3460	16627	29647	1.29	1.0E-74	AA258549.1	EST_HUMAN	zr60c01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667776 5'
4031	17187	30197	0.84	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4031	17187	30198	0.84	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4075	17231	30237	5.41	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4175	17325	30316	0.85	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-f06 BT0642 Homo sapiens cDNA
4382	17525	30508	0.87	1.0E-74	BE467769.1	EST_HUMAN	hz73h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:B0511.12 CE17351 ;
6844	19997	33404	1.29	1.0E-74	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
7804	20860	34353	1.05	1.0E-74	11417977	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8246	21328	34844	1.27	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8246	21328	34845	1.27	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9005	22084	35627	7.81	1.0E-74	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9034	22113	35656	0.67	1.0E-74	BF351951.1	EST_HUMAN	MR0-HT0559-230500-021-a03 HT0559 Homo sapiens cDNA
10445	23480	37086	0.65	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10445	23480	37087	0.65	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10699	23732	37337	1.77	1.0E-74	11420549	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
12154	25124	38826	1.94	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12238	25182		4.97	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12386	15433	28566	1.61	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12925	25510		1.38	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2709	15827		5.1	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12552	25375		3.07	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2395	15526	28654	1.25	6.0E-75	AI817415.1	EST_HUMAN	wk38a08.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
11780	24770	38466	1.39	6.0E-75	BE791831.1	EST_HUMAN	601586109F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940130 5'
9109	22188	35731	1.09	5.0E-75	BE272325.1	EST_HUMAN	601126068F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989865 5'
9317	22393	35944	0.77	5.0E-75	AA132611.1	EST_HUMAN	zo17e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
9395	22470	36034	0.47	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9395	22470	36035	0.47	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9573	22715	36283	1.1	5.0E-75	BF690254.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
10439	23474	37078	2.64	5.0E-75	AI638623.1	EST_HUMAN	tt31c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361 HYPOTHETICAL 20.1 KD PROTEIN ;
115	13346	26373	2.1	4.0E-75	BE081333.1	EST_HUMAN	QV1-BT0632-210200-079-e02 BT0632 Homo sapiens cDNA
471	13666		1.68	4.0E-75	N36757.1	EST_HUMAN	yx90h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:269055 5'
1805	14954	28048	1.08	4.0E-75	AW897230.1	EST_HUMAN	CM0-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
2910	16088	29101	5.64	4.0E-75	BE409464.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
5646	18840	32120	0.68	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5646	18840	32121	0.68	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6399	19568	32929	5.18	4.0E-75	5579457	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110kD) (EIF3S8), mRNA
6898	20048	33458	1.4	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6898	20048	33459	1.4	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10924	24007	37642	10.52	4.0E-75	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1027	14198	27256	3.6	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1028	14198	27256	3.59	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1883	15027	28134	2.23	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2180	15315	28444	1.44	3.0E-75	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
2494	15621	28740	4.39	3.0E-75	4759153	NT	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA
3086	16262	29279	0.96	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3258	16432	29449	1.09	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3431	16599	29616	0.93	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3431	16599	29617	0.93	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3833	16993	29995	0.6	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4283	17428	30418	2.92	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
5365	18568	31434	1.15	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA

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5365	18558	31435	1.15	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6637	19796	33185	0.59	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6637	19795	33186	0.59	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6909	20224	33654	1.57	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6909	20224	33655	1.57	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7285	20368	33821	4.12	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7285	20368	33822	4.12	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7800	20856	34346	2.66	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7800	20856	34347	2.66	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
9185	22263	35805	1.33	3.0E-75	11420804	NT	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNAI1), mRNA
9880	22920	36504	0.83	3.0E-75	11420222	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
5790	18982		1.34	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cdA Homo sapiens cDNA clone cdABED02 5'
8950	22029	35570	1.36	2.0E-75	AI311783.1	EST_HUMAN	qo91e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE ;
2377	15508	28635	10.98	1.0E-75	AW168135.1	EST_HUMAN	xg60d02.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.t1 PTR7 repetitive element ;
3012	16188	29213	2.95	1.0E-75	X52221.1	NT	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
7762	20821	34311	0.64	1.0E-75	BE082528.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
7762	20821	34312	0.64	1.0E-75	BE082528.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
8609	21689		3.12	1.0E-75	AA399270.1	EST_HUMAN	zt57h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gb:M13932 40S RIBOSOMAL PROTEIN S17 (HUMAN);
9628	22683	36253	3.95	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
9628	22683	36254	3.95	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
11122	24194		6.68	1.0E-75	AA664377.1	EST_HUMAN	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
11351	24413	38067	2.22	1.0E-75	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12440	18502	31538	1.97	1.0E-75	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
45	13284	26292	0.89	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1 ;
45	13284	26293	0.89	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1 ;
2486	15613		0.94	9.0E-76	AA702415.1	EST_HUMAN	zl85b07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10105	23143	36741	5.44	9.0E-76	M12937.1	NT	Human ferritin Heavy subunit mRNA, complete cds
961	14134	27194	1.18	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
961	14134	27195	1.18	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2978	16152	29173	0.95	8.0E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
6300	19473	32828	5.84	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7658	20725	34200	1.17	8.0E-76	11435215	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
7739	20800	34289	1.05	8.0E-76	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8492	21573	35110	0.69	8.0E-76	11416961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
10589	23624	37231	1.26	8.0E-76	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
10903	23987	37619	4.29	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
12824	25550		2.51	8.0E-76	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
797	13976	27029	1.69	7.0E-76	5016092	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3366	16538	29551	3.84	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3372	16544	29558	9.08	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4491	17631	30612	5.52	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4491	17631	30613	5.52	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1262	14419		37.29	6.0E-76	BE396253.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
11753	23939	37565	2.52	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'
1997	15138	28243	9.61	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1997	15138	28244	9.61	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1997	15138	28245	9.61	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3278	16452	29473	0.64	4.0E-76	BE814096.1	EST_HUMAN	QV3-BN0047-270700-283-g06 BN0047 Homo sapiens cDNA
5384	18586	31455	1.13	4.0E-76	BE783412.1	EST_HUMAN	601471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
10230	23265	36854	5.48	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5'
10230	23265	36855	5.48	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5'
646	13831	26856	2.01	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
646	13831	26857	2.01	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1629	14781	27866	8.04	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1629	14781	27867	8.04	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3515	16681	29691	5.75	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3515	16681	29692	5.75	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5352	18480	38822	1.82	3.0E-76	Z41314.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							za73c07.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592524 5' similar to gb:L32976 MIXED LINEAGE KINASE 1 (HUMAN);
			0.92	3.0E-76	AA160611.1	EST_HUMAN	gb:L32976 MIXED LINEAGE KINASE 1 (HUMAN);
5851	19041	32347	0.61	3.0E-76	AW027705.1	EST_HUMAN	ww75c05.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2535368 3'
6110	19290	32675	8.19	3.0E-76	AF286598.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
6498	19664	33027	1.27	3.0E-76	N42671.1	EST_HUMAN	Homo sapiens melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2773009 3'
8344	21425	34961	3.03	3.0E-76	AW289353.1	EST_HUMAN	yy20g10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:757461 5'
9917	22957	36544	1.08	3.0E-76	AA442309.1	EST_HUMAN	xc49h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:757461 5'
9942	22981	36572	1.08	3.0E-76	AA442309.1	EST_HUMAN	zr54d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
9942	22981	36573	2.1	3.0E-76	AW967984.1	EST_HUMAN	zr54d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
12144	26943	31763	6.95	3.0E-76	AW956455.1	EST_HUMAN	EST380525 MAGE resequences, MAGD Homo sapiens cDNA
12251	26184	31642	1.11	2.0E-76	D84295.1	NT	EST368525 MAGE resequences, MAGD Homo sapiens cDNA
292	13509	26544	3.21	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
352	13563	26590	3.21	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
352	13563	26591	0.96	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
473	13668		1.07	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
603	13792	26812	1.66	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1056	14222	27291	11.31	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1568	14719	27799	11.31	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1566	14719	27800	0.99	2.0E-76	AA253954.1	EST_HUMAN	Homo sapiens schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
1932	15125	28227	2.13	2.0E-76	P23266	SWISSPROT	zs60h11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB3_HUMAN
2904	16092	29097	2.21	2.0E-76	AA445992.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3369	16541	29555					zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3369	16541	29556	2.21	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to TR:O14591 P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3565	16730	29746	0.93	2.0E-76	AI821149.1	EST_HUMAN	ac83b02.y5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:O14591 O14591 SIMILARITY TO P22059 ;
4254	13509	26544	1.01	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
4663	17789	30773	0.91	2.0E-76	AL163283.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
5062	18190	31165	11.15	2.0E-76	AW879618.1	EST_HUMAN	Homo sapiens cDNA
5163	18285	31249	3.13	2.0E-76	6174586	NT	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5424	18625		2.99	2.0E-76	AF127845.1	NT	Homo sapiens murine retrovirus integration site 1 homolog (MRVI1) mRNA
5736	18929	32226	4.83	2.0E-76	AB029004.1	NT	Homo sapiens mRNA for KIAA1061 protein, partial cds
7570	20642	34119	0.66	2.0E-76	11421326	NT	Gorilla gorilla olfactory receptor (GGO18) gene, partial cds
7592	20663	34139	0.66	2.0E-76	11426908	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
							Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), mRNA

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7840	20895	34397	1.82	2.0E-76	11427410	NT	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA
10489	23524	37134	1.42	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63150), mRNA
11161	24232	37862	2.44	2.0E-76	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA
4412	17554	30539	2.49	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4412	17554	30540	2.49	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5564	18761	31801	5.93	1.0E-76	BE796537.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6374	19543		0.7	1.0E-76	AA333207.1	EST_HUMAN	EST37301 Embryo, 8 week I Homo sapiens cDNA 5' end
7063	20116	33530	4.56	9.0E-77	BE889525.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
13003	25652		1.98	9.0E-77	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
192	13414	26443	0.77	8.0E-77	R83144.1	EST_HUMAN	yp11h02.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:187155 5' similar to SP:ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
4644	17780	30762	1.41	8.0E-77	BF205181.1	EST_HUMAN	601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
5569	18766	31807	1.37	8.0E-77	4506230	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA
11669	24746	38438	1.78	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11669	24746	38439	1.78	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
12979	25637	31982	32.5	8.0E-77	R00245.1	EST_HUMAN	ye69f04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element ;
1983	15126	28228	2.2	7.0E-77	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2482	15609	28733	2.78	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2482	15609	28734	2.78	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
273	13491	26522	4	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1165	14329	27384	1.05	6.0E-77	AW957753.1	EST_HUMAN	EST369823 MAGE resequences, MAGE Homo sapiens cDNA
1574	14727	27808	3.29	6.0E-77	AI204066.1	EST_HUMAN	qe77h12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
1264	14421	27486	2.89	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1391	14545	27621	3.46	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2749	15866	28977	1.75	5.0E-77	AF162665.1	NT	Homo sapiens tousled-like kinase 1 (TLK1) mRNA, complete cds
2822	15936	29046	1.58	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3611	16775	29791	0.65	5.0E-77	6394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4825	17958	30944	0.97	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4825	17958	30945	0.97	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
5052	18180	31156	3.57	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'
6922	20237	33671	0.65	5.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7480	20555	34027	0.59	5.0E-77	X98296.1	NT	H.sapiens mRNA for ubiquitin hydrolase

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Table 4

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Probe. SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7767	20555	34027	0.72	5.0E-77	X98296.1	NT	H.sapiens mRNA for ubiquitin hydrolase
8563	21644	35183	1.21	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8563	21644	35184	1.21	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9769	22765	36335	2.61	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9769	22765	36336	2.61	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10708	23741	37346	0.97	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
10708	23741	37347	0.97	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
2029	15170	28277	1.39	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
2029	15170	28278	1.39	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10496	23531	37139	0.9	3.0E-77	H65167.1	EST_HUMAN	yu64g01.r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10496	23531	37140	0.9	3.0E-77	H65167.1	EST_HUMAN	yu64g01.r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
11115	24187	37819	2.83	3.0E-77	BF359917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1383	14538	27612	1.74	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBTF10 5'
1464	14618	27702	9.74	2.0E-77	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2157	15293	28419	1.1	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2170	15305	28432	2.75	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2659	16087	28895	1.69	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2659	16087	28896	1.69	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4143	17295	30287	1.98	2.0E-77	BE044316.1	EST_HUMAN	ho43b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4534	17672	30656	0.67	2.0E-77	AI613519.1	EST_HUMAN	tw22g02.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN. ;
4534	17672	30657	0.67	2.0E-77	AI613519.1	EST_HUMAN	tw22g02.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN. ;
4891	18021	31006	2.34	2.0E-77	AA653025.1	EST_HUMAN	ns68g12.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1] ;contains element MSR1 repetitive element ;
6075	19257	32586	2.08	2.0E-77	BE298940.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
6301	19474	32829	1.86	2.0E-77	BE787143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
7325	20407	33869	15.02	2.0E-77	AI833003.1	EST_HUMAN	at74a09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP151. [1] ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8726	21806	35343	0.86	2.0E-77	AI362707.1	EST_HUMAN	qy70c09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017360 3' similar to WP:F29D11.1 CE05765 LOW DENSITY LIPID RECEPTOR-RLATED PROTEIN ;
9728	22793	36366	5.68	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
9728	22793	36367	5.68	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10199	23236	36825	0.47	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
10199	23236	36826	0.47	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
44	13282	26288	2.62	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
44	13282	26289	2.62	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
283	13501	26533	1.68	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
283	13501	26534	1.68	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	16025	27140	3.4	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	16025	27141	3.4	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1969	15112	28213	1.36	1.0E-77	AW058119.1	EST_HUMAN	wv83e05.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2536160 3'
2515	15641	28763	1.17	1.0E-77	AB029024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3110	16286	29300	2.28	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4473	17613	30592	4.24	1.0E-77	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4646	17782	30764	22.17	1.0E-77	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4774	17909	30892	2.05	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4815	17948	30933	0.61	1.0E-77	AI273014.1	EST_HUMAN	qv09g04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981110 3'
6051	19233	32557	1.48	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6051	19233	32558	1.48	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6172	19348	32694	1.72	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6577	19739	33120	1.1	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
7198	20063	33473	15.97	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7844	20899	34402	0.82	1.0E-77	11420159	NT	Homo sapiens cullin 1 (CUL1), mRNA
7940	20990	34500	0.71	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9465	22522	36085	0.83	1.0E-77	X94354.1	NT	H.sapiens DNA for Cone cGMP-PDE gene
9465	22522	36086	0.83	1.0E-77	X94354.1	NT	H.sapiens DNA for Cone cGMP-PDE gene
10742	23775	37387	1.05	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10742	23775	37388	1.05	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10773	23806	37429	2.76	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA
6576	19738	33118	2.29	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
6576	19738	33119	2.29	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
88	13323	26351	1.66	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
88	13323	26352	1.66	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3389	16559	29574	0.9	6.0E-78	BF344101.1	EST_HUMAN	602016926F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4152511 5'
6690	19848		2.54	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
224	13446	26474	6.13	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2629	15752	28887	5.71	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48B6A.6 CE22121 ;
3472	16639	29659	5.09	5.0E-78	M55586.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5528	18725	31741	2.73	5.0E-78	AF038536.1	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
5693	18887	32177	18.13	5.0E-78	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
7304	20386	33846	2.18	5.0E-78	AW953120.1	EST_HUMAN	EST365190 MAGE resequences, MAGB Homo sapiens cDNA
9284	22360	35910	7.02	5.0E-78	U60889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
9285	22361	35911	2.94	5.0E-78	BE960836.1	EST_HUMAN	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
1160	14324	27379	1.29	4.0E-78	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
1547	14699	27778	1.81	4.0E-78	AL355841.1	NT	Novel human gene mapping to chomosome 22
2392	15523	28652	5.1	4.0E-78	AF107405.1	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4442	17582	30560	6.17	4.0E-78	7656876	NT	Homo sapiens syncytin (LOC30816), mRNA
4896	18026	31012	1.2	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptido (PIK4CA) mRNA
4896	18026	31013	1.2	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5888	19076	32385	1.25	4.0E-78	11420732	NT	Homo sapiens SFRS protein kinase 2 (SRPK2), mRNA
6302	19475	32830	0.71	4.0E-78	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
6302	19475	32831	0.71	4.0E-78	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
6703	19861	33251	0.74	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7660	20727	34203	0.69	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9054	22133	35677	1.15	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9054	22133	35678	1.15	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9568	22710	36276	0.61	4.0E-78	11417251	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10660	23694	37303	1.95	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10660	23694	37304	1.95	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11705	24702	38394	1.84	4.0E-78	AF169148.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11854	24842	38538	6.72	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12855	25568	31991	3.93	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
165	13390	26417	1.69	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
165	13390	26418	1.69	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
2488	15615	28736	1.01	3.0E-78	7706705	NT	Homo sapiens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA
3860	17020		0.81	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
3918	17077	30074	0.78	3.0E-78	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
4221	17077	30074	0.82	3.0E-78	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
10493	23528		5.44	3.0E-78	BE144758.1	EST_HUMAN	CM0-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA
11227	24296	37937	2.5	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
3191	16366		2.49	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4122	17276		1.99	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
7631	20700	34177	1.09	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-aaj-g-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7631	20700	34178	1.09	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-aaj-g-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7908	20960	34466	3.36	2.0E-78	BF689800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'
8230	21312	34832	2.49	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
8646	21726	35262	1.72	2.0E-78	AI557509.1	EST_HUMAN	Pt2.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8646	21726	35263	1.72	2.0E-78	AI557509.1	EST_HUMAN	Pt2.1_16_B07.r tumor2 Homo sapiens cDNA 3'
11336	24399	38048	9.58	2.0E-78	AI197837.1	EST_HUMAN	qi50h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1859961 3' similar to WP:R90.1 CE06325 PROTEIN KINASE ;
11358	24420		1.47	2.0E-78	BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
11386	24447	38108	3.01	2.0E-78	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
5420	18621	31597	3.16	1.0E-78	11417304	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
7094	18521	31514	0.82	1.0E-78	AV648699.1	EST_HUMAN	AV648699 GLC Homo sapiens cDNA clone GLCBMC01 3'
8353	21434		1.81	1.0E-78	U52373.1	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
12324	25234	32107	1.83	1.0E-78	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12422	25299	32086	2.44	1.0E-78	11435903	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA
4820	17953	30938	4.04	9.0E-79	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
4986	18115	31093	1.6	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
5549	18746	31781	16.98	9.0E-79	AB028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6470	19837	32996	2.52	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
6752	19908	33301	0.98	9.0E-79	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA

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7505	25846		0.99	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7748	20808	34298	0.63	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7748	20808	34299	0.63	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
8541	21622	35158	0.52	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8541	21622	35159	0.52	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9263	22340	35890	4.78	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9263	22340	35891	4.78	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9580	22722	36292	0.66	9.0E-79	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10574	23609	37214	0.82	9.0E-79	11438643	NT	Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA
10632	23666	37274	1.05	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10632	23666	37275	1.05	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
11322	24385	38029	1.61	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11802	24792	38489	2.94	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
11802	24792	38490	2.94	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
13088	25711	31967	1.4	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3836	16996	29998	1.18	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3325	16498	29516	6.36	7.0E-79	BE619648.1	EST_HUMAN	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
8844	21923		0.62	6.0E-79	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12169	25132		5.44	6.0E-79	AA699829.1	EST_HUMAN	zj94e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
11786	24776	38473	3.63	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
323	13537	26569	1.74	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1001	14172	27233	1.22	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cln) gene, complete cds
3168	16343	29351	1.74	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5477	18676	31689	7.05	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5841	19031	32337	1.69	3.0E-79	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5866	19056	32363	0.93	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5866	19056	32364	0.93	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5889	19077	32386	3.87	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5889	19077	32387	3.87	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6884	20036	33445	0.84	3.0E-79	BE256893.1	EST_HUMAN	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
7206	20071	33481	2.58	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
7206	20071	33482	2.58	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8012	21062	34574	0.87	3.0E-79	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8358	21439	34961	0.78	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
9603	22658	36230	0.59	3.0E-79	10835036	NT	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA
10555	23590		0.62	3.0E-79	AV698115.1	EST_HUMAN	AV698115 GKC Homo sapiens cDNA clone GKCAHE11 5'
298	13515		1.4	2.0E-79	H63129.1	EST_HUMAN	yr48f03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208541 3'
651	13837	26864	1.05	2.0E-79	BE379926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
951	14124	27186	1.14	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1007	14178	27239	4.97	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1007	14178	27240	4.97	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1060	14226		2.15	2.0E-79	AI523747.1	EST_HUMAN	th18h07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2118685 3'
2215	15349	28478	6.17	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2215	15349	28479	6.17	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2266	15399	28527	1.35	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2387	15516	28648	1.1	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
2780	15896	29006	1.2	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0937 protein, partial cds
4023	17179	30188	0.69	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLC4 (ClC4) mRNA, complete cds
4280	17425	30414	1.25	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4813	17946	30931	0.83	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5788	18980		1.06	2.0E-79	AA312223.1	EST_HUMAN	EST182926 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid B0303.15
5844	19034	32340	0.9	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6373	19542	32901	1.19	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
7100	18527	31519	0.69	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7317	20399	33861	2.09	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7317	20399	33862	2.09	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
8292	21374	34894	1.1	2.0E-79	4506442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8714	21794	35331	2.13	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8965	22044	35587	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8965	22044	35588	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9205	22283	35823	0.69	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 (H. sapiens) (LOC63961), mRNA
10297	23332	36935	1.98	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10297	23332	36936	1.98	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
11284	24350	37987	2.94	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11284	24350	37988	2.94	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
12208	18498	31534	4.27	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12298	25219	32100	2.3	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12531	25362	32067	3.08	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6718	25830		3.28	1.0E-79	BF363071.1	EST_HUMAN	MR0-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA
6833	19986	33394	0.65	1.0E-79	AI613480.1	EST_HUMAN	ty37e08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623 TEKTIN C1. ;
6833	19986	33395	0.65	1.0E-79	AI613480.1	EST_HUMAN	ty37e08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623 TEKTIN C1. ;
8439	21520	35049	0.9	1.0E-79	BE394211.1	EST_HUMAN	601311517F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632909 5'
11922	24908	38609	1.9	1.0E-79	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
12328	26107		1.44	1.0E-79	AI460115.1	EST_HUMAN	ar79a04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
3215	16389	29399	6.95	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3215	16389	29400	6.95	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
10217	23253	36842	1.3	9.0E-80	BE798603.1	EST_HUMAN	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5'
11554	24609	38288	7.63	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
11554	24609	38289	7.63	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
3691	16853		1.01	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7780	20836	34328	2.82	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7780	20836	34329	2.82	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
9602	22657	36228	2.2	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9602	22657	36229	2.2	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7114	18540	31497	0.61	7.0E-80	AF127882.1	NT	Callithrix jacchus olfactory receptor (CJA80) gene, partial cds
923	14098	27162	0.74	6.0E-80	AI422197.1	EST_HUMAN	tf58d02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
1675	14827	27910	2.41	6.0E-80	U64898.1	NT	Homo sapiens NRD convertase mRNA, complete cds
2372	15503	28628	1.14	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
2372	15503	28629	1.14	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
5922	19109	32422	1.46	6.0E-80	11421462	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6200	19375	32726	3.35	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6358	19528	32886	4.07	6.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6402	19571		1.08	6.0E-80	7662393	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
6452	19619	32982	0.82	6.0E-80	M18533.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
9024	22103	35643	3.4	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9024	22103	35644	3.4	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9221	22299	35842	1.57	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9559	22624	36196	0.66	6.0E-80	AF161495.1	NT	Homo sapiens HSPC146 mRNA, complete cds
10065	23103	36706	1.83	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
11183	24252	37887	2	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11498	24556	38231	20.88	6.0E-80	AF226730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
12053	25034	38740	1.48	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
12176	14098	27162	1.75	6.0E-80	AI422197.1	EST_HUMAN	tl58d02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
12309	25972		2	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12512	25351		3.32	6.0E-80	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
13081	26115		2.69	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
601	13790	26811	1.7	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
858	14035	27097	1.89	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
858	14035	27098	1.89	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1216	14377		1.49	5.0E-80	X91647.1	NT	H.sapiens ncx1 gene (exon 12)
1485	14638		2.89	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2501	15628	28748	3.51	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2855	15969	29078	1.78	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4150	17302	30295	0.9	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4150	17302	30296	0.9	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
5068	18196	31170	1.23	5.0E-80	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8552	21633	35170	1.28	5.0E-80	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9458	22574	36140	5.03	4.0E-80	F26915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
223	13445		6.03	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5028	18157		2.3	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
5941	19127	32440	1.78	3.0E-80	AI091675.1	EST_HUMAN	oo23e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1667054 3' similar to TR:O35790 O35790 PIG-L. ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1841	14987	28087	4.85	2.0E-80	R35321.1	EST_HUMAN	yg65a08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:38060 5'
1908	15051	28163	1.57	2.0E-80	AI444821.1	EST_HUMAN	RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
2116	15253	28372	7.03	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1323 5'
6944	20257	33696	0.95	2.0E-80	AA582952.1	EST_HUMAN	nn80d01.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1090177 3'
7053	20106	33522	1.89	2.0E-80	11421930	NT	Homo sapiens Golgi transport complex protein (90 kDa) (GTC90), mRNA
7401	20479	33947	0.89	2.0E-80	T75215.1	EST_HUMAN	yc86f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22851 5' similar to SP:K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B ;
9360	22435	35994	1.21	2.0E-80	AW964270.1	EST_HUMAN	EST376343 MAGE resequences, MAGH Homo sapiens cDNA
9970	23009	36603	0.99	2.0E-80	AJ007379.1	NT	Homo sapiens GGT gene, exon 6
11109	24181	37815	6.84	2.0E-80	AA393362.1	EST_HUMAN	zt70f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315 G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
350	13561		1.52	1.0E-80	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
822	14001	27055	1.3	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
2009	15149		2.42	1.0E-80	AI732656.1	EST_HUMAN	nn01f12.x5 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.t1 OFR repetitive element ;
4583	17720	30703	0.95	1.0E-80	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
5343	18456		3.32	1.0E-80	Y13932.1	NT	Homo sapiens PRKY exon 7
5442	18642		5.25	1.0E-80	BE386615.1	EST_HUMAN	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
6093	19274	32603	6.12	1.0E-80	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
6627	19787	33175	1.17	1.0E-80	5174540	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
7356	20435	33897	1.18	1.0E-80	AJ224172.1	NT	Homo sapiens mRNA for lipophilin B
7747	20807	34296	8.03	1.0E-80	AI948731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3'
7747	20807	34297	8.03	1.0E-80	AI948731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3'
8426	21507	35039	0.67	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
8897	21976	35514	0.76	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
8897	21976	35515	0.76	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9485	22542	36104	1.17	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
9485	22542	36105	1.17	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10640	23674	37284	0.7	1.0E-80	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10887	23971	37601	4.9	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
10887	23971	37602	4.9	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
12593	25399	32042	1.32	1.0E-80	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12862	25573		1.28	1.0E-80	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10923	24006	37640	1.93	8.0E-81	AI251752.1	EST_HUMAN	qh90g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
10923	24006	37641	1.93	8.0E-81	AI251752.1	EST_HUMAN	qh90g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
11422	24483	38147	5.99	8.0E-81	BE394525.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
2280	15412	28543	0.94	7.0E-81	AA011080.1	EST_HUMAN	ze21d10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:359835 5' similar to SW:KRHA_RABIT Q02957 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. [1] ;contains element MER22 repetitive element ;
7402	20480	33948	3.69	7.0E-81	AI822115.1	EST_HUMAN	za91c08.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299918 3'
4506	17645	30632	3.73	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4506	17645	30633	3.73	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5397	18599	31569	2.28	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5397	18599	31570	2.28	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
9437	22511	36076	1.24	6.0E-81	AA360017.1	EST_HUMAN	EST69129 Fetal lung II Homo sapiens cDNA 5' end
12747	25495	32030	3.38	6.0E-81	BF679022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
12747	25495	32031	3.38	6.0E-81	BF679022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2291	15423	28557	2.98	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8607	21688	35226	3.06	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8607	21688	35227	3.06	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9848	22888	36467	1.25	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9848	22888	36468	1.25	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11883	24871	38568	1.76	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
720	13902	26943	0.64	4.0E-81	AI521435.1	EST_HUMAN	th60e12.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560 ;
1867	15013	28121	1.54	4.0E-81	AW779612.1	EST_HUMAN	hn98d02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:COPG_BOVIN P53620 COATOMER GAMMA SUBUNIT ;
3239	16413	29428	3.91	4.0E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3718	16879	29884	0.89	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815 STRIATIN. ;
4276	17421	30408	2.94	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4276	17421	30409	2.94	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
7427	20504	33974	0.91	4.0E-81	4757893	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2) mRNA
7559	20631	34106	0.59	4.0E-81	11420544	NT	Homo sapiens ets variant gene 1 (ETV1), mRNA
8482	21563	35098	2.36	4.0E-81	X06989.1	NT	Human mRNA for amyloid A4(751) protein
8742	21821	35355	2.2	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8742	21821	35356	2.2	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9427	22501	36067	3.35	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10306	23341	36946	1.4	4.0E-81	11425281	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10374	23409	37018	0.65	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
10374	23409	37019	0.65	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11461	24520	38189	4.74	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
11461	24520	38190	4.74	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
12200	26039	31682	8.38	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12200	26039	31683	8.38	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12796	25532	32009	1.63	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12796	25532	32010	1.63	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12956	25623	31978	4.21	4.0E-81	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1296	14452	27516	9.06	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1296	14452	27517	9.06	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2444	15572	28701	1.72	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3055	16231	29250	6.11	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3055	16231	29251	6.11	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2894	16073	29090	2.29	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2894	16073	29091	2.29	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3873	17032	30031	0.8	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
8144	21226	34746	0.69	2.0E-81	8923839	NT	Homo sapiens hypothetical protein (LOC55586), mRNA
13129	17032	30031	5.68	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
4638	17774	30754	2.86	1.0E-81	AA040370.1	EST_HUMAN	zk45h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly ;
4768	17903	30885	9.54	1.0E-81	BE047996.1	EST_HUMAN	tz45c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291526 5'
5241	18363	31331	0.6	1.0E-81	9966844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
5351	18479	38821	6.18	1.0E-81	U87928.1	NT	Human aconitate hydratase (ACO2) gene, exon 3
5469	18669	31648	3.8	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5469	18669	31649	3.8	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5619	18813	31881	0.76	1.0E-81	AA255569.1	EST_HUMAN	zr85d06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:682475 5' similar to SW:PRI2_HUMAN P49643 DNA PRIMASE 58 KD SUBUNIT ;
5771	18963	32264	3.18	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds

WO 01/57272 PCT/US01/00663

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5771	18963	32265	3.18	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds
6274	19448	32797	1.81	1.0E-81	BF674641.1	EST_HUMAN	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
6877	20029	33439	1.09	1.0E-81	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7949	20999	34509	7.94	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
7972	21022	34535	0.61	1.0E-81	AJ250408.1	NT	Homo sapiens GLI3 gene for GLI3 protein
9978	23017	36610	0.89	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9978	23017	36611	0.89	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
10174	23211	36804	5.13	1.0E-81	BE564367.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
10308	23343	36948	0.81	1.0E-81	AA630784.1	EST_HUMAN	ec14d06.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW:YB36_YEAST P38126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION. ;
10310	23345	36950	3.72	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10310	23345	36951	3.72	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10726	23759	37367	1.41	1.0E-81	AW897550.1	EST_HUMAN	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA
10884	23896	37519	0.49	1.0E-81	AW250322.1	EST_HUMAN	2822127.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822127 5'
11182	24251	37886	1.97	1.0E-81	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11347	24409	38061	1.56	1.0E-81	AW844986.1	EST_HUMAN	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA
11347	24409	38062	1.56	1.0E-81	AW844986.1	EST_HUMAN	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA
11352	24414	38068	2.93	1.0E-81	AW798167.1	EST_HUMAN	RC3-UM0046-290200-011-a06 UM0046 Homo sapiens cDNA
11352	24414	38069	2.93	1.0E-81	AW798167.1	EST_HUMAN	RC3-UM0046-290200-011-a06 UM0046 Homo sapiens cDNA
11550	18490	31529	2.46	1.0E-81	AW960658.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
11812	24802	38501	1.89	1.0E-81	BF204253.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
12417	25295	32085	3.6	1.0E-81	11418138	NT	Homo sapiens phorbolin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
13	13251	26251	1.59	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
109	13251	26251	1.35	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
274	13492	26523	1.58	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
837	14015	27070	1.87	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
910	14085	27150	1.84	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1520	14673	27755	2.24	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1690	14842	27927	1.39	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4198	17348	30339	0.74	8.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4358	17501	30483	0.83	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA

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1481	14634		1.18	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
2825	15939	29049	1.62	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
1705	14857	27944	22.54	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5613	18807	31874	0.87	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-f08 HT0540 Homo sapiens cDNA
5613	18807	31875	0.87	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-f08 HT0540 Homo sapiens cDNA
5876	19066	32374	1.1	4.0E-82	M25833.1	NT	Human von Willebrand factor gene, exon 9
12016	26000	38702	4.71	4.0E-82	AI937300.1	EST_HUMAN	wp75e09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:O75276 O75276 PKD1 ;
12683	25455		3.78	4.0E-82	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
288	13506	26540	15.3	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
721	13903	26944	2.5	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-f02 BN0120 Homo sapiens cDNA
810	13989	27043	8.44	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
893	14069	27134	5.31	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1086	14252		15.73	3.0E-82	AA725848.1	EST_HUMAN	al23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1386	14541	27617	1.22	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1494	14647	27729	5.59	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1950	15093	28194	2.14	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
2062	15202	28318	1.11	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA
3345	16518		2.42	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
8346	21427	34952	2.66	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8753	21832	35371	0.89	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8753	21832	35372	0.89	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
10029	23067	36665	4.01	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10029	23067	36666	4.01	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
610	13799	26818	2.49	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
610	13799	26819	2.49	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1720	14870	27962	2.23	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: hres3) Homo sapiens cDNA clone DKFZp434M117 5'
3949	17107	30104	0.93	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4131	17284	30279	0.68	2.0E-82	U76833.1	NT	Human integral membrane serine protease Seprase mRNA, complete cds
4348	17491	30473	0.9	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4680	17815	30803	1.52	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds

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4680	17815	30804	1.52	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4992	18121	31100	2.86	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5191	18313	31290	1.56	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5191	18313	31281	1.56	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5587	18782	31827	2.89	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6304	19477	32832	4.63	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
7858	26222		1.19	2.0E-82	AI476428.1	EST_HUMAN	tm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
7988	21038	34550	0.8	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8500	21581	35117	1.81	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
8869	21948	35482	0.58	2.0E-82	7657340	NT	Homo sapiens microrchidia (mouse) homolog (MORC), mRNA
8869	21948	35483	0.58	2.0E-82	7657340	NT	Homo sapiens microrchidia (mouse) homolog (MORC), mRNA
10315	23350	36956	1.16	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10315	23350	36957	1.16	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11547	24603	38279	1.74	2.0E-82	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11547	24603	38280	1.74	2.0E-82	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11588	24641	38322	2.6	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11588	24641	38323	2.6	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
12230	25177		2.81	2.0E-82	N94950.1	EST_HUMAN	zb31d10.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'
12818	25545		3.72	2.0E-82	AA011278.1	EST_HUMAN	zi01g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
605	13794	26813	1.59	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1235	14394		3.19	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1314	14470	27536	1.38	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1315	14471	27537	0.8	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
9143	22222	35765	0.9	1.0E-82	AB037838.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
9853	22893	36474	0.51	1.0E-82	AB014562.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
10451	23486		1.4	1.0E-82	BF515938.1	EST_HUMAN	UI-H-BW1-aoa-f-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
10984	24063	37698	2.49	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11258	24327	37966	1.49	1.0E-82	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5307	18424	31394	1.05	9.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8912	21991	35530	4.99	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291661 5'
10481	23516	37128	0.72	9.0E-83	BE253347.1	EST_HUMAN	601117160F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357734 5'
1446	14599	27676	2.97	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1715	15992	27956	10.59	8.0E-83	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
1388	14543	27618	1.2	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-271299-068-h11 LT0016 Homo sapiens cDNA
2928	16105		1.64	7.0E-83	AA584655.1	EST_HUMAN	no12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4936	18066		6.85	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y3I6 Q9Y3I6 DJ207H1.1 ;
6176	19352	32699	0.95	7.0E-83	11428657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
416	13611	26650	1.39	6.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1828	14976	28071	1.79	6.0E-83	AW573088.1	EST_HUMAN	hf31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN HI0034. ;
3082	16258	29277	0.68	6.0E-83	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
3116	16292		0.7	6.0E-83	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3653	16816	29828	0.92	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5408	18610	31582	1.73	6.0E-83	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6147	19324	32669	1.31	6.0E-83	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7671	20737	34215	2	6.0E-83	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
9878	22918	36503	3.51	6.0E-83	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
9971	23010	36604	0.71	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
9971	23010	36605	0.71	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
11821	24810		2.31	6.0E-83	AA486105.1	EST_HUMAN	ab14e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR.t2 THR repetitive element ;
12179	25139		4.14	6.0E-83	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
969	14142		1.24	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2108	15996		3	5.0E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3728	16889	29893	0.91	5.0E-83	AL133207.2	NT	Novel human gene mapping to chomosome X
4015	17172	30180	0.73	5.0E-83	4885190	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
4554	17692	30672	0.61	5.0E-83	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5190	18312	31278	13.87	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5190	18312	31279	13.87	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
657	13843	26870	1.87	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1022	14193		4.09	3.0E-83	AA368311.1	EST_HUMAN	EST79542 Placenta I Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2837	15951		1.6	3.0E-83	AA632654.1	EST_HUMAN	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.t2 THR repetitive element ;
6708	19866		0.82	3.0E-83	AI217223.1	EST_HUMAN	qf73e06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755682 3'
1843	14989	28089	1.37	2.0E-83	AA993492.1	EST_HUMAN	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216. ;
1843	14989	28090	1.37	2.0E-83	AA993492.1	EST_HUMAN	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216. ;
1978	15121	28222	9.11	2.0E-83	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
2251	15384	28512	1.57	2.0E-83	AB033098.1	NT	Homo sapiens mRNA for KIAA1272 protein, partial cds
2913	16091	29103	1.33	2.0E-83	BE828694.1	EST_HUMAN	RC6-ET0046-280600-013-H12 ET0046 Homo sapiens cDNA
3342	16515		2.16	2.0E-83	11430834	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3874	17033		0.94	2.0E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4456	17596	30576	4.95	2.0E-83	AF202879.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4775	17910	30893	3.19	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4775	17910	30894	3.19	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5385	18587	31559	0.91	2.0E-83	U06679.1	NT	Human carcinoembryonic antigen gene family member 18 (CGM18) gene, exons A1 and B1
5967	19153	32468	0.67	2.0E-83	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
6086	19268	32597	1.2	2.0E-83	BE885401.1	EST_HUMAN	601507482F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909068 5'
6885	20037	33446	0.72	2.0E-83	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
7593	20364	34140	5.15	2.0E-83	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
7987	21036	34548	0.58	2.0E-83	BF105097.1	EST_HUMAN	601822090F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042318 5'
8026	21109	34626	0.63	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
8026	21109	34627	0.63	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
8175	21257	34779	1.46	2.0E-83	U66707.1	NT	Rattus norvegicus densin-180 mRNA, complete cds
8509	21590	35124	2.52	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8509	21590	35125	2.52	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
9793	22833	36412	0.54	2.0E-83	5453881	NT	Homo sapiens phosphorylase kinase, gamma 1 (muscle) (PHKG1) mRNA
9793	22833	36413	0.54	2.0E-83	5453881	NT	Homo sapiens phosphorylase kinase, gamma 1 (muscle) (PHKG1) mRNA
10240	23275	36866	3.2	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10240	23275	36867	3.2	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10322	23357	36967	1.35	2.0E-83	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
10392	23427	37034	0.78	2.0E-83	AW505600.1	EST_HUMAN	UI-HF-BN0-amd-h-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081852 5'
11086	24160	37796	3.24	2.0E-83	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11168	24239	37870	1.64	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547J135 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11168	24239	37871	1.64	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547J135 5'
12859	25570		3.26	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1444	14597	27673	2.28	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1444	14597	27674	2.26	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2076	15216	28335	1.15	1.0E-83	4503652	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA
2722	15840	28951	1.21	1.0E-83	BE883690.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3251	16425	29443	0.72	1.0E-83	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
3972	17129	30132	7.76	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds
4359	17502	30484	2.22	1.0E-83	225822.1	NT	H.sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
5008	18137	31111	2.74	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
6835	19988	33397	1.59	1.0E-83	AI027614.1	EST_HUMAN	ov89b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM PROTEIN (HUMAN);
3897	17056	30056	3.62	7.0E-84	BE901209.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1323	14479	27544	2.96	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
1323	14479	27545	2.96	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2471	15588	28723	17.98	6.0E-84	AA776574.1	EST_HUMAN	ae86a03.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5354	18481		2.18	6.0E-84	AL042853.2	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434H0322 5'
5635	18829	31905	1.91	6.0E-84	AA897339.1	EST_HUMAN	ai47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480600 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
5777	18969	32273	0.99	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA
5777	18969	32274	0.99	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA
7642	20711	34190	3.14	6.0E-84	BE810371.1	EST_HUMAN	PM0-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA
7868	20922	34429	1.05	6.0E-84	AF038391.1	NT	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
8264	21346	34861	2	6.0E-84	BE770199.1	EST_HUMAN	PM4-FT0054-160600-004-e10 FT0054 Homo sapiens cDNA
732	13914	26955	1.32	5.0E-84	AA382811.1	EST_HUMAN	EST96094 Testis I Homo sapiens cDNA 5' end
3079	16255		1.91	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
6232	19407	32756	0.62	5.0E-84	AA167678.1	EST_HUMAN	zq39e07.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632100 5' similar to TR:G483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q.;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11838	24827	38516	2.85	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11952	24938	38640	1.99	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11952	24938	38641	1.99	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1407	14561	27635	1.34	4.0E-84	AB037735.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds
1443	14596	27672	4.47	4.0E-84	AI685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN O43847 NARDILYSIN PRECURSOR ;
5064	18192	31167	0.66	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
5065	18193	31168	1.52	4.0E-84	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5377	18579	31448	1.62	4.0E-84	AF022835.1	NT	Homo sapiens multidrug resistance protein (MRP), exon 13
5680	18874	32162	1.8	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5680	18874	32163	1.8	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6398	19567	32928	2.14	4.0E-84	AF059650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7825	20880	34381	13.68	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9112	22191	35735	1.12	4.0E-84	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9112	22191	35736	1.12	4.0E-84	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
11158	24229	37859	4.76	4.0E-84	AB032956.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
326	13540	26572	2.16	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1178	14341	27395	1.53	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2015	15155	28260	2.39	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2063	15203	28319	2.36	3.0E-84	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3843	17002	30005	5.53	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA, complete cds
11118	24190		5.78	3.0E-84	AI983801.1	EST_HUMAN	wu20d05.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);
2172	15307	28435	6.46	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2172	15307	28436	6.46	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
3009	16185	29209	9.21	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-l) mRNA, complete cds
3027	16203	29226	1.22	2.0E-84	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
5643	18837	31914	0.93	2.0E-84	BF511575.1	EST_HUMAN	UI-H-BI4-aol-a-02-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
5643	18837	31915	0.93	2.0E-84	BF511575.1	EST_HUMAN	UI-H-BI4-aol-a-02-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
6774	19929	33325	0.92	2.0E-84	H63370.1	EST_HUMAN	yr56e11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:209324 3'
8247	21329		1.55	2.0E-84	AI298674.1	EST_HUMAN	qm87c09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895728 3'
8579	21660	35200	0.58	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8579	21660	35201	0.58	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9546	22611	36179	1.24	2.0E-84	AU120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9933	22972	36564	0.64	2.0E-84	H22841.1	EST_HUMAN	ym49e11.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:51383 5' similar to SP:APOH_RAT P26644 BETA-2-GLYCOPROTEIN I ;
12449	25316	32092	1.81	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathatic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1 ;
12449	25316	32093	1.81	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathatic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1 ;
322	13536	26568	1.5	1.0E-84	AF114488.1	NT	Homo sapiens clone IMAGE:3626257 3'
563	13755	26781	10.87	1.0E-84	4507952	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
738	13920		1.19	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1321	14477	27542	2.63	1.0E-84	AA984379.1	EST_HUMAN	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2114	16252	28371	3.11	1.0E-84	BE392137.1	EST_HUMAN	am85b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:3626257 5'
2298	16430	28562	1.53	1.0E-84	11427197	NT	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:1239106 3'
3845	17005	30007	2.78	1.0E-84	AA720851.1	EST_HUMAN	Homo sapiens pericentriolar material 1 (PCM1), mRNA
4538	17676	30659	5.89	1.0E-84	AJ229041.1	NT	nw12e06.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4821	17954	30939	3.03	1.0E-84	AL043314.2	EST_HUMAN	Homo sapiens 969 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5031	17676	30659	3.56	1.0E-84	AJ229041.1	NT	Homo sapiens 969 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6043	19226	32549	0.88	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
6319	19491	32849	2.84	1.0E-84	S73482.1	NT	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
7020	20156	33576	1.42	1.0E-84	AL049784.1	NT	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
7020	20156	33577	1.42	1.0E-84	AL049784.1	NT	Homo sapiens AML1 and CBR1 on chromosome 21q22; segment 1/3
7256	20339	33789	2.53	1.0E-84	AL049784.1	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
7637	20706	34185	10.45	1.0E-84	8393994	NT	uterine water channel=28 kda erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
7737	20798	34287	1.07	1.0E-84	11430846	NT	Novel human gene mapping to chomosome 13
7777	20798	34287	2.34	1.0E-84	11430846	NT	Novel human gene mapping to chomosome 13
9736	22800		2.79	1.0E-84	5031984	NT	Novel human gene mapping to chomosome 13
9972	23011	36606	0.6	1.0E-84	AF224511.1	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
9994	18488	31527	1.6	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9994	18488	31528	1.6	1.0E-84	4507848	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
12325	25235		2.62	1.0E-84	11417812	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
12438	25311	32088	3.77	1.0E-84	11418185	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
989	14161		1.94	9.0E-85	AL163209.2	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
							Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
							Homo sapiens chromosome 21 segment HS21C009

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1098	14263	27319	2.89	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1098	14263	27320	2.89	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1609	14762	27841	1.12	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1609	14762	27842	1.12	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1709	14860	27949	3.59	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
3870	17029		0.8	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4366	17509	30490	0.92	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5001	18130	31105	0.99	9.0E-85	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
5032	18160	31137	1.16	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
13046	14860	27949	1.78	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
1159	14323	27378	4.64	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11943	24929		5.61	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11702	24699	38391	2.56	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11702	24699	38392	2.56	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
12060	25041	38750	2	6.0E-85	AA403053.1	EST_HUMAN	zi62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 G1335769 GAG-POL POLYPROTEIN. ;
2410	15540	28668	4.09	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4552	17690		0.71	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
5567	18764	31804	1.59	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862402 5'
5567	18764	31805	1.59	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862402 5'
11381	24442	38101	2.31	5.0E-85	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
13127	17690		1.72	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
6276	19450	32798	1.39	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6276	19450	32799	1.39	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
8021	21074	34586	3.43	4.0E-85	BE882304.1	EST_HUMAN	601505022F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906940 5'
10798	23831		1.8	4.0E-85	BE079263.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
1327	14484	27551	0.91	3.0E-85	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1821	14970	28062	4.8	3.0E-85	T97495.1	EST_HUMAN	ye53g09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
5019	18148	31125	1.03	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA

WO 01/57272 PCT/US01/00663

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5019	18148	31126	1.03	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5080	18208	31180	0.91	3.0E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5517	18715	31729	6.35	3.0E-85	11436001	NT	Homo sapiens lacrimal proline rich protein (LPRP), mRNA
6210	19385	32734	0.72	3.0E-85	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6262	19436	32782	4.92	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6262	19436	32783	4.92	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
7091	20185		7.95	3.0E-85	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7555	20627	34103	0.84	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0621 protein (KIAA0621), mRNA
8056	21139	34659	1.44	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
8706	21786	35319	0.48	3.0E-85	11525829	NT	Homo sapiens CGI-61 protein (LOC51108), mRNA
9178	22256	35798	4.39	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9506	22772	36343	0.84	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B* (SNRPB2), mRNA
9508	22772	36344	0.84	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B* (SNRPB2), mRNA
10700	23733	37338	0.72	3.0E-85	AF098642.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11796	24786	38484	1.48	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
12999	25648		3.02	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
985	14157	27218	0.62	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1065	14231	27289	2.35	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1438	14589	27662	1.19	2.0E-85	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
1451	14604	27682	13.02	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1451	14604	27683	13.02	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2304	15436	28568	2.92	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2884	14523		4.22	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3087	16263	29280	3.57	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4454	17594	30574	4.66	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4687	17822	30810	0.74	2.0E-85	4826977	NT	Homo sapiens reelin (RELN) mRNA
5030	18159	31136	1.21	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9473	22530	36094	1.78	2.0E-85	AI760820.1	EST_HUMAN	wi67h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element MSR1 repetitive element ;
9849	22889	36469	0.82	2.0E-85	AI914459.1	EST_HUMAN	wd49d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331461 3'
10469	23504	37118	0.94	2.0E-85	AI886384.1	EST_HUMAN	wm94d12.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443607 3'
2360	15491		3.55	1.0E-85	BE794306.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2467	15594	28719	9.36	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2467	15594	28720	9.36	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
7983	21032	34545	0.61	1.0E-85	BE062951.1	EST_HUMAN	MR0-BT0264-221199-002-f03 BT0264 Homo sapiens cDNA
9984	23023	36615	2.13	1.0E-85	BE257917.1	EST_HUMAN	601109738F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350553 5'
10415	23450	37055	0.76	1.0E-85	AW813525.1	EST_HUMAN	RC1-ST0196-081099-011-c05 ST0196 Homo sapiens cDNA
11164	24235	37865	2.79	1.0E-85	AA778785.1	EST_HUMAN	zj45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
11164	24235	37866	2.79	1.0E-85	AA778785.1	EST_HUMAN	zj45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
11245	24314	37953	1.86	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
11245	24314	37954	1.86	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
12068	25049	38757	3.29	1.0E-85	AI198420.1	EST_HUMAN	qi56a07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1860468 3'
12330	25404	32045	4.68	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12601	25404	32045	2.92	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1460	14613		25.01	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
6254	19428	32774	0.62	8.0E-86	11424140	NT	Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA
233	13454	26480	2.2	7.0E-86	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
960	14133	27192	1.03	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
960	14133	27193	1.03	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6325	19497	32853	0.97	7.0E-86	9966886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6325	19497	32854	0.97	7.0E-86	9966886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7116	18542	31499	6.43	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
8943	22022	35562	3.98	7.0E-86	L38557.1	NT	Homo sapiens galactocerebrosidase (GALC) gene, exon 15
9901	22941		1.13	7.0E-86	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9960	22999	36595	1.68	7.0E-86	11526307	NT	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA
11204	24273	37909	1.44	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
11204	24273	37910	1.44	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
12117	25097	38802	1.99	7.0E-86	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
1322	14478	27543	1.87	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA
217	13439	26471	2.15	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
6159	19335	32680	11.61	4.0E-86	BE295343.1	EST_HUMAN	601176865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
11517	13439	26471	2.34	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4404	17547	30531	0.94	3.0E-86	BE867703.1	EST_HUMAN	601443262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847455 5'
5713	18906	32201	6.19	3.0E-86	AW340946.1	EST_HUMAN	xz92h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
8457	21538	35087	1.21	3.0E-86	AV722329.1	EST_HUMAN	AV722329 HTB Homo sapiens cDNA clone HTBBSD04 5'
10425	23460	37065	3.54	3.0E-86	BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10425	23460	37066	3.54	3.0E-86	BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11720	23906	37529	4.87	3.0E-86	AI659240.1	EST_HUMAN	tw18b02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2251371 3'
11803	24793	38491	1.37	3.0E-86	AV690469.1	EST_HUMAN	AV690469 GKC Homo sapiens cDNA clone GKCBSE02 5'
12300	25971		3.38	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
277	13495	26525	1.56	2.0E-86	AA306264.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
427	13622		2.69	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1217	14378	27437	3.33	2.0E-86	N58977.1	EST_HUMAN	yz19a08.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:283478 5'
2265	15398	28526	8.53	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
2342	15473	28607	1.56	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3502	16669	29679	1.51	2.0E-86	AW966142.1	EST_HUMAN	EST378215 MAGE resequences, MAGI Homo sapiens cDNA
3840	16999	30001	2.29	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3840	16999	30002	2.29	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4151	17303		2.59	2.0E-86	AW515742.1	EST_HUMAN	hd87g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2916542 3'
4910	18040	31030	3.21	2.0E-86	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5993	19178	32499	1.32	2.0E-86	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
5993	19178	32500	1.32	2.0E-86	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
7221	25837	33501	0.78	2.0E-86	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
8199	21281	34803	0.58	2.0E-86	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8772	21851	35392	2.52	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8772	21851	35393	2.52	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
9104	22183	35728	0.68	2.0E-86	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9519	22584	36153	1.96	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
10664	23698	37307	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10664	23698	37308	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10667	23701	37311	0.48	2.0E-86	11417120	NT	Homo sapiens hypothetical protein FLJ20125 (FLJ20125), mRNA
10721	23754	37360	1.25	2.0E-86	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11143	24215	37842	1.76	2.0E-86	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
12789	25527	32006	6.3	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12980	25638		2.56	2.0E-86	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1627	14779	27864	2.15	1.0E-86	4826855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA

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3231	16405	29417	1.68	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3307	16481	29502	2.39	1.0E-86	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3368	16540	29553	1.74	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3368	16540	29554	1.74	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4380	17523	30504	5.41	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4743	17878	30861	0.94	1.0E-86	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
5670	18864	32149	1.85	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11905	18864	32149	1.53	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5472	18672		1.84	9.0E-87	AI150703.1	EST_HUMAN	qb77c09.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
7606	20676	34150	1.82	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7606	20676	34151	1.82	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
492	13686	26720	49.59	8.0E-87	X62245.1	NT	O.cuniculus mRNA for elongation factor 1 alpha
2369	15500	28626	3.27	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2369	15500	28627	3.27	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6530	19694	33067	1.38	7.0E-87	AW890336.1	EST_HUMAN	MR0-NT0039-020500-004-a11 NT0039 Homo sapiens cDNA
8384	21465	34990	3	7.0E-87	BF352776.1	EST_HUMAN	IL3-HT0619-060700-198-D10 HT0619 Homo sapiens cDNA
9653	21096	34610	0.66	7.0E-87	BE712961.1	EST_HUMAN	IL5-HT0702-160600-103-d06 HT0702 Homo sapiens cDNA
10278	23311	36907	3.38	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
10276	23311	36908	3.38	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
10686	25865		0.53	7.0E-87	AI081565.1	EST_HUMAN	ox59h01.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660657 3'
11129	24201	37825	6.59	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
11129	24201	37826	6.59	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
3615	16779	29794	1.19	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
6551	19713	33089	1.47	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
10963	24044		4.48	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1184	14347	27404	1.62	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis I Homo sapiens cDNA 5' end
12603	14347	27404	2.58	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis I Homo sapiens cDNA 5' end
988	14160	27220	1.37	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1199	14361	27420	7.91	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1461	14614	27696	1.31	4.0E-87	R78133.1	EST_HUMAN	yi80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2086	15226	28348	2.28	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2143	15279	28402	1.29	4.0E-87	R78133.1	EST_HUMAN	yi80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2143	15279	28403	1.29	4.0E-87	R78133.1	EST_HUMAN	yi80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2493	15620	28738	0.99	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
2493	15620	28739	0.99	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
3553	16718	29732	3.61	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
5562	18759	31798	4.6	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5869	19059	32366	0.58	4.0E-87	U85429.1	NT	Human transcription factor NFATx3 mRNA, complete cds
6170	19346	32692	4.34	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
7848	20903	34406	0.71	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7848	20903	34407	0.71	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7950	21000	34510	3.64	4.0E-87	L48524.1	NT	Homo sapiens tuberin (TSC2) gene, exon 10
11437	24498	38165	3.42	4.0E-87	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
12705	26023	31671	1.27	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12705	26023	31672	1.27	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12896	25593		58.7	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2836	15950	29057	14.35	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
3884	17043	30042	1.02	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
5033	18161	31138	3.2	2.0E-87	BF376311.1	EST_HUMAN	CM0-TN0038-150900-552-h08 TN0038 Homo sapiens cDNA
5076	18204	31176	0.8	2.0E-87	BE175478.1	EST_HUMAN	RC5-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
5778	18970	32275	12.22	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5778	18970	32276	12.22	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6456	19623		4.87	2.0E-87	BE567193.1	EST_HUMAN	601341383F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683348 5'
6838	19991	33399	0.79	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
6920	20235	33668	0.75	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLC Homo sapiens cDNA clone GLCDSG04 3'
7324	20406	33868	1.35	2.0E-87	BE294432.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
7374	20453	33918	0.7	2.0E-87	11433046	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
7611	20681	34157	36.59	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
7864	20918	34424	35.3	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
8589	21670	35209	3.35	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
9988	23027		4.86	2.0E-87	BE531136.1	EST_HUMAN	601278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1209	15989		2.2	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1463	14616	27698	1.61	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1463	14616	27699	1.61	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3801	16962	29966	5.18	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3828	16988	29991	2.3	1.0E-87	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
6356	19526	32883	1.63	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6356	19526	32884	1.63	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7333	20414	33876	1.09	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7558	20630	34105	1.05	1.0E-87	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7707	20772	34257	0.92	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
8307	21389	34912	9.93	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9110	22189	35732	0.95	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9110	22189	35733	0.95	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9833	22873	36456	2.92	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
9833	22873	36457	2.92	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
10584	23619	37225	0.88	1.0E-87	M34426.1	NT	Human L-plastin mRNA, 5' end
10970	24050	37683	2.11	1.0E-87	5729867	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
11247	24316		1.66	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12701	26190		2.31	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
13228	25798	31890	1.22	1.0E-87	AF169558.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
13228	25798	31891	1.22	1.0E-87	AF169558.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
1130	14295	27350	8.48	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1380	14535	27609	2.94	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1380	14535	27610	2.94	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2189	15324	28449	0.99	9.0E-88	7661701	NT	Homo sapiens DKFZP586P1522 protein (DKFZP586P1522), mRNA
3717	16878	29883	1	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4384	17527	30508	2.97	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
4384	17527	30509	2.97	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
9223	22301	35845	4.04	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1875	15019		1.22	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2704	15822	28939	3.65	5.0E-88	N89399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3064	16240	29260	0.62	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3075	16251	29272	0.71	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3075	16251	29273	0.71	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3476	16643		2.78	5.0E-88	AI693217.1	EST_HUMAN	wd68h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element;contains element MER22 MER22 repetitive element ;
3625	16789	29806	0.75	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
4859	17992	30979	0.71	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
6910	20225	33656	2.67	5.0E-88	H10932.1	EST_HUMAN	ym06b10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:47129 5'
8114	21196	34715	2.67	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9512	22577	36143	0.53	5.0E-88	BF680206.1	EST_HUMAN	602154958F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295775 5'
1360	14515	27589	0.96	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1360	14515	27590	0.96	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
5244	18365	31333	0.65	4.0E-88	BF670714.1	EST_HUMAN	602149762F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290975 5'
7392	20470	33936	1.7	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
11150	24221	37849	1.54	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
11779	24769	38464	1.72	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11779	24769	38465	1.72	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
750	13931	26974	1.25	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1855	15001		3.09	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
3013	16189	29214	6.08	3.0E-88	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
4355	17498	30477	0.81	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4355	17498	30478	0.81	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4600	17737		4.81	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5414	18616	31590	2.79	3.0E-88	11429587	NT	Homo sapiens valosin-containing protein (VCP), mRNA
5703	18896	32188	3.63	3.0E-88	9966888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5822	19012	32318	3.9	3.0E-88	11420697	NT	Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6290	19463	32815	0.72	3.0E-88	11417370	NT	Homo sapiens interleukin 13 (IL13), mRNA
6543	25826	33080	0.84	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6543	25826	33081	0.84	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7211	20076	33489	15.52	3.0E-88	AF279265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7712	20777	34263	5.53	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
8105	21187	34707	9.3	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8390	21471	34997	1.58	3.0E-88	AF034374.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9634	21077	34589	2.14	3.0E-88	11526262	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
10132	23170	36767	0.76	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10132	23170	36768	0.76	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10162	23199	36794	0.6	3.0E-88	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12424	25301		2.49	3.0E-88	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
12439	26030	31676	1.63	3.0E-88	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13223	25796	31889	1.31	3.0E-88	11526140	NT	Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA
1061	14227	27283	6.85	2.0E-88	7305198	NT	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1653	14806	27891	4.24	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1789	14938	28031	6.83	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3554	16719	29733	2.9	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4545	17683	30665	1.93	2.0E-88	5031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
6032	19215	32536	4.98	1.0E-88	AW139565.1	EST_HUMAN	UI-H-BI1-aea-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718760 3'
6032	19215	32537	4.98	1.0E-88	AW139565.1	EST_HUMAN	UI-H-BI1-aea-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6783	19938	33334	21.66	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6783	19938	33335	21.66	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7271	20354	33807	1.52	1.0E-88	AI969034.1	EST_HUMAN	wq70a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2476606 3'
7334	20415	33877	3.7	1.0E-88	AA488981.1	EST_HUMAN	aa54a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2 CE00851 ;
8331	21413	34939	0.51	1.0E-88	AF135183.1	NT	Homo sapiens Recq helicase 5 (RECQ5) gene, alternative splice products, complete cds
9443	22559	36122	0.76	1.0E-88	AA190368.1	EST_HUMAN	zp87c02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627170 5' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN ;
9778	22818	36396	2.83	1.0E-88	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
11730	23916	37541	3.35	1.0E-88	AA991479.1	EST_HUMAN	os91g03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
12665	25442		4.28	1.0E-88	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
13232	25800	31850	1.54	1.0E-88	AW451790.1	EST_HUMAN	UI-H-BI3-alk-b-03-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737084 3'
11194	24263	37898	8.14	9.0E-89	11421238	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA
2795	15910	29019	1.75	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
7072	20125	33541	1.14	8.0E-89	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
446	13642	26680	1.41	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
446	13642	26681	1.41	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5005	18134	31108	2.71	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5046	18174	31151	7.29	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E246 5'
5547	18744	31778	1.22	7.0E-89	X99832.1	NT	H.sapiens CLN3 gene, complete CDS
5547	18744	31779	1.22	7.0E-89	X99832.1	NT	H.sapiens CLN3 geno, complete CDS
6473	19640	33000	1.57	7.0E-89	7549808	NT	Homo sapiens plastin 3 (T isoform) (PLS3), mRNA
6473	19640	33001	1.57	7.0E-89	7549808	NT	Homo sapiens plastin 3 (T isoform) (PLS3), mRNA
7668	20734	34211	1.84	7.0E-89	11420754	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
8063	21145	34664	0.68	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8063	21145	34665	0.68	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA, complete cds
8674	21754	35289	0.53	7.0E-89	J02923.1	NT	Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds
10750	23783	37395	1.34	7.0E-89	X62048.1	NT	H.sapiens Wee1 hu gene
10750	23783	37396	1.34	7.0E-89	X62048.1	NT	H.sapiens Wee1 hu gene
10768	23801	37423	1.35	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10768	23801	37424	1.35	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
11515	24572	38260	2.66	7.0E-89	M59783.1	NT	Human aldose reductase (AR) gene, segment 2
1048	14214	27271	1.39	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2287	15419	28551	2.52	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2504	15631	28750	1.61	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2504	15631	28751	1.61	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
4759	17894	30873	3.79	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4759	17894	30874	3.79	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5295	18413	31379	0.81	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5295	18413	31380	0.81	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5186	18308	31273	3.36	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5186	18308	31274	3.36	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
7761	20820	34310	1.02	4.0E-89	BE762749.1	EST_HUMAN	EST388290 MAGE resequences, MAGN Homo sapiens cDNA clone IMAGE:1844915 3'
2941	16118	29131	1.83	3.0E-89	AW976181.1	EST_HUMAN	qh17b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2591485'
7290	20372	33828	1.3	3.0E-89	AI217359.1	EST_HUMAN	qh17b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2591485'
11039	24118	37751	2.29	3.0E-89	N57357.1	EST_HUMAN	yw86e11.r1 Soares_placenta_8to9weeks_2NbHPatog9W Homo sapiens cDNA clone IMAGE:259148 5'
12790	25916	31863	1.52	3.0E-89	AV708431.1	EST_HUMAN	similar to SW:P14K_HUMAN P42356 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA ;
12886	25587	31969	1.82	3.0E-89	AV705749.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
							AV705749 ADB Homo sapiens cDNA clone ADBBGA01 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
129	13616	26656	0.73	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
129	13616	26657	0.73	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26656	0.89	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26657	0.89	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
543	13736	26760	0.63	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2945	16122	29135	1.53	2.0E-89	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
4263	17408	30394	1.18	2.0E-89	AF089897.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4269	17414	30402	5.14	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4269	17414	30403	5.14	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4469	17609	30587	1.13	2.0E-89	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4619	17756	30738	1	2.0E-89	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5459	18659		1.39	2.0E-89	BE541744.1	EST_HUMAN	601065996F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5598	18793	31842	3.55	2.0E-89	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
5909	19098	32412	1.5	2.0E-89	U03985.1	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
6339	19509	32865	0.79	2.0E-89	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7847	20902	34405	5.28	2.0E-89	U81004.1	NT	Human GT24 (GT24) mRNA, partial cds
8119	21201	34722	3.11	2.0E-89	11428801	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8612	21692	35229	0.9	2.0E-89	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
9453	22569	36136	0.72	2.0E-89	AB037754.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
10015	23053	36647	1.22	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
10015	23053	36648	1.22	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
11655	24734	38425	2.63	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11871	24859	38554	3.52	2.0E-89	11433673	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
12017	25001	38703	1.64	2.0E-89	U10692.1	NT	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds
12877	25584		4.25	2.0E-89	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
11877	24865	38561	6.88	1.0E-89	BF196052.1	EST_HUMAN	hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;
11877	24885	38562	6.88	1.0E-89	BF196052.1	EST_HUMAN	hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8422	21503	35035	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8422	21503	35036	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1088	14254	27309	4.38	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1089	14254	27309	2.91	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1361	16035	27591	3.26	8.0E-90	BE670561.1	EST_HUMAN	7e36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1361	16035	27592	3.26	8.0E-90	BE670561.1	EST_HUMAN	7e36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8757	21836	35377	0.6	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-120400-022-b08 HT0598 Homo sapiens cDNA
10939	24021	37654	1.38	8.0E-90	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
10939	24021	37655	1.38	8.0E-90	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
859	14036		6.81	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8619	21699		2.14	7.0E-90	AA782977.1	EST_HUMAN	al63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
9166	22244	35787	2.13	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
9166	22244	35788	2.13	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10220	23256	36844	0.46	7.0E-90	AW273794.1	EST_HUMAN	xv24a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814026 3'
10340	23375	36985	4.2	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10340	23375	36986	4.2	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10672	23705	37314	0.62	7.0E-90	BF526089.1	EST_HUMAN	602071208F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214257 5'
3136	16312	29324	1.16	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
3136	16312	29325	1.16	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
4342	17485	30467	11.21	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4342	17485	30468	11.21	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6105	19285	32618	2.84	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6105	19285	32619	2.84	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8522	21603	35140	4.01	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8522	21603	35141	4.01	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
159	13384		27.59	5.0E-90	AB035344.1	NT	Homo sapiens TCL6 gene, exon 1-10b
1219	14380	27439	6.22	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1864	15010	28116	1.07	5.0E-90	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
1864	15010	28117	1.07	5.0E-90	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
2622	15745	28859	2.37	5.0E-90	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
4662	17797	30784	4.51	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4683	17818	30806	0.78	5.0E-90	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5708	18901	32196	2.85	5.0E-90	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
5726	18919		0.72	5.0E-90	AF008915.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
5810	19000	32307	1.32	5.0E-90	AB015617.1	NT	Homo sapiens ELKS mRNA, complete cds
5886	18901	32196	1.88	5.0E-90	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
6869	20021	33430	0.95	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6869	20021	33431	0.95	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7364	20443	33905	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds
7364	20443	33906	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds
7736	20797	34286	7.98	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
8488	21569	35107	4.89	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
9882	22922	36506	1.17	5.0E-90	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10488	23523	37133	0.71	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10663	23697	37306	9.66	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10723	23756	37362	0.53	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10723	23756	37363	0.53	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
12948	25659		1.77	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13000	25649		4.54	5.0E-90	AI523366.1	EST_HUMAN	er78h05.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'
313	13529	26562	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
313	13529	26563	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1110	14275	27332	4.36	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1724	14874	27966	13.42	4.0E-90	X99033.1	NT	H.sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
2923	16101	29114	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2923	16101	29115	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Excn SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Datebase Source	Top Hit Descriptor
3088	16264	29281	0.93	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3088	16264	29282	0.93	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4779	17914	30900	3.63	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4919	18049	31037	2.1	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4939	18059	31047	1.91	4.0E-90	M95987.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 8
12885	16101	29114	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12885	16101	29115	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8036	21119	34638	0.91	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-any-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
8036	21119	34639	0.91	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-any-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11930	24916	38619	28.7	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
220	13442	26473	4.5	2.0E-90	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1200	14362	27421	6.48	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1200	14362	27422	6.48	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3948	17106	30103	2.95	2.0E-90	AI138213.1	EST_HUMAN	qc54c02.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1713410 3' similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3. ;
4811	17944	30930	1.05	2.0E-90	AB006627.1	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5029	18158	31135	10.16	2.0E-90	5729855	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5896	19084	32395	0.6	2.0E-90	11525901	NT	Homo sapiens RaP2 interacting protein 8 (RPIP8), mRNA
5896	19084	32396	0.6	2.0E-90	11525901	NT	Homo sapiens RaP2 interacting protein 8 (RPIP8), mRNA
5903	19092	32406	3.89	2.0E-90	AW672686.1	EST_HUMAN	ba49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to TR:O75208 O75208 HYPOTHETICAL 35.5 KD PROTEIN. ;
9993	23032	36623	0.99	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
9993	23032	36624	0.99	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10165	23202	36795	1.46	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
10165	23202	36796	1.46	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11758	23944	37571	3.06	2.0E-90	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
287	13505	26539	4.1	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
385	15983	26628	2.28	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
386	15983	26628	1.56	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
713	13895	26932	1.92	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
713	13895	26933	1.92	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
748	13929	26971	17.93	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
748	13929	26972	17.93	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1134	14299		2.25	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1334	14491	27560	3.46	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1334	14491	27561	3.46	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1701	14853		2.61	1.0E-90	BE379884.1	EST_HUMAN	601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511118 5'
1951	15094	28195	3.73	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
2915	16093	29106	6.46	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3954	17112	30112	0.59	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3954	17112	30113	0.59	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4543	17681	30663	1.68	1.0E-90	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5792	18983	32286	2.08	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5959	19145	32460	0.9	1.0E-90	11426910	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7220	20085	33500	0.73	1.0E-90	U91934.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7849	20904	34408	2.31	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
9021	22100	35640	3	1.0E-90	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9493	22550		0.92	1.0E-90	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9516	22581	36148	1.4	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9516	22581	36149	1.4	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
4313	17456	30444	8.29	8.0E-91	D12234.1	EST_HUMAN	HUM000S381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
8501	21582	35118	1.14	7.0E-91	11419234	NT	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA
10507	23542	37153	0.65	7.0E-91	AI904151.1	EST_HUMAN	CM-BT043-090299-075 BT043 Homo sapiens cDNA
3563	16728	29744	1.85	5.0E-91	AA702794.1	EST_HUMAN	zi90b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4639	17775	30755	1.14	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4639	17775	30756	1.14	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4930	18060	31042	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4930	18060	31043	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6750	19906	33300	1.25	5.0E-91	AI879995.1	EST_HUMAN	au49f09.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW:ASPG_FLAME Q47898 N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR ;
8400	21481	35009	1.33	5.0E-91	BF314682.1	EST_HUMAN	601901624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
8960	22039	35581	1.47	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8960	22039	35582	1.47	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
12971	25631		1.61	5.0E-91	AI193566.1	EST_HUMAN	qe70f11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains MIR.b2 MIR MIR repetitive element ;
3272	16446	29465	1.58	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3272	16446	29466	1.58	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
11171	24242	37875	3.22	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12376	25267	32074	3.27	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12376	25267	32119	3.27	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12685	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12685	25457	32020	1.16	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
1647	14800	27885	2.17	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1647	14800	27886	2.17	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1832	15993	28077	1.1	3.0E-91	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
3420	16589	29605	1.29	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3551	16716	29729	4.85	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3551	16716	29730	4.85	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3888	17047	30047	0.93	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4714	17849	30832	4.41	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5094	18222	31193	1.48	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5094	18222	31194	1.48	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5803	18993	32296	3.55	3.0E-91	11434964	NT	Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA
6434	19602		2.56	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6713	19871	33262	2.98	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6713	19871	33263	2.98	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7816	20871	34368	4.48	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7816	20871	34369	4.48	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8132	21214	34735	0.69	3.0E-91	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8970	22049	35592	2.73	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9488	22545	36108	0.73	3.0E-91	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11480	24539	38207	1.49	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11480	24539	38208	1.49	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
13037	18486	31430	8.54	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
13037	18485	31431	8.54	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
49	13288	26300	2.94	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1274	14431	27502	2.74	1.0E-91	AW449746.1	EST_HUMAN	UI-H-BI3-aks-d-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
5529	18726	31742	0.78	1.0E-91	11434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
6983	20211	33640	1.96	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
6983	20211	33641	1.96	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
12130	25110	38814	1.48	1.0E-91	AV763053.1	EST_HUMAN	AV763053 MDS Homo sapiens cDNA clone MDSBEC05 5'
12540	26114		1.5	1.0E-91	H15212.1	EST_HUMAN	ym30e03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:49587 5'
1270	14428	27496	5.77	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1270	14428	27497	5.77	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5309	18426	31396	0.66	9.0E-92	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5579	18774	31820	5.86	9.0E-92	J03007.1	NT	Human Na+,K+ ATPase alpha-subunit mRNA, partial cds
5722	18915	32210	2.62	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
6583	19745	33127	3.77	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
8041	21124	34644	0.55	9.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8041	21124	34645	0.55	9.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8569	21650	35191	1.53	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8569	21650	35192	1.53	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9474	22531	36095	1.83	9.0E-92	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
95	13330	26357	6.63	8.0E-92	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
296	13513	26547	3.09	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
1866	15012	28119	1.43	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
1866	15012	28120	1.43	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
5508	18707	31722	0.68	8.0E-92	AB046820.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds
5615	18809	31877	0.8	8.0E-92	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6677	19836	33225	1.28	8.0E-92	AJ000979.1	NT	Homo sapiens MCP-4 gene
6680	19839	33228	0.91	8.0E-92	AF179428.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
8283	21365		0.55	8.0E-92	11416961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8620	21700	35235	5.05	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8620	21700	35236	5.05	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8721	21801	35337	0.71	8.0E-92	11426569	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
9262	22339	35889	2.53	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10232	23267	36857	0.91	8.0E-92	Y13629.1	NT	Homo sapiens mRNA for MBNL protein
11043	24121	37755	2.86	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11642	24722	38415	1.93	8.0E-92	4503340	NT	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
12740	25491	32028	1.59	8.0E-92	11434704	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
68	13305	26328	1.91	7.0E-92	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
246	16008	26498	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
246	16008	26499	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
604	13793		1.68	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds
1309	14465	27533	1.94	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2260	15393	28519	3.85	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2260	15393	28520	3.85	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2630	15753	28868	6.13	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2787	15903	29010	5.84	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
3426	18466	29609	0.7	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3426	18466	29610	0.7	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4710	17845	30828	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4710	17845	30829	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
5284	18403	31371	0.98	7.0E-92	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5375	18578	31446	5.51	7.0E-92	AA446206.1	EST_HUMAN	zw66d12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'
2178	15313	28441	0.96	3.0E-92	11434814	NT	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), mRNA
2178	15313	28442	0.96	3.0E-92	11434814	NT	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), mRNA
2824	15938	29048	2.74	3.0E-92	BE909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
5997	19182	32504	3.96	3.0E-92	AA378336.1	EST_HUMAN	EST91020 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to ribosomal protein S13
11002	24081	37716	3.26	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
11002	24081	37717	3.26	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin

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12878	26198		1.67	3.0E-92	BF367138.1	EST_HUMAN	RC1-GN0021-240800-012-e11 GN0021 Homo sapiens cDNA
26	13264	26266	1.54	2.0E-92	4501898	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
183	13405	26433	4.28	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA
183	13405	26434	4.28	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA
768	13949	26997	5.49	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
768	13949	26998	5.49	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1752	14901	.	1.62	2.0E-92	S78653.1	NT	mrg=mas-related [human, Genomic, 2416 nt]
1990	15132	28236	2.53	2.0E-92	AI818119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1990	15132	28237	2.53	2.0E-92	AI818119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2020	15161	28265	1.01	2.0E-92	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2020	15161	28266	1.01	2.0E-92	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2106	15245	28366	5.35	2.0E-92	4506860	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
2725	15843	28954	22.36	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3701	16862	29864	1.02	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3701	16862	29865	1.02	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3777	16938	29944	7.02	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4403	17546	30530	1.17	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5108	18236		4.1	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0414 5'
5879	19069	32377	0.64	2.0E-92	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6431	19599		7.19	2.0E-92	4504756	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
6748	19904	33297	2.6	2.0E-92	AB028991.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7627	20697		0.61	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7657	20697		0.64	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
9056	22135	35680	1.26	2.0E-92	AW340174.1	EST_HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
10997	24076	37709	4.68	2.0E-92	11434900	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
11257	24326	37965	3.22	2.0E-92	11434759	NT	Homo sapiens zinc finger protein 198 (ZNF198), mRNA
11409	24470	38134	5.71	2.0E-92	AW836290.1	EST_HUMAN	CM4-LT0026-161299-062-g06 LT0026 Homo sapiens cDNA
11409	24470	38135	5.71	2.0E-92	AW836290.1	EST_HUMAN	CM4-LT0026-161299-062-g06 LT0026 Homo sapiens cDNA
12758	25502	32035	8.46	2.0E-92	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12782	25524	32005	1.36	2.0E-92	AF106556.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
13066	15843	28954	73.58	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1897	15040	28150	2.95	1.0E-92	R78078.1	EST_HUMAN	yi80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1897	15040	28151	2.95	1.0E-92	R78078.1	EST_HUMAN	yi80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2135	15271	28392	35.12	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8441	21522	35051	0.82	1.0E-92	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
9365	22440	35999	3.24	1.0E-92	AI380356.1	EST_HUMAN	tg01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element ;
9365	22440	36000	3.24	1.0E-92	AI380356.1	EST_HUMAN	tg01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element ;
2085	15225	28347	3.53	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2100	15240		20.41	9.0E-93	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2712	15830		1.69	9.0E-93	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3703	16864	29867	1.35	9.0E-93	BE388671.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
11947	24933		7.79	9.0E-93	11418526	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
6723	19880	33271	2.4	8.0E-93	BF036364.1	EST_HUMAN	Homo sapiens NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
256	13475	26506	7.25	7.0E-93	AF231918.1	NT	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
3144	16320	29332	0.74	6.0E-93	11526176	NT	Homo sapiens chromosome 21 unknown mRNA
6819	19972	33380	0.97	6.0E-93	AB033093.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
7056	20109	33525	7.64	6.0E-93	AF095771.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
1412	14566	27640	0.99	5.0E-93	AB014511.1	NT	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds
1439	14592	27666	4.61	5.0E-93	AI674184.1	EST_HUMAN	Homo sapiens mRNA for KIAA0611 protein, partial cds
1439	14592	27667	4.61	5.0E-93	AI674184.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2314670 3'
1504	14657		4.17	5.0E-93	AL163201.2	NT	wc09c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'
1869	16049	28123	1.03	5.0E-93	AJ297710.1	NT	Homo sapiens chromosome 21 segment HS21C001
3305	16479	29500	3.73	5.0E-93	X04201.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 2
5920	19107	32420	1.09	5.0E-93	M22878.1	NT	Homo sapiens mRNA for tropomyosin
6235	19410		1.75	5.0E-93	AF045555.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
							Human somatic cytochrome c (HC1) processed pseudogene, complete cds
							Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and
							replication factor C subunit 2 (RFC2) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7892	20944	34450	3.52	5.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8804	21883	35422	0.73	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8804	21883	35423	0.73	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9822	22862	36443	2.02	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10012	23050	36644	1.35	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
10275	23310	36906	1.78	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
11064	24140	37775	1.92	5.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12651	25791	31921	2.31	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
90	13325		5.63	4.0E-93	AA459933.1	EST_HUMAN	zx50e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM ;
458	13653	26690	2.38	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
458	13653	26691	2.38	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
793	13972	27024	1.16	4.0E-93	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
793	13972	27025	1.16	4.0E-93	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
1210	14371	27431	2.12	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
2033	15174	28284	4.37	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2318	15450	28582	1.19	4.0E-93	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2672	15792	28909	1.16	4.0E-93	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3656	16819	29831	0.73	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4159	17310	30306	1.51	4.0E-93	4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5136	16819	29831	0.75	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5760	18952	32255	5.01	4.0E-93	T46864.1	EST_HUMAN	yb94c12.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN ,
11398	24459	38123	10.47	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKC Homo sapiens cDNA clone GKCDRF07 5'
3742	16903	29906	12.26	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3742	16903	29907	12.26	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4350	17493		2.6	3.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
6693	19851	33242	1.31	3.0E-93	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
11040	24119	37752	2.86	3.0E-93	AI824829.1	EST_HUMAN	wb02d05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304489 3'
195	13418	26447	5.59	2.0E-93	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
195	13418	26448	5.59	2.0E-93	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
333	13547	26578	13.77	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
334	13547	26578	6.74	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1646	14799	27884	3.9	2.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
2199	15334	28461	2.23	2.0E-93	U40763.1	NT	Human Clk-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2555	15680	28805	1.02	2.0E-93	BE252982.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5254	18374	31340	1.19	2.0E-93	BE253201.1	EST_HUMAN	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
5533	18730	31746	5.08	2.0E-93	AW964386.1	EST_HUMAN	EST376458 MAGE resequences, MAGH Homo sapiens cDNA
5544	18741	31775	0.7	2.0E-93	4758153	NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5660	18854		0.64	2.0E-93	BF351459.1	EST_HUMAN	QV3-HT0513-290300-126-h04 HT0513 Homo sapiens cDNA
5754	18946	32248	1.08	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
5768	18960	32261	0.76	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-86
6822	19975		1.2	2.0E-93	AW502002.1	EST_HUMAN	UI-HF-BN0-aks-g-09-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
11333	24396	38044	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
11333	24396	38045	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
12525	25358		1.78	2.0E-93	AA126735.1	EST_HUMAN	zl29c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3'
12624	25420		3.25	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12930	25613		5.34	2.0E-93	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
105	13341	26368	1.38	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
105	13341	26369	1.38	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
531	13724	26750	7.76	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
613	13802	26822	3.32	1.0E-93	AI146755.1	EST_HUMAN	oy84b08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384 ZINC FINGER PROTEIN. ;
895	14071	27136	3.43	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1194	14356	27414	0.6	1.0E-93	4503872	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD67, mRNA
1265	14422	27487	7.22	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1265	14422	27488	7.22	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1376	14531	27604	9.7	1.0E-93	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2414	15544	28672	1.08	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2534	15659	28783	3.06	1.0E-93	AF055066.1	NT	Homo sapiens MHC class 1 region
2576	15702		1.29	1.0E-93	AL137200.1	NT	Novel human gene mapping to chomosome 1
2883	14480	27546	1.32	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2883	14480	27547	1.32	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3000	16176	29197	5.86	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3287	16461		1.23	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4549	17687	30668	3.28	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5348	18461	31426	0.92	1.0E-93	AF123498.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
5348	18461	31427	0.92	1.0E-93	AF123498.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
5684	18878	32167	2.39	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5684	18878	32168	2.39	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5885	19074	32383	1.2	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6037	19220	32543	10.78	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6326	19498	32855	4.8	1.0E-93	7662241	NT	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA
6931	20246	33679	1.94	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7400	20478	33946	3.24	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
8455	21536	35066	2.29	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8740	21819	35353	1.15	1.0E-93	Y10183.1	NT	H.sapiens mRNA for MEMD protein
8850	21929	35468	1.14	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9651	21094	34608	2.03	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9655	21098	34612	1.14	1.0E-93	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9787	22827	36403	3.9	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9787	22827	36404	3.9	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9926	22966	36555	1.24	1.0E-93	AL049801.1	NT	Novel human gene mapping to chomosome 13, similar to rat RhoGAP
10349	23384	36994	0.59	1.0E-93	11433646	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
12820	25547		1.62	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12923	25608		3.71	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
13108	25723	31941	1.36	1.0E-93	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13123	26173		1.42	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10819	23852		1.13	8.0E-94	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4070	17226	30233	1.94	8.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
5483	18682	31698	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5483	18682	31699	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6173	19349	32695	2.24	5.0E-94	AA722434.1	EST_HUMAN	zg87g06.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409594 3'
7150	20285	33726	1.45	5.0E-94	AI015800.1	EST_HUMAN	ot83d05.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'

WO 01/57272 PCT/US01/00663

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8840	21919	35457	0.85	5.0E-94	BF529115.1	EST_HUMAN	602042163F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180023 5'
11215	24284	37922	1.43	5.0E-94	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
11215	24284	37923	1.43	5.0E-94	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
12503	26177	31558	3.6	5.0E-94	T89398.1	EST_HUMAN	yd98b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:116239 3'
1890	15034		16.49	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2723	15841	28952	0.99	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3762	16923	29925	1.12	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3762	16923	29926	1.12	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4840	17973	30983	3.06	4.0E-94	AI591312.1	EST_HUMAN	tw11f10.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE ;
6597	19757	33144	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6597	19757	33145	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7052	20105		0.9	4.0E-94	L27386.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
626	13811	26833	1.76	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
739	13921	26961	1.13	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1779	14928	28021	12.9	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1779	14928	28022	12.9	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1813	14962	28055	3.18	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4306	17449	30435	0.67	3.0E-94	AA464605.1	EST_HUMAN	zw63g08.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
4437	17577	30567	0.72	3.0E-94	AA781836.1	EST_HUMAN	ai59h06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375163 3'
5798	18988	32292	3.21	3.0E-94	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6279	19453	32801	1.13	3.0E-94	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6581	19743	33125	3.84	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
7978	21027	34541	0.63	3.0E-94	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8393	21474	35001	0.96	3.0E-94	AF152309.1	NT	Homo sapiens protocedherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8787	21866	35408	4.41	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
9791	22831	36410	7.29	3.0E-94	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
11362	24423	38079	1.94	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
11976	24960	38662	2.11	3.0E-94	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
9954	22993	36587	0.67	2.0E-94	AI910393.1	EST_HUMAN	wi30h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
9954	22993	36588	0.67	2.0E-94	AI910393.1	EST_HUMAN	wi30h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
153	13378	26410	3.07	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3158	16333	29342	2.05	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3158	16333	29343	2.05	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4478	17618	30600	1.11	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
6198	19373	32724	0.69	1.0E-94	AE000269.1	NT	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6396	19565	32925	1.91	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G0314 5'
6405	19574	32936	0.82	1.0E-94	H08270.1	EST_HUMAN	yi87f02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:45053 5'
6648	19807	33194	0.66	1.0E-94	AV725992.1	EST_HUMAN	AV725992 HTC Homo sapiens cDNA clone HTCBEF05 5'
8304	21386	34908	0.8	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8304	21386	34909	0.8	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9456	22572	36138	2.17	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
9990	23029	36620	1.35	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872099 5'
11321	24384	38028	3.11	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11597	24650	38334	1.88	1.0E-94	AI272244.1	EST_HUMAN	ap22e02.x1 Schiller oligoden:droglioma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR:Q62845 Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. ;
12051	25032	38738	1.34	1.0E-94	11418871	NT	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
12639	13378	26410	2.02	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
12968	13378	26410	1.73	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1506	14659	27741	6.05	9.0E-95	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3224	16398	29409	1.09	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3224	16398	29410	1.09	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5521	18718	31733	1.46	9.0E-95	X82569.1	NT	M.musculus glyT1 gene (exons 1c and 2)
5521	18718	31734	1.46	9.0E-95	X82569.1	NT	M.musculus glyT1 gene (exons 1c and 2)
8446	21527	35054	1.58	9.0E-95	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
149	13374	26407	2.9	8.0E-95	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
4658	17794	30779	1.68	8.0E-95	AI700998.1	EST_HUMAN	we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
4658	17794	30780	1.68	8.0E-95	AI700998.1	EST_HUMAN	we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
7087	20181	33605	0.73	8.0E-95	11419376	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
7390	20468	33934	1.4	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
7390	20468	33935	1.4	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8391	21472	34998	2.08	8.0E-95	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
9565	22707	36273	1.98	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9565	22707	36274	1.98	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10053	23091	36693	2.45	8.0E-95	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
10083	23121		2.92	8.0E-95	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10440	23475	37079	0.81	8.0E-95	9845523	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
10953	24035	37670	1.59	8.0E-95	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
11773	24765	38461	1.72	8.0E-95	10864024	NT	Homo sapiens HCF-binding transcription factor Zhangfel (ZF), mRNA
11982	24967	38669	1.32	8.0E-95	7019572	NT	Homo sapiens zinedin (ZIN), mRNA
11982	24967	38670	1.32	8.0E-95	7019572	NT	Homo sapiens zinedin (ZIN), mRNA
12887	25588		17.21	8.0E-95	AA629056.1	EST_HUMAN	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.t1 L1 repetitive element ;
286	13504	26537	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
286	13504	26538	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2519	15645	28767	1.37	7.0E-95	M75973.1	NT	Human hepatocyte growth factor gene, exon 8
2519	15645	28768	1.37	7.0E-95	M75973.1	NT	Human hepatocyte growth factor gene, exon 8
4486	17626	30608	15.92	7.0E-95	M95708.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4535	17673		1.09	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9418	22492	36058	0.62	4.0E-95	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
215	13438	26468	0.82	3.0E-95	AV648361.1	EST_HUMAN	AV648361 GLC Homo sapiens cDNA clone GLCBIF01 3'
5558	18756	31794	1.52	3.0E-95	BF526041.1	EST_HUMAN	602071146F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214147 5'
5791	25811	32285	0.94	3.0E-95	4503354	NT	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA
7315	20397	33859	0.73	3.0E-95	AA412321.1	EST_HUMAN	zt97d01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7315	20397	33860	0.73	3.0E-95	AA412321.1	EST_HUMAN	zt97d01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7525	20598	34071	2.01	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGE resequences, MAGE Homo sapiens cDNA
7525	20598	34072	2.01	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGE resequences, MAGE Homo sapiens cDNA
9555	22620	36190	1.62	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9555	22620	36191	1.62	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9948	22987	36581	0.86	3.0E-95	BF213446.1	EST_HUMAN	601845212F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070451 5'
1676	14828	27911	3.52	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1676	14828	27912	3.52	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1995	15136	28242	73.27	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1998	15139	28246	3.97	2.0E-95	BE393873.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2497	15624	28743	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2497	15624	28744	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2536	15661	28784	3.62	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2582	15707	28826	1.34	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2662	15784		0.99	2.0E-95	R16245.1	EST_HUMAN	ya49d08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53393 3'
3226	16400	29412	2.1	2.0E-95	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3655	16818	29829	3.6	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3655	16818	29830	3.6	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3706	16867	29870	0.81	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3844	17004	30006	0.62	2.0E-95	AI290264.1	EST_HUMAN	qm01c02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705 ;
4481	17621	30602	1.36	2.0E-95	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
5151	18273	31242	3.5	2.0E-95	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5230	18352	31321	0.99	2.0E-95	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5597	18792	31840	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5597	18792	31841	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5815	19005	32310	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5815	19005	32311	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5855	19045	32352	0.63	2.0E-95	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6270	19444	32793	3.86	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6579	19741	33122	0.9	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6579	19741	33123	0.9	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6700	19858	33248	3.25	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6903	20218	33647	1.47	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9343	22419	35973	1.48	2.0E-95	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10592	23627	37236	0.56	2.0E-95	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10962	24043	37678	1.98	2.0E-95	4757853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPR1A) mRNA
11138	24210	37836	1.35	2.0E-95	7661993	NT	Homo sapiens Ste20-related serine/threonine kinase (KIAA0204), mRNA
12002	24987	38691	1.69	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12002	24987	38692	1.69	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12103	25083		1.57	2.0E-95	AF161420.1	NT	Homo sapiens HSPC302 mRNA, partial cds
12608	25407	32047	2.31	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
			1.3	2.0E-95	11417860	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
12721	25480		7.4	2.0E-95	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
13067	25698	31966					zf23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6 ;
5732	18925	32219	8.06	1.0E-95	AA284651.1	EST_HUMAN	zf23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6 ;
5732	18925	32220	8.06	1.0E-95	AA284651.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
7683	20748	34229	4.11	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3922423 5'
7683	20748	34230	4.11	1.0E-95	BF370000.1	EST_HUMAN	yg09b06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:3899761 5'
9663	22625	36197	0.45	1.0E-95	R17806.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3899761 5'
8388	21469	34996	1.56	9.0E-96	BE897259.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
455	16012	26687	0.88	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA
455	16012	26688	0.88	8.0E-96	BE907607.1	EST_HUMAN	PM0-LT0019-090300-002-d09 LT0019 Homo sapiens mRNA
5628	18822		2.8	8.0E-96	AW836047.1	NT	Homo sapiens chromosome 21 unknown mRNA
4018	17175	30183	1.25	7.0E-96	AF231920.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
2334	15465	28600	2.48	6.0E-96	BE171984.1	NT	MR0-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
3394	16564	29579	0.71	6.0E-96	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3571	16736	29751	10.25	6.0E-96	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
11839	24828	38517	2.41	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11839	24828	38518	2.41	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11891	24879	38576	1.94	6.0E-96	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
12064	25045	38753	1.32	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12064	25045	38754	1.32	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
330	13544	26574	3.55	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
865	14041	27104	3.4	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
865	14041	27105	3.4	5.0E-96	AB032998.1	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2684	15804		1.72	5.0E-96	11416767	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3092	16268	29284	0.71	5.0E-96	6912735	NT	Homo sapiens mRNA for monoamine oxidase type A (7) (partial)
5024	18153		1.69	5.0E-96	X60812.1	NT	H.sapiens DNA for monoamine oxidase type A (7) (partial) cds
5296	18414	31381	0.79	5.0E-96	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
6788	19943	33341	1.1	5.0E-96	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6851	20004	33413	0.58	5.0E-96	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
6921	20236	33669	3.68	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6921	20236	33670	3.68	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA

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7163	20296	33740	0.91	5.0E-96	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7684	20749	34231	0.76	5.0E-96	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8297	21379	34900	1.87	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8297	21379	34901	1.87	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
12083	25063	38769	1.33	5.0E-96	7661973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4308	17451		15.95	3.0E-96	H68656.1	EST_HUMAN	yr87h12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5'
428	13623		5.76	2.0E-96	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
766	13947	26994	1.1	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1834	14981	28079	1.03	2.0E-96	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
4880	18011	30995	1.56	2.0E-96	BE148074.1	EST_HUMAN	RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
7620	20690	34165	0.59	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
7620	20690	34166	0.59	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
9181	22259		4.9	2.0E-96	AV689461.1	EST_HUMAN	AV689461 GKC Homo sapiens cDNA clone GKCFMD07 5'
12288	25214		2.54	2.0E-96	AW249440.1	EST_HUMAN	2819351.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819351 5'
638	13823	26845	0.86	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
638	13823	26846	0.86	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
688	13872	26905	3.08	1.0E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1822	14971	28063	9.97	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
1822	14971	28064	9.97	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
5331	18444		1.59	1.0E-96	5453913	NT	Homo sapiens phospholipid transfer protein (PLTP) mRNA
7105	18532	31487	1.19	1.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7194	20059	33470	0.71	1.0E-96	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8407	21488	35017	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8407	21488	35018	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8913	21992	35531	21.44	1.0E-96	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
9051	22130	35674	2.22	1.0E-96	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10362	23397	37007	0.68	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
10362	23397	37008	0.68	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
12274	13823	26845	3.29	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
12274	13823	26846	3.29	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3405	16575	29590	0.72	6.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
7730	20792		3.4	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9134	22213	35757	0.75	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
9134	22213	35758	0.75	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
10821	23854	37475	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
10821	23854	37476	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
11692	24690	38381	2.42	6.0E-97	X15804.1	NT	Human mRNA for alpha-actinin
8204	21286	34809	1.73	5.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
8336	21417	34943	11.21	5.0E-97	AA418026.1	EST_HUMAN	zv97e12.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125 G1304125 PMS4 MRNA ;
9877	22917	36502	3.12	5.0E-97	BF154912.1	EST_HUMAN	RC0-BT0812-250900-032-e09 BT0812 Homo sapiens cDNA
11840	24829	38519	1.68	5.0E-97	BE148597.1	EST_HUMAN	MR0-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
11840	24829	38520	1.68	5.0E-97	BE148597.1	EST_HUMAN	MR0-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
962	14135	27196	2.13	4.0E-97	BE004436.1	EST_HUMAN	CM0-BN0106-170300-293-a06 BN0106 Homo sapiens cDNA
1959	15102	28202	1.41	4.0E-97	5463672	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
5683	18877	32166	0.92	4.0E-97	4557326	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
6962	20190	33615	6.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
6962	20190	33616	6.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
7161	20294	33737	1.09	4.0E-97	7710125	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
7214	20079	33492	0.92	4.0E-97	11422155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8329	21411	34937	1.06	4.0E-97	4557708	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8553	21634	35171	1.43	4.0E-97	11421793	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
8779	21858	35401	0.51	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
8820	21899	35438	0.82	4.0E-97	11423233	NT	Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA
9449	22565	36128	1.06	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9449	22565	36129	1.06	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10652	23686	37296	0.55	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
11435	24496	38162	1.99	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11435	24496	38163	1.99	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11719	23905	37528	4.51	4.0E-97	AB042557.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
12472	25325		5.26	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
253	13473	26504	1.58	3.0E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
897	14073	27138	7.16	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
897	14073	27139	7.16	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1473	16039	27712	1.94	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2508	15998	28755	2.4	3.0E-97	U36255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3333	16506	29523	0.96	3.0E-97	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
4902	18032	31021	22.23	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6557	19719	33095	2.72	1.0E-97	BE566486.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5'
7039	20092	33509	0.69	1.0E-97	5453881	NT	Homo sapiens phosphorylase kinase, gamma 1 (muscle) (PHKG1) mRNA
9966	23005	36600	1.02	1.0E-97	R10887.1	EST_HUMAN	yf38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
10945	24027	37663	2.84	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
10945	24027	37684	2.84	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11589	24642	38324	1.38	1.0E-97	AA553761.1	EST_HUMAN	nk29g02.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014962 3'
11756	23942	37568	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11756	23942	37569	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
924	14099	27163	2.34	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1305	14461	27528	1.32	9.0E-98	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6432	19600		0.79	9.0E-98	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
8020	21072	34583	4.13	9.0E-98	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8020	21072	34584	4.13	9.0E-98	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8109	21191	34711	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8109	21191	34712	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9316	22392	35943	1.78	9.0E-98	X06989.1	NT	Human mRNA for amyloid A4(751) protein
9425	22499	36064	1.12	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9492	22549	36112	1.6	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9540	22605		0.81	9.0E-98	AF057726.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9567	22709	36276	1.28	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9567	22709	36277	1.28	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10467	23502	37115	0.67	9.0E-98	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
10575	23610	37215	0.5	9.0E-98	11431544	NT	Homo sapiens protease-activated receptor 3 (PAR3), mRNA
11253	24322	37962	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11253	24322	37963	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12487	14099	27163	4.97	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1403	14557	27631	0.93	8.0E-98	AB033768.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
1591	14743	27825	1.1	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1591	14743	27826	1.1	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1765	14914	28009	2.79	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1765	14914	28010	2.79	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3896	17055	30055	6.45	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
6207	19382	32732	0.96	5.0E-98	BE885873.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909097 5'
2247	15380	28508	1.35	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone I8
2673	15793	28910	2.1	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2807	15921		5.04	3.0E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7085	20179	33602	1.99	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7085	20179	33603	1.99	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
8951	22030	35571	4.07	3.0E-98	H46698.1	EST_HUMAN	yo17g09.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178240 5'
9497	22553	36116	0.54	3.0E-98	8922096	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
10087	23125	36726	1.82	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone I8
10087	23125	36727	1.82	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone I8
10691	23724	37330	0.89	3.0E-98	BE900454.1	EST_HUMAN	601673686F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
11195	24264	37899	2.56	3.0E-98	U59309.1	NT	Human fumarase precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
11819	24808	38504	2.22	3.0E-98	AI159975.1	EST_HUMAN	qb80h02.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706451 3'
13138	25739		3.01	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
754	13935	26980	0.67	2.0E-98	BE261694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2141	15277	28399	4.06	2.0E-98	BE294281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2311	15443	28578	2.21	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4411	17553	30538	0.82	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4459	17599	30577	4.23	2.0E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4948	18078	31052	1.39	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 16
4948	18078	31053	1.39	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 16
5492	18691	31708	4.76	2.0E-98	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor I (LOC51735), mRNA
6793	19948	33347	1.7	2.0E-98	4505798	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7801	20857	34348	1.25	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7801	20857	34349	1.25	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8807	21886	35426	4.44	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8807	21886	35427	4.44	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8889	21968	35503	0.8	2.0E-98	L76656.1	NT	Homo sapiens NKAT4b mRNA, complete cds
8889	21968	35504	0.8	2.0E-98	L76656.1	NT	Homo sapiens NKAT4b mRNA, complete cds
9737	22802	36376	1.56	2.0E-98	X12664.1	NT	H.sapiens arginase gene exon 3 (EC 3.5.3.1)
10624	23658		1.65	2.0E-98	7705868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
12136	25116		1.61	2.0E-98	AB046813.1	NT	Homo sapiens mRNA for KIAA1593 protein, partial cds
12492	25340	32062	2.23	2.0E-98	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
418	13613	26653	27.52	1.0E-98	AI862007.1	EST_HUMAN	tw36b04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ;
467	13662	26698	3.27	1.0E-98	AW998511.1	EST_HUMAN	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
1840	14986	28086	26.16	1.0E-98	N49818.1	EST_HUMAN	yv23f05.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human ;
5432	18632	31610	3.3	1.0E-98	AA195854.1	EST_HUMAN	zp98c09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562 G806562 NEBULIN. ;
5687	18881	32172	0.97	1.0E-98	BE390627.1	EST_HUMAN	601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
5687	18881	32173	0.97	1.0E-98	BE390627.1	EST_HUMAN	601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
9199	22277	35815	0.59	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
9199	22277	35816	0.59	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5939	19125	32438	1.05	9.0E-99	AI905004.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
5939	19125	32439	1.05	9.0E-99	AI905004.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
6165	19341	32588	4.01	9.0E-99	AW968635.1	EST_HUMAN	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
11384	24445	38105	1.85	9.0E-99	AI479829.1	EST_HUMAN	tm69h07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11384	24445	38106	1.85	9.0E-99	AI479829.1	EST_HUMAN	tm69h07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11700	24697	38389	1.72	9.0E-99	AA134604.1	EST_HUMAN	zn90d02.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to TR:G662994 G662994 GPI-ANCHORED PROTEIN P137. ;
8924	22003	35542	1.19	8.0E-99	9635487	NT	Human endogenous retrovirus, complete genome
5956	19142	32458	9.25	7.0E-99	AF035808.1	NT	Homo sapiens oscillin (hLn) gene, exon 5
11909	24896	38599	1.91	7.0E-99	AF001886.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
484	13678	26713	0.72	6.0E-99	U10991.1	NT	Human G2 protein mRNA, partial cds
2196	15331	28456	6.2	6.0E-99	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
2196	15331	28457	6.2	6.0E-99	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
3995	17152	30160	2.8	6.0E-99	AW976364.1	EST_HUMAN	EST388473 MAGE resequences, MAGN Homo sapiens cDNA
4870	18003	30988	1.42	6.0E-99	4502660	NT	Homo sapiens CD34 antigen (CD34) mRNA

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6732	19888	33280	0.94	6.0E-99	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
6816	19969	33376	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6816	19969	33377	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8296	21378	34899	1.85	6.0E-99	X99101.1	NT	H.sapiens mRNA for estrogen receptor
8314	21396	34921	0.59	6.0E-99	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8964	22043	35586	2.67	6.0E-99	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
9064	22143	35688	7.6	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
9064	22143	35689	7.6	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
9123	22202	35744	0.59	6.0E-99	11431994	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9123	22202	35745	0.59	6.0E-99	11431994	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
10958	24039	37674	3.15	6.0E-99	11526299	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
11742	23928	37553	2.02	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
11742	23928	37554	2.02	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
2022	15163	28268	1	5.0E-99	Y11365.1	NT	H.sapiens IMPA gene, exon 8
4686	17821	30809	1.81	5.0E-99	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12502	25346		2.49	5.0E-99	BE890177.1	EST_HUMAN	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
8516	21597		4.95	3.0E-99	M95586.1	NT	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds
1268	14426		7.26	2.0E-99	AW274792.1	EST_HUMAN	xp09e06.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3331	16504	29522	1.4	2.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4665	17800	30787	1.82	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7851	20906	34410	0.76	2.0E-99	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8904	21983	35523	10.79	2.0E-99	W23507.1	EST_HUMAN	zb46d06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
9353	22428	35986	0.75	2.0E-99	R78254.1	EST_HUMAN	yi81b09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145625 5'
11367	24428	38085	3.16	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
12081	25061	38767	1.64	2.0E-99	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
325	13539	26571	1.49	1.0E-99	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
390	13596	26632	1.75	1.0E-99	11526150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1452	14605	27684	3.61	1.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1587	14739	27819	1.16	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1587	14739	27820	1.16	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1980	15123	28224	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products

WO 01/57272 PCT/US01/00663

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1980	15123	28225	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3154	16329	29339	0.93	1.0E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4499	17639	30621	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4499	17639	30622	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6943	20256	33694	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6943	20256	33695	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7289	25842	33827	0.81	1.0E-99	X98022.1	NT	H.sapiens E6-AP gene exon 2
9400	22474		0.75	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
9720	22785	36356	1.7	1.0E-99	AW340174.1	EST_HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
11403	24464	38128	2.56	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11403	24464	38129	2.56	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11462	24521	38191	1.68	1.0E-99	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11659	24738	38429	2.83	1.0E-99	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11996	24981	38687	2.45	1.0E-99	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
12257	25193		4.52	1.0E-99	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	13241	26241	1.7	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	13241	26241	2.91	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
70	13307	26329	1.62	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
70	13307	26330	1.62	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
89	13324	26353	0.82	1.0E-100	AW275237.1	EST_HUMAN	xv78b11.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2824605 3'
173	13397	26425	0.89	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
327	13541	26573	1.84	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
353	13564	26592	1.87	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR32
450	13646		2.24	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
502	13697		5.88	1.0E-100	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
522	13715	26742	1.21	1.0E-100	BE180609.1	EST_HUMAN	RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cDNA
1044	14210	27266	4.57	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1044	14210	27267	4.57	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1577	14730		1.3	1.0E-100	AW207555.1	EST_HUMAN	UI-H-BI1-afk-c-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1581	14733	27814	1.66	1.0E-100	AI200857.1	EST_HUMAN	qf62f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA P81061 CYSTATIN ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2315	15447		1.14	1.0E-100	D83349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2507	15634	28754	1.41	1.0E-100	X62468.1	NT	H.sapiens mRNA for IFN-gamma (pKC-0)
2771	15886	28996	2.5	1.0E-100	11418976	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
3083	16259		6.55	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4326	17469	30456	1.67	1.0E-100	AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4351	17494	30474	2.28	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5202	18323	31291	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5202	18323	31292	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5404	18606	31578	1.74	1.0E-100	BF244218.1	EST_HUMAN	601863164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5'
5625	18819	31893	0.76	1.0E-100	AW075983.1	EST_HUMAN	xa82f01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN);
5818	19008	32314	1.45	1.0E-100	AU118182.1	EST_HUMAN	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5864	19054	32361	1.78	1.0E-100	AF135116.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
5960	19146	32461	0.85	1.0E-100	X14690.1	NT	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
6292	19465	32817	0.9	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6292	19465	32818	0.9	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6626	19786	33174	5.62	1.0E-100	AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6824	19977	33384	1.36	1.0E-100	R10887.1	EST_HUMAN	yf38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
6908	20223	33653	1.77	1.0E-100	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6982	20210	33638	1.02	1.0E-100	AA496841.1	EST_HUMAN	ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418 G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
6982	20210	33639	1.02	1.0E-100	AA496841.1	EST_HUMAN	ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418 G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
7026	20162	33583	1.18	1.0E-100	BF376478.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
7026	20162	33584	1.18	1.0E-100	BF376478.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
7033	20169	33591	6.2	1.0E-100	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
8729	21809	35345	3.53	1.0E-100	BF103853.1	EST_HUMAN	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
8766	21845		5.59	1.0E-100	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9216	22294	35837	0.47	1.0E-100	AU116951.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9216	22294	35838	0.47	1.0E-100	AU116951.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9433	22507	36073	3.88	1.0E-100	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9510	22776		1.65	1.0E-100	AI972388.1	EST_HUMAN	wr37g09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element MER22 repetitive element ;
9633	21076	34588	2.28	1.0E-100	AW998611.1	EST_HUMAN	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9687	22736		0.84	1.0E-100	AU127720.1	EST_HUMAN	AU127720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
9782	22822	36400	2.17	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
9782	22822	36401	2.17	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
10048	23086	36687	1.81	1.0E-100	AW630487.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
10048	23086	36688	1.81	1.0E-100	AW630487.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
10688	23721	37327	0.64	1.0E-100	BF347519.1	EST_HUMAN	602020554F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156165 5'
10782	23815		1.35	1.0E-100	Y10391.1	NT	Human endogenous retrovirus HERV-K, pol gene
10996	24075	37708	6.64	1.0E-100	BF327292.1	EST_HUMAN	MR0-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
11564	24619	38300	1.56	1.0E-100	X94633.1	NT	H.sapiens CD97 gene exon 4
11564	24619	38301	1.55	1.0E-100	X94633.1	NT	H.sapiens CD97 gene exon 4
11635	24715	38405	3.91	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11635	24715	38406	3.91	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11665	13241	26241	3.07	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11977	24962		2.21	1.0E-100	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
12128	25108	38812	1.93	1.0E-100	AJ131034.1	NT	Homo sapiens otase gene, exon 12
12177	25137	38832	7.59	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12312	26037		1.78	1.0E-100	BF446549.1	EST_HUMAN	7q86h03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to TR:Q21997 Q21997 COSMID R151. [2] TR:Q9UA08 ;
12493	25341	32063	4.97	1.0E-100	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12754	25500	32033	1.31	1.0E-100	11418123	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
13195	25778	31935	6.91	1.0E-100	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
79	13315	26342	0.92	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
79	13315	26343	0.92	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
704	13887	26919	1.4	1.0E-101	AB007915.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
722	13904	26945	6.12	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
722	13904	26946	6.12	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
792	13971	27023	1.37	1.0E-101	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
876	14052	27117	1.35	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) mRNA
948	14121	27182	0.85	1.0E-101	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
1009	14180	27243	6.07	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5'
1077	14243	27299	1.39	1.0E-101	AI221878.1	EST_HUMAN	qg99e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1614	14767	27849	1.44	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1614	14767	27850	1.44	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1785	14934	28028	1.57	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1785	14934	28029	1.57	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1999	15140	28247	2.07	1.0E-101	4502996	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2116	15254	28373	2.76	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160600-016-h09 ST0281 Homo sapiens cDNA
2425	16062	28680	1.2	1.0E-101	5729892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2680	15800	28917	4.62	1.0E-101	X72993.1	NT	H.sapiens EWS gene, exon 5
2802	15916	29025	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
2802	15916	29026	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3020	16196		20.16	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3273	16447	29467	2.97	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3313	16486		2.3	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3468	16635	29654	1.82	1.0E-101	AW965556.1	EST_HUMAN	EST377629 MAGE resequences, MAGI Homo sapiens cDNA
3487	15916	29025	3.59	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3487	15916	29026	3.59	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3981	17138	30142	3.81	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5147	18269	31239	1.14	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5147	18269	31240	1.14	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5248	18369	31336	0.6	1.0E-101	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
5248	18369	31337	0.6	1.0E-101	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
5433	18633	31611	1.94	1.0E-101	AW965139.1	EST_HUMAN	EST377212 MAGE resequences, MAGI Homo sapiens cDNA
6126	19305	32645	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6126	19305	32646	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6834	19987	33396	0.96	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7423	20500		1.26	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7473	20548	34019	4.22	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7473	20548	34020	4.22	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7645	20714	34192	7.65	1.0E-101	AW008475.1	EST_HUMAN	wv55f12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
7749	20809		1.99	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349901 5'
7900	20952	34459	6.54	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA
8097	21179	34696	0.74	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
8097	21179	34697	0.74	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
8245	21327	34843	1.6	1.0E-101	BF029174.1	EST_HUMAN	601764686F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8517	21598	35132	0.71	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8517	21598	35133	0.71	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
9212	22290	35832	1.1	1.0E-101	AA036800.1	EST_HUMAN	zk29g08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471998 5' similar to PIR:S54640 S54640 YD9335.03c protein - yeast ;
9531	22596	36167	0.99	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9531	22596	36168	0.99	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9661	21103	34619	17.36	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9661	21103	34620	17.36	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9676	22638	36209	19.41	1.0E-101	9845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
9959	22998	36593	3.36	1.0E-101	BE619667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9959	22998	36594	3.36	1.0E-101	BE619667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
10098	23136	36737	0.68	1.0E-101	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10620	23654	37284	1.94	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10656	23690	37299	4.37	1.0E-101	AI570293.1	EST_HUMAN	to77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10656	23690	37300	4.37	1.0E-101	AI570293.1	EST_HUMAN	to77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10771	23804	37426	0.83	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10771	23804	37427	0.83	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
11371	24432	38089	1.31	1.0E-101	AB020626.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
12059	25040	38748	1.85	1.0E-101	AI908168.1	EST_HUMAN	RC-BT163-290499-085 BT163 Homo sapiens cDNA
12059	25040	38749	1.85	1.0E-101	AI908168.1	EST_HUMAN	RC-BT163-290499-085 BT163 Homo sapiens cDNA
12738	25489		2.24	1.0E-101	BE163587.1	EST_HUMAN	QV3-HT0460-230200-101-d03 HT0460 Homo sapiens cDNA
12793	25529		12.79	1.0E-101	AW939051.1	EST_HUMAN	QV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
40	13278	26284	0.61	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pI4K230) mRNA, complete cds
351	13562	26589	4.57	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
635	13820	26844	0.61	1.0E-102	BE252470.1	EST_HUMAN	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
796	13975	27028	1.06	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1141	14306	27362	1.9	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1297	14453	27518	2.05	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1297	14453	27519	2.05	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1450	14603	27681	355.9	1.0E-102	BE408447.1	EST_HUMAN	601299982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2383	15514	28642	1.91	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
2383	16514	28643	1.91	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
3090	16266		0.74	1.0E-102	Y13932.1	NT	Homo sapiens PRKY exon 7
3133	16309	29322	1.47	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3203	16378	29387	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3203	16378	29388	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4347	17490	30472	1.74	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4533	17671	30655	2.57	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
5224	18346	31316	1.28	1.0E-102	R66488.1	EST_HUMAN	yi32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'
5487	18686	31704	1.6	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5887	19057		6.87	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5905	19094	32408	3.25	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5905	19094	32409	3.25	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5912	19100	32414	0.81	1.0E-102	11433046	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
6422	19591	32956	2.81	1.0E-102	AI459825.1	EST_HUMAN	ar82f09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52. ;
7227	20090	33507	0.7	1.0E-102	AW451643.1	EST_HUMAN	UI-H-BI3-alj-d-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736835 3'
7286	20369	33823	0.91	1.0E-102	BE729323.1	EST_HUMAN	601561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7314	20396	33858	1.02	1.0E-102	BE386106.1	EST_HUMAN	601277215F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618243 5'
7429	20506	33977	1.5	1.0E-102	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7510	20584	34057	8.03	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
7802	20858	34350	2.61	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5'
8418	21499	35031	3.85	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT0025-210600-236-h08 NT0025 Homo sapiens cDNA
8691	21771	35301	1.71	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'
8691	21771	35302	1.71	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'
8802	21881	35419	0.81	1.0E-102	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9131	22210	35754	1.2	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9131	22210	35755	1.2	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9481	22538	36102	0.84	1.0E-102	AV755842.1	EST_HUMAN	AV755842 BM Homo sapiens cDNA clone BMFAUD06 5'
9522	22587	36155	2	1.0E-102	T70393.1	EST_HUMAN	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
9522	22587	36156	2	1.0E-102	T70393.1	EST_HUMAN	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
9611	22666	36237	3.11	1.0E-102	AU124629.1	EST_HUMAN	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10593	23628		0.64	1.0E-102	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10647	23681	37291	0.67	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10647	23681	37292	0.67	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10687	23720	37325	3.26	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
10687	23720	37326	3.26	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
10748	23781	37394	1.5	1.0E-102	AA970786.1	EST_HUMAN	on57h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2. [1];
11323	24386	38030	1.37	1.0E-102	BE897468.1	EST_HUMAN	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5'
11327	24390	38035	2.44	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11327	24390	38036	2.44	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11600	24653	38337	1.47	1.0E-102	AA868675.1	EST_HUMAN	ak49h10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409347 3'
11690	24688	38378	2.47	1.0E-102	BF359243.1	EST_HUMAN	RC6-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA
12009	24994	38699	2.83	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
12182	25142		5.69	1.0E-102	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
12775	25517	32000	5.67	1.0E-102	AW300862.1	EST_HUMAN	xk07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'
12831	25553	32015	1.25	1.0E-102	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA
71	13308	26331	0.85	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
71	13308	26332	0.85	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
102	13338	26365	8.24	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
213	13436	26466	0.84	1.0E-103	5453793	NT	Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA
1004	14175	27234	74.34	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1272	14429	27500	7.08	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1626	14778	27863	3.51	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
1964	15107	28207	1.02	1.0E-103	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2031	15172	28280	0.95	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2031	15172	28281	0.95	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2379	15510	28638	1.95	1.0E-103	AU134991.1	EST_HUMAN	AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000965 5'
2523	15648	28772	1.84	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2685	15805	28921	1	1.0E-103	N32770.1	EST_HUMAN	yw91d08.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259599 3'
3137	16313		2.76	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3467	16634	29853	5.33	1.0E-103	AW298245.1	EST_HUMAN	UI-H-BW0-ajt-h-11-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'

WO 01/57272 PCT/US01/00663

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3526	16691	29700	0.95	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3850	17010		5.46	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3894	17053	30053	0.9	1.0E-103	AA485683.1	EST_HUMAN	ab10d12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element ;
3933	17092	30090	1.54	1.0E-103	11430876	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
4110	17264	30264	4.63	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
5325	18438		0.63	1.0E-103	AA451616.1	EST_HUMAN	zx43b04.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789199 5' similar to TR:G292352 G292352 COLLAGEN CHAIN RH ;
6056	19238	32563	0.9	1.0E-103	BF569527.1	EST_HUMAN	602186023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310573 5'
6063	19245	32571	1.67	1.0E-103	AF179995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6397	19566	32926	0.8	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6397	19566	32927	0.8	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6587	19748	33130	0.84	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGE resequences, MAGC Homo sapiens cDNA
6587	19748	33131	0.84	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGE resequences, MAGC Homo sapiens cDNA
6725	25831	33273	1.15	1.0E-103	AA781442.1	EST_HUMAN	aj26e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391452 3'
6768	19924	33318	0.91	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6859	20011	33422	1.66	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;
6859	20011	33423	1.66	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;
6987	18506	31521	1.77	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6987	18506	31522	1.77	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7108	18535	31490	1.04	1.0E-103	11431100	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7178	20310	33753	0.98	1.0E-103	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
7375	20454	33919	1.88	1.0E-103	AW965776.1	EST_HUMAN	EST377849 MAGE resequences, MAGI Homo sapiens cDNA
7488	20563	34032	3.6	1.0E-103	BE748158.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
7951	21001	34511	4	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;
7951	21001	34512	4	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8484	21565	35101	0.59	1.0E-103	T31080.1	EST_HUMAN	EST27193 Human Brain Homo sapiens cDNA 5' end similar to None
8822	21901	35440	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8822	21901	35441	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8900	21979	35518	1.34	1.0E-103	BF109244.1	EST_HUMAN	7l60e03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525964 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
9307	22383	35934	3.18	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9307	22383	35935	3.18	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9349	22425	35980	0.97	1.0E-103	AA581086.1	EST_HUMAN	nd13c02.s1 NCI_CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
10263	23298	36896	2.04	1.0E-103	Z37976.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10304	23339	36944	2.07	1.0E-103	AW963676.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
10443	23478	37083	10.79	1.0E-103	AI878956.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:O15046 O15046 KIAA0338 ;
10878	23963	37591	1.52	1.0E-103	BE549706.1	EST_HUMAN	7b41f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
10971	24051	37684	9.5	1.0E-103	AI792759.1	EST_HUMAN	ol02d06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
11072	24147	37785	2.45	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11072	24147	37786	2.45	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11083	24157	37794	2.4	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11083	24157	37795	2.4	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11656	24735	38426	2.67	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
11731	23917	37542	4.1	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11968	24953		1.71	1.0E-103	AB024759.1	NT	Homo sapiens TSA305 gene, exon 16
12044	25025	38730	2.26	1.0E-103	BE644611.1	EST_HUMAN	7e68a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.t3 MER29 repetitive element ;
12178	25138		3.4	1.0E-103	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12209	25162		1.22	1.0E-103	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12414	26293	32083	1.71	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
243	13465	26494	2.46	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
243	13465	26495	2.46	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1937	15080	28182	1.92	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2267	15400	28528	33.29	1.0E-104	AA132975.1	EST_HUMAN	zo22c06.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14116_rna1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2277	15409	28540	4.55	1.0E-104	BE744628.1	EST_HUMAN	601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2442	15570	28698	9.73	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2442	15570	28699	9.73	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2506	15633	28753	2	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2934	16111	29125	17.99	1.0E-104	M34671.1	NT	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds
2983	16159		2.15	1.0E-104	Y11151.1	NT	H.sapiens gene encoding phenylpyruvate tautomerase II
3337	16510	29526	0.99	1.0E-104	AU133926.1	EST_HUMAN	AU133926 OVARC1 Homo sapiens cDNA clone OVARC1000936 5'
3478	16645		2.33	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3690	16852	29860	0.65	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3690	16852	29861	0.65	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4053	17209	30219	0.71	1.0E-104	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4248	17394	30383	0.71	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4496	17636	30618	33.95	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4732	17867	30849	1.2	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4732	17867	30850	1.2	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
6061	19243	32567	1.05	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6061	19243	32568	1.05	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6108	19288	32623	0.93	1.0E-104	AB017332.1	NT	Homo sapiens alk3 mRNA for Aurora/Ipl1-related kinase 3, complete cds
6596	19756	33142	8.5	1.0E-104	AI768797.1	EST_HUMAN	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN. ;contains element LTR7 repetitive element ;
6596	19756	33143	8.5	1.0E-104	AI768797.1	EST_HUMAN	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN. ;contains element LTR7 repetitive element ;
6786	19941	33339	0.74	1.0E-104	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor I (LOC51735), mRNA
6942	20255	33692	3.39	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6942	20255	33693	3.39	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7373	20452	33917	2.01	1.0E-104	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8796	21875	35414	0.87	1.0E-104	BF509244.1	EST_HUMAN	UI-H-BI4-aow-b-09-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086176 3'
9368	22443	36004	2.41	1.0E-104	BF448230.1	EST_HUMAN	nad16g11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
9463	22520	36082	0.46	1.0E-104	AA682308.1	EST_HUMAN	zj98b05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9484	22541		1.03	1.0E-104	T74219.1	EST_HUMAN	yc83f02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22440 5'
9515	22580	36146	5	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9515	22580	36147	5	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9641	21084	34597	4.14	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9641	21084	34598	4.14	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9955	22994	36589	0.92	1.0E-104	AW103848.1	EST_HUMAN	xd76d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116 Q24116 HYPOTHETICAL 29.4 KD PROTEIN. ;
9955	22994	36590	0.92	1.0E-104	AW103848.1	EST_HUMAN	xd76d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116 Q24116 HYPOTHETICAL 29.4 KD PROTEIN. ;
10153	23190	36787	0.49	1.0E-104	AF113514.1	NT	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10298	23333	36937	3.15	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10298	23333	36938	3.15	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10611	23645	37253	1.49	1.0E-104	AV728070.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
10657	23691	37301	4.47	1.0E-104	AU130765.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
10757	23790	37407	0.54	1.0E-104	AA931321.1	EST_HUMAN	oo06a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1565370 3'
10757	23790	37408	0.54	1.0E-104	AA931321.1	EST_HUMAN	oo06a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1565370 3'
10774	23807	37430	5.4	1.0E-104	U66535.1	NT	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
10791	23824		0.74	1.0E-104	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11577	24632	38310	44.86	1.0E-104	BE720191.1	EST_HUMAN	RC0-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11577	24632	38311	44.86	1.0E-104	BE720191.1	EST_HUMAN	RC0-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11611	24663	38350	4.1	1.0E-104	BF684288.1	EST_HUMAN	602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
12082	25062	38768	46.12	1.0E-104	11434729	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5), mRNA
13073	25702		1.32	1.0E-104	BE393892.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658676 5'
289	15981	26541	2.57	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
438	13238	26238	6.69	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
607	13796	26815	2.51	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
607	13796	26816	2.51	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1865	15011	28118	10.24	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1979	15122	28223	2.39	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2263	15398	28524	3.06	1.0E-105	AA318369.1	EST_HUMAN	EST20609 Spleen I Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit
2398	15529		1.18	1.0E-105	BE891766.1	EST_HUMAN	601434491F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919511 5'
2784	15900		0.98	1.0E-105	AA584808.1	EST_HUMAN	no10d05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
3071	16247		2.79	1.0E-105	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3432	16600	29618	0.86	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3432	16600	29619	0.86	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4213	17362	30350	2.23	1.0E-105	AW961688.1	EST_HUMAN	EST373761 MAGE resequences, MAGG Homo sapiens cDNA

WO 01/57272 PCT/US01/00663

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5053	18181		5.34	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5259	18378	31344	1.08	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5445	18545	31623	1.18	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5513	18711		1.12	1.0E-105	11420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7045	20098	33513	1.44	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7045	20098	33514	1.44	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7121	18547	31458	3.78	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7121	18547	31459	3.78	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7167	20300	33743	0.72	1.0E-105	AW951634.1	EST_HUMAN	EST363689 MAGE resequences, MAGB Homo sapiens cDNA
7436	20513	33986	0.72	1.0E-105	BE902616.1	EST_HUMAN	601677279F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960019 5'
8043	21126	34647	0.93	1.0E-105	X12556.1	NT	Human mRNA for dbl proto-oncogene
8217	21299	34820	11.05	1.0E-105	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR32
8592	21673	35211	1.63	1.0E-105	AW007194.1	EST_HUMAN	ws50c10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2500626 3' similar to SW:ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
9128	22207	35750	0.82	1.0E-105	AW840817.1	EST_HUMAN	RC1-CN0008-070100-011-e05 CN0008 Homo sapiens cDNA
9250	22327	35874	2.51	1.0E-105	AW016879.1	EST_HUMAN	UI-H-BI0p-abi-b-12-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9404	22478	36041	0.83	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9404	22478	36042	0.83	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9767	22764	36333	0.75	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
9767	22764	36334	0.75	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11173	24243	37876	4.82	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11506	24564	38241	1.42	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for a6(IV) collagen, exon 31
11559	24614	38293	1.85	1.0E-105	7705936	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11887	24875	38572	2.52	1.0E-105	AW027554.1	EST_HUMAN	wv74f07.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892 P87892 PROTEASE ;
11972	24957	38659	1.48	1.0E-105	BF430921.1	EST_HUMAN	7o18c10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR:P97680 P97680 RIN1. ;
12111	25091	38794	1.3	1.0E-105	AF218896.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 8
155	13380		0.66	1.0E-106	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
210	13433	26464	5.14	1.0E-106	AI565065.1	EST_HUMAN	tq79c01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2215008 3'
555	13748	26774	1.89	1.0E-106	AW965556.1	EST_HUMAN	EST377629 MAGE resequences, MAGI Homo sapiens cDNA
620	13807	26828	0.8	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
621	13807	26828	1.13	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1554	14707	27787	8.84	1.0E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1736	14885	27978	7.83	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1757	14906	28000	1.33	1.0E-106	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1846	14992	28093	5.51	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ;
1846	14992	28094	5.51	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ;
2191	15326	28451	1.94	1.0E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2391	15522	28651	3.62	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2574	15699	28821	2.19	1.0E-106	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2667	15788	28904	1.93	1.0E-106	U64675.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2669	15790	28906	2.01	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2815	15929	29041	8.05	1.0E-106	AI276526.1	EST_HUMAN	q76h10.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678307 3'
2886	14617	27700	1.84	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2886	14617	27701	1.84	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2939	16116	29128	1.18	1.0E-106	BE384296.1	EST_HUMAN	601272675F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
3007	16182	29204	5.7	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3007	16182	29205	5.7	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3248	16422	29438	2.5	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3248	16422	29439	2.5	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3461	16628	29648	1.04	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3527	16692	29701	1.07	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3527	16692	29702	1.07	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4149	17301	30293	9.2	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGE resequences, MAGN Homo sapiens cDNA
4149	17301	30294	9.2	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGE resequences, MAGN Homo sapiens cDNA
4723	17858	30840	2.27	1.0E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
5485	18684	31701	2.95	1.0E-106	AA781155.1	EST_HUMAN	aj24b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN);
5976	19161	32480	0.95	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5976	19161	32481	0.95	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6026	19209	32529	0.61	1.0E-106	AA434168.1	EST_HUMAN	zw28d12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770615 3'
6116	19296	32631	1	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6116	19296	32632	1	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6227	19402	32752	8.39	1.0E-106	BF679574.1	EST_HUMAN	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295067 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6336	19507	32864	0.81	1.0E-106	BE897112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6526	19507	32864	0.66	1.0E-106	BE897112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6549	19711	33087	15.91	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6549	19711	33088	15.91	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
7528	20601	34075	5.69	1.0E-106	AA663779.1	EST_HUMAN	ae72e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7582	20654	34130	4.17	1.0E-106	11429617	NT	Homo sapiens XPMC2 protein (LOC57109), mRNA
7672	20738	34216	1.64	1.0E-106	BE292722.1	EST_HUMAN	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5'
7787	20843	34335	8.06	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7787	20843	34336	8.06	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7994	21044	34556	0.6	1.0E-106	AU116850.1	EST_HUMAN	AU116850 HEMBA1 Homo sapiens cDNA clone HEMBA1000129 5'
8173	21255	34776	3.62	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8173	21255	34777	3.62	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8368	21449	34972	2.21	1.0E-106	AI523066.1	EST_HUMAN	ar68a07.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233 CALGRANULIN B (HUMAN);
8830	21909	35447	0.64	1.0E-106	BE387950.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
8830	21909	35448	0.64	1.0E-106	BE387950.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
8903	21982	35522	2.77	1.0E-106	AI654123.1	EST_HUMAN	ty62a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN Q05084 69 KD ISLET CELL AUTOANTIGEN ;
9252	22329	35876	0.83	1.0E-106	AW838831.1	EST_HUMAN	CM4-LT0059-150200-096-e06 LT0059 Homo sapiens cDNA
9348	22424	35978	2.34	1.0E-106	AA825307.1	EST_HUMAN	oc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
9348	22424	35979	2.34	1.0E-106	AA825307.1	EST_HUMAN	oc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
9486	22543	36106	0.77	1.0E-106	AI750447.1	EST_HUMAN	cn03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn03a04 random
9629	22684	36255	1.94	1.0E-106	AI479569.1	EST_HUMAN	tm41f02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3 TAR1 PTR5 repetitive element ;
9629	22684	36256	1.94	1.0E-106	AI479569.1	EST_HUMAN	tm41f02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3 TAR1 PTR5 repetitive element ;
10205	23241	36832	0.6	1.0E-106	BE389234.1	EST_HUMAN	601282367F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604217 5'
10289	23324	36926	1.09	1.0E-106	BF027310.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10289	23324	36927	1.09	1.0E-106	BF027310.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10446	23481	37088	10.7	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10446	23481	37089	10.7	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10492	23527	37136	1.83	1.0E-106	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10497	23532	37141	0.66	1.0E-106	11436432	NT	Homo sapiens multimerin (MMRN), mRNA
10497	23532	37142	0.66	1.0E-106	11436432	NT	Homo sapiens multimerin (MMRN), mRNA
10678	23712	37320	0.65	1.0E-106	AL039886.1	EST_HUMAN	DKFZp434F0712_r1 434 (synonym: hfes3) Homo sapiens cDNA clone DKFZp434F0712 5'
10807	23840	37464	4.26	1.0E-106	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11135	24207	37832	4.81	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
11135	24207	37833	4.81	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
11317	24380	38025	2.06	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11317	24380	38026	2.06	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11694	24692	38383	1.35	1.0E-106	BE257385.1	EST_HUMAN	601109219F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349997 5'
11837	24826	38514	1.89	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
11837	24826	38515	1.89	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
12253	25946		4.3	1.0E-106	AW410405.1	EST_HUMAN	fh05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961644 5'
12484	25336	32059	1.97	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12484	25336	32060	1.97	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12717	25477		3.71	1.0E-106	BE695905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
244	13466		4.52	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
275	13493		0.9	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
637	13822		1.03	1.0E-107	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
647	13832	26858	2.34	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
836	14014	27069	1.02	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
909	14084	27149	1.38	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
991	14163	27223	9.71	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1307	14463	27531	1.06	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1600	14753	27836	3.81	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1791	14940	28033	5.42	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
1887	15031	28138	1.52	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1887	15031	28139	1.52	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2282	15414	28546	3.77	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2435	15563	28691	4.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2435	15563	28692	4.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3072	16248	29268	6.14	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3072	16248	29269	6.14	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3169	16344	29352	2.9	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3931	17090	30087	4.89	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5742	18935	32235	0.64	1.0E-107	AW969038.1	EST_HUMAN	EST381115 MAGE resequences, MAGK Homo sapiens cDNA
5986	19171	32493	2.71	1.0E-107	BE867469.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846494 5'
7520	20593	34067	1.33	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BN0-alf-c-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7520	20593	34068	1.33	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BN0-alf-c-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7698	20763	34247	1.36	1.0E-107	AI765078.1	EST_HUMAN	wh56h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
7909	20961	34467	0.59	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7909	20961	34468	0.59	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
9587	22729	36299	0.99	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'
10889	23973	37604	1.92	1.0E-107	BE168726.1	EST_HUMAN	QV1-HT0516-140300-107-c10 HT0516 Homo sapiens cDNA
10944	24026	37662	2.96	1.0E-107	AI392850.1	EST_HUMAN	tg10d06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICDI P05095 ALPHA-ACTININ 3, NON MUSCULAR ;
11189	24258	37894	1.58	1.0E-107	L49141.1	NT	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11202	24271	37907	2.3	1.0E-107	BF666511.1	EST_HUMAN	602123963F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
11603	24656	38341	3.91	1.0E-107	BE540550.1	EST_HUMAN	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11676	23904	37526	4.29	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11676	23904	37527	4.29	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
12322	26100		7.14	1.0E-107	AA001415.1	EST_HUMAN	ze45e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1 THR repetitive element ;
13211	25790	31920	1.24	1.0E-107	BE798189.1	EST_HUMAN	601582652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937188 5'
977	14150	27210	1.72	1.0E-108	BE296042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1294	14450	27515	2.41	1.0E-108	Y18000.1	NT	Homo sapiens NF2 gene
2140	15276	28398	1.02	1.0E-108	BF026728.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2407	15538	28665	12.11	1.0E-108	AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2407	15538	28666	12.11	1.0E-108	AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2499	15626	28746	11.96	1.0E-108	BE206694.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3025	16201	29224	0.64	1.0E-108	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3430	16598	29614	0.64	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3430	16598	29615	0.64	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4273	17418	30406	1.57	1.0E-108	AW664438.1	EST_HUMAN	hi12a11.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 3BP-1. ;
4647	17783	30765	2.62	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4647	17783	30766	2.62	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4927	18057	31040	3.37	1.0E-108	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5037	18165	31141	0.63	1.0E-108	AW504799.1	EST_HUMAN	UI-HF-BN0-aln-e-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080166 5'
5063	18191	31166	3.18	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5596	18791	31839	1.24	1.0E-108	AW384094.1	EST_HUMAN	RC0-HT0372-241199-031-d03 HT0372 Homo sapiens cDNA
5644	18838	31916	2.56	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5644	18838	31917	2.56	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
6049	19232		0.66	1.0E-108	AF012623.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6125	19304	32644	0.74	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6267	19441	32789	6.14	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6267	19441	32790	6.14	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6392	19561	32921	1.22	1.0E-108	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6489	19304	32644	1.09	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6753	19909	33302	0.64	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6753	19909	33303	0.64	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7308	20390	33850	4.52	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA
7597	20667	34143	2.12	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADSD6) mRNA
7646	20715	34193	1.32	1.0E-108	BE252607.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354064 5'
7674	20739	34218	0.73	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
7674	20739	34219	0.73	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
8254	21336		1.72	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8306	21388	34910	0.61	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BM0-ads-e-12-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8306	21388	34911	0.61	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BM0-ads-e-12-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
9247	22324	35869	0.77	1.0E-108	AF203977.1	NT	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
9287	22363	35912	0.46	1.0E-108	N44974.1	EST_HUMAN	yy35h10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773 A45773 kelch protein, long form - fruit fly ;
10847	23880	37500	1.08	1.0E-108	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10904	21037	34549	2.09	1.0E-108	BE535227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
11066	18501	31537	2.67	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
11319	24382	38027	1.35	1.0E-108	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11549	24605	38283	3.46	1.0E-108	AW966185.1	EST_HUMAN	EST378258 MAGE resequences, MAGI Homo sapiens cDNA
11605	24658	38343	1.71	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11605	24658	38344	1.71	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11652	24731		2.77	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11688	15538	28665	2.99	1.0E-108	AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11688	15538	28666	2.99	1.0E-108	AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11712	24752	38446	1.72	1.0E-108	D63539.1	NT	Homo sapiens COL4A6 gene for a6(IV) collagen, exon 23
12499	25344	32064	4.15	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12940	25618		5.09	1.0E-108	BF346356.1	EST_HUMAN	602018571F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154297 5'
43	13281	26287	1.01	1.0E-109	AW803116.1	EST_HUMAN	IL2-UM0077-260400-079-D06 UM0077 Homo sapiens cDNA
66	13303	26326	1.17	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
225	13447	26475	3.34	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
235	13456	26482	2.77	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
479	13674	26705	2.28	1.0E-109	4507712	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA
611	13800	26820	14.77	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
611	13800	26821	14.77	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1037	14205	27262	1.62	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1229	14389	27451	8.5	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1230	14389	27451	6.38	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1573	14726	27806	0.99	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
1573	14726	27807	0.99	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
1923	15066	28170	2.3	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2314	15446	28580	5.46	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2325	15457	28589	3.65	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2687	15807	28923	19.35	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 O02197 CIRCULATING CATHODIC ANTIGEN. ;
2687	15807	28924	19.35	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 O02197 CIRCULATING CATHODIC ANTIGEN. ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2688	15808	28925	2.68	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3125	16301	29314	3.37	1.0E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3475	16642	29661	2.08	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3475	16642	29662	2.08	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3606	16770	29785	1.1	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3945	17104		1.31	1.0E-109	BE146144.1	EST_HUMAN	MR0-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
4264	17409	30395	4.35	1.0E-109	AI655417.1	EST_HUMAN	ts98e06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 CE16100 ;
4524	17663	30650	2.67	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4722	17857	30839	1.7	1.0E-109	7662083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5165	18287	31252	0.72	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
5165	18287	31253	0.72	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
5361	18564	31480	0.67	1.0E-109	AU137282.1	EST_HUMAN	AU137282 PLACE1 Homo sapiens cDNA clone PLACE1006159 5'
5374	18577	31445	0.92	1.0E-109	BF673718.1	EST_HUMAN	602136446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'
5428	18628	31604	2.92	1.0E-109	5174622	NT	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
5724	18917		1.23	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6050	25817	32556	1.23	1.0E-109	BF379688.1	EST_HUMAN	CM1-UT0038-060900-399-h07 UT0038 Homo sapiens cDNA
6119	18917		1.41	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6721	19878	33269	0.85	1.0E-109	AI221385.1	EST_HUMAN	qg86h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 3'
6907	20222	33651	0.69	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6907	20222	33652	0.69	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7389	20467	33933	0.67	1.0E-109	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7738	20799	34288	3.75	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7740	20801	34290	4.91	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
7740	20801	34291	4.91	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8366	21447	34970	1.35	1.0E-109	AL049784.1	NT	Novel human gene mapping to chomosome 13
8480	21561	35096	1.39	1.0E-109	AW749130.1	EST_HUMAN	PM0-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA
8857	21936		2.84	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
8932	22011	35549	4.36	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8932	22011	35550	4.36	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9177	22255	35797	0.57	1.0E-109	BE145672.1	EST_HUMAN	IL0-HT0205-071199-142-g01 HT0205 Homo sapiens cDNA
9439	22513	36077	1.65	1.0E-109	H84860.1	EST_HUMAN	ys90g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491 A53491 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER - SPINY ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9550	22615	36184	0.64	1.0E-109	BE397068.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9550	22615	36185	0.64	1.0E-109	BE397068.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9685	22734	36304	1.37	1.0E-109	F06604.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
11013	24092	37730	1.8	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11013	24092	37731	1.8	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11046	24123	37757	19.68	1.0E-109	BF694831.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
11387	24448	38109	1.57	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'
11651	24730	38422	2.18	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
11693	24691	38382	4.5	1.0E-109	W16510.1	EST_HUMAN	zb08b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat ;
11884	24872	38569	1.64	1.0E-109	BE045560.1	EST_HUMAN	hh23f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2955969 3' similar to TR:Q9Z124 Q9Z124 YGR163W MRNA HOMOLOGUE, COMPLETE CDS. ;
11948	24934	38636	1.5	1.0E-109	AL119824.1	EST_HUMAN	DKFZp761I1124_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761I1124 5'
11984	24969	38673	1.31	1.0E-109	11418618	NT	Homo sapiens single-minded (Drosophila) homolog 1 (SIM1), mRNA
12126	25106	38810	2.26	1.0E-109	AB007932.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
12397	15457	28589	2.32	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12636	15457	28589	3.2	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12762	25506	32036	8.36	1.0E-109	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3	13242	26242	1.4	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
38	13276	26281	3.96	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
38	13276	26282	3.96	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
112	13242	26242	1.83	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
305	13521	26555	1.31	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
540	13733	26757	1.04	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1207	14369	27429	0.89	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1308	14464	27532	1.02	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1973	15116	28217	1.51	1.0E-110	BE379477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2118	15256		1.66	1.0E-110	BF508896.1	EST_HUMAN	UI-H-BI4-aos-b-05-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2903	16081		7.19	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3156	16331		1.48	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3264	16438	29457	2.66	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3264	16438	29458	2.66	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4320	17463	30449	1.09	1.0E-110	M15918.1	NT	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4758	17893	30872	2.04	1.0E-110	AI017213.1	EST_HUMAN	ou32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to SW:N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4777	17912	30897	3.01	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5088	18216		2.28	1.0E-110	7662441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5409	18611	31583	2.23	1.0E-110	BE299406.1	EST_HUMAN	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
5843	19033	32339	0.78	1.0E-110	BE621069.1	EST_HUMAN	601493677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895795 5'
5860	19050	32356	8.61	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5860	19050	32357	8.61	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6858	25835	33421	5.43	1.0E-110	M55112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7179	20311	33754	0.59	1.0E-110	BE251496.1	EST_HUMAN	601109388F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350277 5'
7251	20334	33782	0.85	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7251	20334	33783	0.85	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7477	20552	34025	0.78	1.0E-110	AI560289.1	EST_HUMAN	tn12d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN P50549 ETS TRANSLOCATION VARIANT 1 ;
7583	20655	34131	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7583	20655	34132	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7613	20683	34159	2.87	1.0E-110	AB020675.1	NT	Homo sapiens mRNA for KIAA0868 protein, partial cds
7743	20804	34293	0.96	1.0E-110	AU137923.1	EST_HUMAN	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'
9536	22601	36174	1.09	1.0E-110	BE302594.1	EST_HUMAN	ba68f01.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905561 5' similar to TR:O77258 O77258 EG:114D9.2 PROTEIN. ;
9777	22817	36395	2.46	1.0E-110	AW838394.1	EST_HUMAN	QV2-LT0053-020400-119-e04 LT0053 Homo sapiens cDNA
10529	23564	37171	3.38	1.0E-110	11432732	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
10986	24065	37700	3.2	1.0E-110	Y12337.1	NT	H.sapiens mRNA for myotonic dystrophy protein kinase like protein
11209	24278	37916	3.64	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11209	24278	37917	3.64	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11608	24661	38347	1.89	1.0E-110	M10051.1	NT	Human insulin receptor mRNA, complete cds
11728	23914	37539	1.7	1.0E-110	AA446529.1	EST_HUMAN	zw67g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816 G1145816 FKBP54 ;
12211	25164		2.47	1.0E-110	BE897218.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
12341	25246		2.86	1.0E-110	AW062258.1	EST_HUMAN	IL0-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
12594	25400		2.96	1.0E-110	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12746	26113		6.01	1.0E-110	BF364546.1	EST_HUMAN	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA
13071	15256		1.16	1.0E-110	BF508896.1	EST_HUMAN	UI-H-BI4-aos-b-05-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
179	13402		11.92	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
201	13424	26455	1.64	1.0E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
753	13934		1.99	1.0E-111	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
762	13943	26989	4.13	1.0E-111	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
950	14123	27185	2.5	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
4286	17431	30419	1.15	1.0E-111	7661569	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4449	17589	30570	4.59	1.0E-111	K02268.1	NT	Human enkephalin B (enkB) gene, exon 4 and 3' flank and complete cds
5593	18788	31835	0.75	1.0E-111	AA151017.1	EST_HUMAN	zl47b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5593	18788	31836	0.75	1.0E-111	AA151017.1	EST_HUMAN	zl47b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5749	18941	32242	0.88	1.0E-111	BE867909.1	EST_HUMAN	601443690F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847655 5'
5862	19052	32359	0.66	1.0E-111	U19969.1	NT	Human two-handed zinc finger protein ZEB mRNA, partial cds
6156	19332	32678	2.09	1.0E-111	AI344679.1	EST_HUMAN	qp09g12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS-RELATED PROTEIN RAL-A (HUMAN);
6818	19971	33379	0.96	1.0E-111	AL040762.1	EST_HUMAN	DKFZp434C1815_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1815 5'
6945	20258	33697	1.31	1.0E-111	AW294648.1	EST_HUMAN	UI-H-BW0-all-d-03-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729525 3'
7605	20675	34149	3.04	1.0E-111	BF366228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
7704	20769	34254	0.7	1.0E-111	AI761228.1	EST_HUMAN	wi68d01.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813 CYTOCHROME P450 IIIA5 (HUMAN);
7791	20847	34340	0.83	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8286	21368	34888	0.8	1.0E-111	AA278868.1	EST_HUMAN	zs79g03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR. ;
8286	21368	34889	0.8	1.0E-111	AA278868.1	EST_HUMAN	zs79g03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR. ;
8383	21464	34989	0.63	1.0E-111	11431896	NT	Homo sapiens protein x 0001 (LOC51185), mRNA
8435	21516	35047	3.56	1.0E-111	U66533.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
8878	21957	35492	0.96	1.0E-111	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8975	22054	35597	0.64	1.0E-111	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
9008	22087		8.43	1.0E-111	BF214902.1	EST_HUMAN	601847132F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4078303 5'
9085	22164	35708	15.93	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9085	22164	35709	15.93	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9289	22365	35914	3.37	1.0E-111	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9518	22583	36152	0.54	1.0E-111	BF333210.1	EST_HUMAN	QV2-BT0817-270900-398-e06 BT0817 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10355	23390	37000	1.56	1.0E-111	AA504160.1	EST_HUMAN	aa58g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:L09235 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10383	23418		1.04	1.0E-111	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10479	23514	37127	5.58	1.0E-111	AA131248.1	EST_HUMAN	zl31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10995	24074	37707	1.34	1.0E-111	AW296467.1	EST_HUMAN	UI-H-BW0-alq-d-07-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730276 3'
11299	24365	38006	3.29	1.0E-111	U68159.1	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
12167	25130	38828	4.07	1.0E-111	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12741	25492	32029	4.72	1.0E-111	AV708482.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAOB08.5'
12881	25888	31855	4.82	1.0E-111	W22562.1	EST_HUMAN	72C9 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
13041	18504	31539	1.27	1.0E-111	AB035356.1	NT	Homo sapiens mRNA for neurexin I-alpha protein, complete cds
623	13808	26829	2.77	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
625	13810	26831	4.84	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 5
625	13810	26832	4.84	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 5
649	13834	26860	1.82	1.0E-112	BF509039.1	EST_HUMAN	UI-H-BI4-aot-g-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
649	13834	26861	1.82	1.0E-112	BF509039.1	EST_HUMAN	UI-H-BI4-aot-g-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1026	14197	27255	33.06	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1087	14253	27308	1.49	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1718	14868	27958	7.1	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1718	14868	27959	7.1	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1863	15009	28115	1.11	1.0E-112	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
2577	15703	28823	2.83	1.0E-112	BE866859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3147	16323		0.76	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3444	16612	29630	0.61	1.0E-112	AI826511.1	EST_HUMAN	wk45b12.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81650_rna1 SEMENOGELIN 1 PROTEIN PRECURSOR (HUMAN);
3990	17147	30153	0.63	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0590-090300-113-f09 BT0590 Homo sapiens cDNA
4726	17861	30843	0.68	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4875	18007	30990	5.87	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4875	18007	30991	5.87	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5784	18976	32282	36.7	1.0E-112	N46046.1	EST_HUMAN	yy35d07.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273229 5'
6201	19376	32727	1.33	1.0E-112	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6273	19447	32795	0.66	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajs-g-06-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6273	19447	32796	0.66	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajs-g-06-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6379	19548	32904	0.93	1.0E-112	BE741666.1	EST_HUMAN	601594717F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
6588	19749	33132	0.7	1.0E-112	BF672815.1	EST_HUMAN	602152649F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293420 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6773	19928	33323	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6773	19928	33324	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6981	20209	33637	1.51	1.0E-112	BF574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7305	20387	33847	0.68	1.0E-112	AL043299.1	EST_HUMAN	DKFZp434M0523_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M0523 5'
7491	20566	34037	1.49	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7491	20566	34038	1.49	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8387	21468	34995	1.79	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
9158	22236	35781	2.64	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9158	22236	35782	2.64	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
10097	23135	36736	2.37	1.0E-112	BF111413.1	EST_HUMAN	7l30g07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TR:Q9VW35 Q9VW35 CG8743 PROTEIN. ;
11017	24096	37735	16.73	1.0E-112	AW863327.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
11103	24175	37810	1.31	1.0E-112	T93967.1	EST_HUMAN	yd56d10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
11103	24175	37811	1.31	1.0E-112	T93967.1	EST_HUMAN	yd56d10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
11191	24260	37896	3.14	1.0E-112	AJ249900.1	NT	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
11359	24421	38077	2.24	1.0E-112	BE280479.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
11428	24489	38153	2.28	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
11428	24489	38154	2.28	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
11460	24519	38188	4.78	1.0E-112	AW377670.1	EST_HUMAN	PM0-CT0237-141099-001-h02 CT0237 Homo sapiens cDNA
12096	25076	38783	1.66	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
12096	25076	38784	1.66	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
12727	25484		1.31	1.0E-112	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
761	13942	26987	6.82	1.0E-113	AI365586.1	EST_HUMAN	ao95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
761	13942	26988	6.82	1.0E-113	AI365586.1	EST_HUMAN	ao95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
965	14138	27199	2.93	1.0E-113	M11965.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1572	14725	27805	3.23	1.0E-113	AI365586.1	EST_HUMAN	ao95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1993	15994	28240	1.63	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2161	15297	28422	1.49	1.0E-113	BF515218.1	EST_HUMAN	UI-H-BW1-anl-f-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
3200	16375	29385	2.06	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5178	18300	31263	36.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5178	18300	31264	36.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5359	25930		2.4	1.0E-113	BE780858.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5610	18805	31870	6.37	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
6045	19228	32552	3.54	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
6072	19264	32583	1.02	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6195	19371	32722	2.57	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
6285	19458	32809	0.8	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6285	19458	32810	0.8	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6446	19613	32976	0.68	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6446	19613	32977	0.68	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7474	20549	34021	0.63	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
7474	20549	34022	0.63	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
9093	22172	35717	0.5	1.0E-113	8922819	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9296	22372	35921	2.91	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9296	22372	35922	2.91	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9601	22656		0.62	1.0E-113	BE772987.1	EST_HUMAN	RC1-FT0134-280600-021-d02 FT0134 Homo sapiens cDNA
10036	23074	36674	1.27	1.0E-113	11429367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
10256	23291	36888	1.01	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10256	23291	36889	1.01	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10842	23875	37495	0.47	1.0E-113	AW500517.1	EST_HUMAN	UI-HF-BN0-akj-b-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077322 5'
11385	24446	38107	1.89	1.0E-113	AW500519.1	EST_HUMAN	UI-HF-BN0-akj-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
11396	24457	38119	5.42	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN ;
11396	24457	38120	5.42	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN ;
11540	24596	38272	2.91	1.0E-113	BE292968.1	EST_HUMAN	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988366 5'
59	13297	26314	0.75	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
59	13297	26315	0.75	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	13297	26316	0.75	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
662	13848	26876	7.46	1.0E-114	T70551.1	EST_HUMAN	yd15c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);contains Alu repetitive element;
1096	14261	27318	2.54	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1341	14497	27569	4.05	1.0E-114	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1673	14825	27909	1.9	1.0E-114	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1706	14858	27945	5.08	1.0E-114	6679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2145	15281	28406	2.52	1.0E-114	BE171984.1	EST_HUMAN	MR0-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
2330	15462	28595	0.99	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
2865	13283	26290	0.6	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2865	13283	26291	0.6	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3201	16376	29386	2.6	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3240	16414	29429	1.03	1.0E-114	BF206374.1	EST_HUMAN	601869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4124	17278	30275	3.27	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4510	17649	30637	0.7	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
5282	18401	31370	1.1	1.0E-114	AW294203.1	EST_HUMAN	UI-H-BI2-ahc-d-01-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726424 3'
5516	18714	31727	1.68	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5516	18714	31728	1.68	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5712	18905	32200	0.9	1.0E-114	9257201	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA
7224	20088		0.71	1.0E-114	AB041533.1	NT	Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds
7388	20466	33931	1.09	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7388	20466	33932	1.09	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7434	20511	33983	8.2	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7434	20511	33984	8.2	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
8075	21157	34675	1.94	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8360	21441	34963	1.85	1.0E-114	AI363139.1	EST_HUMAN	qy68d06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'
8360	21441	34964	1.85	1.0E-114	AI363139.1	EST_HUMAN	qy68d06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'
8898	21977	35516	2.99	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
8966	22045	35589	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8966	22045	35590	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9384	22459	36022	0.87	1.0E-114	BF109832.1	EST_HUMAN	7l69g12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to TR:Q9UHN6 Q9UHN6 TRANSMEMBRANE PROTEIN 2. ;
9614	22669		1.3	1.0E-114	AW327455.1	EST_HUMAN	dq03f05.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9662	21104	34621	2.67	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
9748	22812		1.36	1.0E-114	M13536.1	NT	Human ceruloplasmin mRNA
10343	23378	36989	1.02	1.0E-114	BE870004.1	EST_HUMAN	601449752F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10364	23399	37010	1.11	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10762	23795	37415	1.18	1.0E-114	BE171984.1	EST_HUMAN	MR0-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
11027	24106		4.31	1.0E-114	BE302866.1	EST_HUMAN	ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
11466	24525	38197	8.11	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
11466	24525	38198	8.11	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
11842	24831	38522	6.28	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
11842	24831	38523	6.28	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
12643	26187		4.63	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12936	25616	31975	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12936	25616	31976	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
24	13262	26264	3.06	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
132	13358	26391	1.09	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
136	13362		18.42	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
303	13519	26552	2.02	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
549	13742	26766	1.68	1.0E-115	AI339206.1	EST_HUMAN	qt06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5 ;
549	13742	26767	1.68	1.0E-115	AI339206.1	EST_HUMAN	qt06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5 ;
809	13988	27041	3	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
809	13988	27042	3	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
811	13990	27044	15.24	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1590	14742	27823	1.15	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1590	14742	27824	1.15	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1888	15032	28140	1.31	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2142	15278	28400	1.13	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2142	15278	28401	1.13	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2150	15286	28411	1.1	1.0E-115	AB007902.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
2374	15505	28631	1.11	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
2912	16090		1.03	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-150-b08 UM0094 Homo sapiens cDNA
3184	16359	29365	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3184	16359	29366	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3561	16726	29742	1.8	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4153	17305	30299	4.2	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4521	17660	30647	2.49	1.0E-115	6912659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4557	17695	30674	4.28	1.0E-115	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4797	17932	30918	2.86	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4797	17932	30919	2.86	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
5026	18156	31132	2.99	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5026	18155	31133	2.99	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5044	18172	31149	1.01	1.0E-115	Y19215.1	NT	Homo sapiens putative psihHbC pseudogene for hair keratin, exons 1 to 9
5304	18421	31391	1.23	1.0E-115	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
5347	18460	31425	0.92	1.0E-115	AB018311.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
5463	18663	31642	2.8	1.0E-115	AW970335.1	EST_HUMAN	EST382416 MAGE resequences, MAGK Homo sapiens cDNA
5540	18737	31754	0.97	1.0E-115	BF665387.1	EST_HUMAN	602119346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276738 5'
5659	18853	32136	1.74	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5659	18853	32137	1.74	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5808	18998	32304	1.15	1.0E-115	AI928799.1	EST_HUMAN	au64g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
5808	18998	32305	1.15	1.0E-115	AI928799.1	EST_HUMAN	au64g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
6391	19560	32919	0.68	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6391	19560	32920	0.68	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6525	19690	33064	9.49	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA
6658	19817	33204	1.68	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6658	19817	33205	1.68	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
7074	20127	33543	0.75	1.0E-115	T86774.1	EST_HUMAN	yd86b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to SP:DPOG_YEAST P15801 DNA POLYMERASE GAMMA ;
7428	20505	33975	1.24	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7428	20505	33976	1.24	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7246	20329	33775	1	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O0127 5'
7776	20833	34324	4.7	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7790	20846	34339	0.72	1.0E-118	L46590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
8159	21241	34761	1.95	1.0E-118	BE781223.1	EST_HUMAN	601469159F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
8577	21658	35198	7	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8577	21658	35199	7	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8583	21664	35204	1.1	1.0E-118	AA443024.1	EST_HUMAN	zx98d07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8583	21664	35205	1.1	1.0E-118	AA443024.1	EST_HUMAN	zx98d07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8873	21952	35488	0.94	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8873	21952	35489	0.94	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8918	21997	35536	1.94	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8918	21997	35537	1.94	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9236	22313	35855	5.15	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
9266	22343	35894	0.55	1.0E-118	AL048474.2	EST_HUMAN	DKFZp586K1824_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586K1824
9792	22832	36411	1.07	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
10541	23576	37184	1.23	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10541	23576	37185	1.23	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10586	23621	37228	1.75	1.0E-118	BF195407.1	EST_HUMAN	7n17e09.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW:ZP3A_HUMAN P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ;
10752	23785	37399	0.59	1.0E-118	AW296351.1	EST_HUMAN	UI-H-BW0-aic-a-07-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729772 3'
11555	24610	38290	3.75	1.0E-118	AA315C07.1	EST_HUMAN	EST186814 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
11855	24843	38539	2.92	1.0E-118	BE908676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11855	24843	38540	2.92	1.0E-118	BE908676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
12071	25052	38761	1.81	1.0E-118	BE218235.1	EST_HUMAN	hv36a06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175474 3' similar to TR:Q9Z2H4 Q9Z2H4 G PROTEIN-COUPLED RECEPTOR LGR4. ;
776	13956	27007	2.46	1.0E-119	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CIC4) mRNA, complete cds
1062	16029	27284	0.93	1.0E-119	7705607	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1987	15129	28232	2.96	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3171	16348	29353	1.01	1.0E-119	8922205	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3312	16485		2.17	1.0E-119	AA916760.1	EST_HUMAN	on10b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2 CE01214 ;
4063	17219	30227	1.22	1.0E-119	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5453	18653	31632	3.96	1.0E-119	AU133399.1	EST_HUMAN	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001991 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5466	18668	31645	15.48	1.0E-119	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
5470	18670	31650	3.29	1.0E-119	BE936121.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5550	18747	31782	1.61	1.0E-119	AV693731.1	EST_HUMAN	AV693731 GKC Homo sapiens cDNA clone GKCDHB03 5'
5707	18900	32194	0.86	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
5707	18900	32195	0.86	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6255	19429	32775	6.7	1.0E-119	AI150703.1	EST_HUMAN	qb77c09.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
6414	19583	32944	0.71	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6414	19583	32945	0.71	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6461	19628	32989	1.22	1.0E-119	AI476732.1	EST_HUMAN	tm23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
6589	19750	33133	2.39	1.0E-119	X06292.1	NT	Human c-fes/fps proto-oncogene
6601	19761	33149	4.01	1.0E-119	AW974193.1	EST_HUMAN	EST386296 MAGE resequences, MAGM Homo sapiens cDNA
7568	20640	34116	1.09	1.0E-119	BE796614.1	EST_HUMAN	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'
8862	21941	35476	0.93	1.0E-119	BE615150.1	EST_HUMAN	601280564F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622526 5'
9957	22996	36592	0.46	1.0E-119	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
10111	23149	36750	0.96	1.0E-119	11036643	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA
10311	23346	36952	0.61	1.0E-119	AI149796.1	EST_HUMAN	qf43a11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752764 3' similar to TR:Q13458 Q13458 GUANINE NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO. ;
10452	23487	37095	2.29	1.0E-119	AA465124.1	EST_HUMAN	aa32f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
10722	23755	37361	1.13	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10766	23799	37420	0.77	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10766	23799	37421	0.77	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10844	23877	37497	0.59	1.0E-119	BE561967.1	EST_HUMAN	601347190F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687887 5'
10849	23882	37502	0.73	1.0E-119	AB032261.1	NT	Homo sapiens Scd mRNA for stearoyl-CoA desaturase, complete cds
11308	24373	38015	1.58	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11308	24373	38016	1.58	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11479	24538		6.62	1.0E-119	BF569571.1	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
12490	26098		5.48	1.0E-119	AW847519.1	EST_HUMAN	RC3-CT0212-240999-011-f03 CT0212 Homo sapiens cDNA
12845	25882		3.03	1.0E-119	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
247	13468	26500	0.68	1.0E-120	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
312	13528	26561	0.97	1.0E-120	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
1066	14232	27290	2.74	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1066	14232	27291	2.74	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1456	14609	27689	3.26	1.0E-120	N44873.1	EST_HUMAN	yy40g12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273766 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1631	14783	27869	11.19	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1849	14995	28098	6.58	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2174	15309	28437	1.83	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2174	15309	28438	1.83	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3382	13528	26561	1.61	1.0E-120	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
4477	17617	30598	2.05	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4477	17617	30599	2.05	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4784	17919	30906	3.11	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4784	17919	30907	3.11	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5853	19043	32349	16.08	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5853	19043	32350	16.08	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
7746	20806	34295	1.84	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
8078	21160	34677	1.38	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8078	21160	34678	1.38	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8527	21608	35147	2.31	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183333 5'
8599	21680	35218	0.9	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8599	21680	35219	0.9	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8603	21684	35221	1.94	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8603	21684	35222	1.94	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8647	21727	35264	1.31	1.0E-120	AB007934.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds
9701	22750	36319	4.67	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9701	22750	36320	4.67	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9946	22985	36578	3.54	1.0E-120	BF306541.1	EST_HUMAN	601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
9962	23001	36597	6.7	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
9979	23018	36612	1.02	1.0E-120	AL049801.1	NT	Novel human gene mapping to chomosome 13, similar to rat RhoGAP
10096	23134		0.55	1.0E-120	AI904151.1	EST_HUMAN	CM-BT043-090299-075 BT043 Homo sapiens cDNA
10281	23316	36916	3.4	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11391	24452	38115	8.66	1.0E-120	BE296387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
11625	24705	38397	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11625	24705	38398	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
12657	25436	32049	1.42	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
75	13311	26337	0.62	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
389	13595	26631	1.35	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
742	16020	26964	1.31	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA

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2023	15164	28269	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2023	15164	28270	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2169	15304	28431	1.22	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2643	15766	28880	1.07	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5'
2643	15766	28881	1.07	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5'
3150	16325	29336	5.8	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3150	16325	29337	5.8	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3626	16790	29807	1.23	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3626	16790	29808	1.23	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3768	16929	29934	8.25	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4450	17590	30571	1.76	1.0E-121	AI263294.1	EST_HUMAN	qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
5091	18219	31189	3.42	1.0E-121	X91937.1	NT	H.sapiens ECE-1 gene (exon 17)
5382	18584	31453	0.84	1.0E-121	BE222250.1	EST_HUMAN	hu09f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119 3'
5679	18873	32161	0.73	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6757	19913	33308	0.64	1.0E-121	M91463.1	NT	Human glucose transporter (GLUT4) gene, complete cds
7028	20164		0.96	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
7102	18529	31483	0.79	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-f02 NN0066 Homo sapiens cDNA
7102	18529	31484	0.79	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-f02 NN0066 Homo sapiens cDNA
8123	21205	34725	1.07	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
8127	21209	34729	2.51	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8127	21209	34730	2.51	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
10062	23100	36702	1.02	1.0E-121	AW683858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
10062	23100	36703	1.02	1.0E-121	AW683858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
11015	24094	37733	3.45	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
11023	24102	37740	1.94	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
11211	24280	37919	5.74	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11243	24312	37950	1.93	1.0E-121	N59624.1	EST_HUMAN	yv74c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3'
278	13496	26526	2.64	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
346	13557	26585	2.33	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
368	13577	26610	2.56	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
905	14080	27146	3.34	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1247	14406	27468	5.19	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1728	14878	27969	18.7	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1750	14899	27995	1.61	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1750	14899	27996	1.61	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1857	15003	28110	6.92	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899368 5'
2560	15685	28810	7.43	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2560	15685	28811	7.43	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2901	16080	29096	4.87	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4971	18100	31076	3.81	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5104	18232		1.41	1.0E-122	AW504645.1	EST_HUMAN	UI-HF-BN0-all-a-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'
5681	18875	32164	1.2	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6896	18875	32164	6.8	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7363	20442	33904	0.64	1.0E-122	AA868671.1	EST_HUMAN	ak49h06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409339 3'
8996	22075	35614	0.6	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
9228	22306	35849	1.17	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9524	22589	36159	0.96	1.0E-122	AI359618.1	EST_HUMAN	qy32h07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1. ;
9524	22589	36160	0.96	1.0E-122	AI359618.1	EST_HUMAN	qy32h07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1. ;
10338	23373	36983	0.64	1.0E-122	AL117234.1	NT	Novel human gene mapping to chomosome X, isoform of dbl (proto-oncogene)
11233	24302	37939	2.12	1.0E-122	AW955834.1	EST_HUMAN	EST367904 MAGE resequences, MAGD Homo sapiens cDNA
11667	24744	38436	1.83	1.0E-122	AB024068.1	NT	Homo sapiens gene for B120, exon 10
12231	25178		5.28	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
789	13968	27019	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
789	13968	27020	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1038	14206	27263	6.18	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1047	14213	27270	3.36	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1267	14424	27491	3.83	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1267	14424	27492	3.83	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2035	15176	28286	0.94	1.0E-123	11422479	NT	Homo sapiens similar to sex comb on midleg (Drosophila)-like 2 (H. sapiens) (LOC63782), mRNA
2166	15301	28427	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28428	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28429	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2389	15520		4.21	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
3322	16495	29512	0.71	1.0E-123	6912617	NT	Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5563	18760	31799	1.62	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5563	18760	31800	1.62	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5699	18893	32185	1.76	1.0E-123	BE799746.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
6598	19758	33146	1.93	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7143	20278	33718	0.91	1.0E-123	H53198.1	EST_HUMAN	yq84a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP:YAK1_YEAST P14680 PROTEIN KINASE YAK1 ;
7156	20290	33733	1.39	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7344	20424	33887	0.71	1.0E-123	U55258.1	NT	Human hBRAVO/Nr-CAM precursor (hBRAVO/Nr-CAM) gene, complete cds
7562	20634	34109	0.83	1.0E-123	11525833	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA
7820	20875	34374	1.31	1.0E-123	11436439	NT	Homo sapiens 2'-5'oligoadenylate synthetase 2 (OAS2), mRNA
7829	20884	34386	2.22	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
7836	20891	34393	0.6	1.0E-123	11437202	NT	Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA
7975	21025	34538	0.6	1.0E-123	N35841.1	EST_HUMAN	yx89d11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein kinase PkpA - Phycomyces blakesleeanus ;
7975	21025	34539	0.6	1.0E-123	N35841.1	EST_HUMAN	yx89d11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein kinase PkpA - Phycomyces blakesleeanus ;
8100	21182	34701	0.79	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8100	21182	34702	0.79	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8732	21812		0.7	1.0E-123	AW371924.1	EST_HUMAN	RC4-BT0311-251199-012-a07 BT0311 Homo sapiens cDNA
9569	22711	36279	2.07	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9705	22754	36325	16.77	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
12020	25004	38705	4.91	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
12020	25004	38706	4.91	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
12114	25094	38798	2.71	1.0E-123	AW450931.1	EST_HUMAN	UI-H-BI3-ail-f-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'
12114	25094	38799	2.71	1.0E-123	AW450931.1	EST_HUMAN	UI-H-BI3-ail-f-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
279	13497	26527	1.02	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
279	13497	26528	1.02	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
285	13503		1.49	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
498	13693	26725	2.26	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
709	13891	26926	4	1.0E-124	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ;
709	13891	26927	4	1.0E-124	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ;
777	13957	27008	3.72	1.0E-124	AF155654.1	NT	Human putative ribosomal protein S1 mRNA
831	14009	27065	2.06	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
927	14102	27165	2.67	1.0E-124	7705446	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
1343	14499	27572	0.66	1.0E-124	11419092	NT	Homo sapiens ring finger protein (RNF), mRNA
1377	14532	27605	6.42	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1377	14532	27606	6.42	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1858	15004	28111	4.06	1.0E-124	AJ131712.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (noH61 gene)
2123	15259	28379	2.16	1.0E-124	BE879524.1	EST_HUMAN	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
2528	15653	28777	0.98	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
3579	16744	29761	1.06	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3579	16744	29762	1.06	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3739	16900	29904	1.24	1.0E-124	X13794.1	NT	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS)
4006	17163	30170	0.64	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4179	17329	30321	0.69	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4187	17337	30330	0.98	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4866	17999	30983	2.51	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
5050	18178		15.32	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5205	18326	31296	0.74	1.0E-124	AW963390.1	EST_HUMAN	EST375463 MAGE resequences, MAGH Homo sapiens cDNA
5412	18614	31588	10.49	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5789	18981	32284	1.2	1.0E-124	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6008	19193	32511	6.89	1.0E-124	BF696135.1	EST_HUMAN	602124644F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
6298	19471	32826	0.8	1.0E-124	AV711263.1	EST_HUMAN	AV711263 Cu Homo sapiens cDNA clone CuAADF07 5'
6563	19725	33103	1.12	1.0E-124	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7152	20286	33728	3.15	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene.
7287	20370	33824	0.94	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5'

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7287	20370	33825	0.94	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5'
7725	20789	34278	2.38	1.0E-124	AA630331.1	EST_HUMAN	ac08h05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:855897 3'
8453	21634	35064	2.73	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8657	21737	35277	1.24	1.0E-124	AW612106.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162 O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
8657	21737	35278	1.24	1.0E-124	AW612106.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162 O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
9363	22438	35996	0.68	1.0E-124	AI799864.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321428 3'
9363	22438	35997	0.68	1.0E-124	AI799864.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321428 3'
9691	22740	36309	1.72	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9691	22740	36310	1.72	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9808	22848	36426	7.77	1.0E-124	AI767133.1	EST_HUMAN	wi93f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
9808	22848	36427	7.77	1.0E-124	AI767133.1	EST_HUMAN	wi93f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
10075	23113	36717	1.46	1.0E-124	AW503755.1	EST_HUMAN	UI-HF-BN0-akz-b-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'
11302	24368	38009	1.57	1.0E-124	U94776.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
11617	24668	38356	3.9	1.0E-124	AW665663.1	EST_HUMAN	hj05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'
11761	23947	37575	2.18	1.0E-124	AI446455.1	EST_HUMAN	tj19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN. ;
11761	23947	37576	2.18	1.0E-124	AI446455.1	EST_HUMAN	tj19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN. ;
12310	13891	26926	4.6	1.0E-124	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
12310	13891	26927	4.6	1.0E-124	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
12780	25522	32004	1.99	1.0E-124	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
13080	26038	31680	2.36	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
329	13543		7.32	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
439	13239	26239	4.69	1.0E-125	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
661	13847	26874	2.02	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
661	13847	26875	2.02	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
746	13927	26968	2.42	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1023	14194	27252	1.54	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1177	14340	27394	1.73	1.0E-125	7662278	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1707	16045	27946	1.44	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1854	15000	28106	5.91	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1854	15000	28107	5.91	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2433	16561	28687	4.81	1.0E-125	AA011278.1	EST_HUMAN	zi01g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
2573	15698	28820	0.96	1.0E-125	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2661	15783	28898	2.34	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INHA) mRNA
2661	15783	28899	2.34	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INHA) mRNA
3961	17119	30123	1.33	1.0E-125	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4672	17807	30796	1.82	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4672	17807	30797	1.82	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4739	17874	30857	0.86	1.0E-125	BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5'
5877	19067	32375	0.65	1.0E-125	BF683645.1	EST_HUMAN	602139874F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'
5994	19179	32501	1.39	1.0E-125	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
6013	19197	32514	1.2	1.0E-125	BE175169.1	EST_HUMAN	QV2-HT0577-010500-165-b06 HT0577 Homo sapiens cDNA
6054	19236	32561	3.53	1.0E-125	BE892660.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6096	19277	32606	0.85	1.0E-125	AI679904.1	EST_HUMAN	tu67c07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2256108 3' similar to WP:C45G9.2 CE01854 ;
6412	19581	32942	0.72	1.0E-125	BE736055.1	EST_HUMAN	601305670F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640097 5'
6711	19869	33259	3.71	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
6711	19869	33260	3.71	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7207	20072	33483	4.06	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
7207	20072	33484	4.06	1.0E-126	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
7700	20765	34249	1.56	1.0E-125	BE278823.1	EST_HUMAN	601159076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
7933	20983	34491	0.59	1.0E-125	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8743	21822	35357	1.49	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
8743	21822	35358	1.49	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9318	22394	35945	4.15	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
9318	22394	35946	4.15	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9581	22723	36293	1.06	1.0E-125	AI565996.1	EST_HUMAN	tn52b03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089 HYPOTHETICAL PROTEIN ;
10670	23704	37313	0.72	1.0E-125	BE794576.1	EST_HUMAN	601590345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944531 5'
10712	23745	37351	1.06	1.0E-125	AB002298.1	NT	Human mRNA for KIAA0300 gene, partial cds
10921	24004	37639	3.03	1.0E-125	AF043458.1	NT	Homo sapiens I-REL gene, exon 5
11091	24165	37802	1.34	1.0E-125	11425570	NT	Homo sapiens ryanodine receptor 1 (skeletal) (RYR1), mRNA
11357	24419	38076	2.42	1.0E-125	AL040655.1	EST_HUMAN	DKFZp434N2414_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N2414 5'
11401	24462	38126	3.35	1.0E-125	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
11538	24594		1.63	1.0E-125	R61450.1	EST_HUMAN	yh15a12.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:37663 5'
11568	24623	38303	2.13	1.0E-125	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11575	24630	38309	5.32	1.0E-125	AF026029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11686	24685	38375	2.27	1.0E-125	AW812899.1	EST_HUMAN	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
11793	24783	38479	4.71	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
11793	24783	38480	4.71	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
795	13974	27027	2.16	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
798	13977	27030	1.74	1.0E-126	M61936.1	NT	Human laminin B1 chain gene, exon 20
942	14116	27175	1.53	1.0E-126	X68735.1	NT	H.sapiens gene for alpha1-antichymotrypsin, exon 3
2663	15785	28900	4.55	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3140	16316	29329	8.12	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3140	16316	29330	8.12	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3719	16880	29885	0.87	1.0E-126	X53941.1	NT	H.sapiens DNA for liver cytochrome b5 pseudogene
3745	16906	29910	2.52	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4908	18038	31026	1.08	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4908	18038	31027	1.08	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4956	18086	31062	1.81	1.0E-126	N34078.1	EST_HUMAN	yx78c06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267850 5'
5820	19010	32316	0.68	1.0E-126	T66998.1	EST_HUMAN	ya52b12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66527 3'
6362	19532	32891	2.91	1.0E-126	AA460075.1	EST_HUMAN	zx66e03.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796444 5' similar to TR:G1145880 G1145880 TITIN ;
6419	19588	32951	4.33	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
6419	19588	32952	4.33	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7669	20735	34212	0.9	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7669	20735	34213	0.9	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8062	21144	34662	0.73	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8062	21144	34663	0.73	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds

WO 01/57272 PCT/US01/00663

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8177	21259	34781	2.42	1.0E-126	X16609.1	NT	Human mRNA for ankyrin (variant 2.1)
8377	21458	34982	0.8	1.0E-126	AA483368.1	EST_HUMAN	ne74b12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909983 similar to SW:TSG6_HUMAN P98066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR ;
10000	23038	36629	0.57	1.0E-126	4505424	NT	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
11099	24172	37807	2.01	1.0E-126	BF683175.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298240 5'
11806	24796	38494	2.2	1.0E-126	BE261660.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
12823	18500	31536	6.48	1.0E-126	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
176	13400	26429	2.92	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
176	13400	26430	2.92	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	26429	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	26430	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
284	13502	26535	2.14	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
284	13502	26536	2.14	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
904	14079	27145	1.17	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
939	14113	27174	4.81	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1726	14876	27967	2.22	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2127	15263	28382	1.97	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2127	15263	28383	1.97	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2273	15406	28535	17.46	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2418	15547	28675	3.12	1.0E-127	AF245505.1	NT	Homo sapiens adlican mRNA, complete cds
2674	15794	28911	21.46	1.0E-127	X12881.1	NT	Human mRNA for cytokeratin 18
3781	16942	29948	0.61	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3913	17072	30070	0.7	1.0E-127	AW161297.1	EST_HUMAN	au80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 repetitive element ;
4232	17379	30368	0.59	1.0E-127	AF135188.1	NT	Homo sapiens delayed rectifier potassium channel subunit IsK mRNA, complete cds
4368	17511	30491	24.93	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4368	17511	30492	24.93	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4618	17755	30737	0.83	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds
4725	17860	30842	6.74	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4755	17890		2.69	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4795	17930	30916	4.36	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5824	19014	32320	1.57	1.0E-127	W03547.1	EST_HUMAN	za01e10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291258 5' similar to SW:PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 ;
5854	19044	32351	0.91	1.0E-127	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5923	19110	32423	4.18	1.0E-127	X85764.1	NT	H.sapiens NOS2 gene, exon 6
6291	19464	32816	2.23	1.0E-127	X84060.1	NT	H.sapiens TCF11 gene, exon 3-6
6451	19618	32981	5.73	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
6797	19952	33352	1.09	1.0E-127	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
7208	20073	33485	0.81	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
7984	21014	34525	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7964	21014	34526	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7973	21023	34536	0.63	1.0E-127	BF671355.1	EST_HUMAN	602151232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292575 5'
9088	22167	35713	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9088	22167	35714	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9840	22880	36462	3.73	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9840	22880	36463	3.73	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10077	23115	36718	0.86	1.0E-127	AI298932.1	EST_HUMAN	qm94h09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896449 3'
10551	23586	37194	0.99	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11426	24487	38150	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11426	24487	38151	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11927	24913	38614	1.55	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
11927	24913	38615	1.55	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
12539	13400	26429	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12539	13400	26430	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12763	25507	32037	1.74	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13170	26044		1.64	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
472	13667	26700	1.56	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
1179	14342	27396	0.96	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1179	14342	27397	0.96	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2132	15268	28387	18.07	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2132	15268	28388	18.07	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2283	15415	28547	37.91	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2516	15642		1.11	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3481	16648	29664	1.17	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4786	17921	30909	7.27	1.0E-128	11426673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5662	18856	32139	0.75	1.0E-128	X69539.1	NT	H.sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6548	19710	33086	1.5	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7070	20123	33538	6.26	1.0E-128	BF224345.1	EST_HUMAN	7q86b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
8745	21824	35360	0.67	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8745	21824	35361	0.67	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10341	23376	36987	1.29	1.0E-128	AA639198.1	EST_HUMAN	ne04a11.r1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS.;
10949	24031	37666	3.54	1.0E-128	11425254	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
10957	24038	37673	3.51	1.0E-128	AA926959.1	EST_HUMAN	om68h08.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
11210	24279	37918	1.98	1.0E-128	BE887554.1	EST_HUMAN	601511912F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913371 5'
12402	25282		4.26	1.0E-128	AW955290.1	EST_HUMAN	EST367360 MAGE resequences, MAGC Homo sapiens cDNA
124	13621	26663	1.93	1.0E-129	S37722.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
426	13621	26663	1.65	1.0E-129	S37722.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1756	14905	27999	3.74	1.0E-129	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1761	14910	28004	1.66	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1761	14910	28005	1.66	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1894	15037	28145	4.07	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
2838	15952	29058	2.93	1.0E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
2838	15952	29059	2.93	1.0E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
3198	16373	29380	1.43	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3198	16373	29381	1.43	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3198	16373	29382	1.43	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4279	17424	30413	2.37	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4395	17538	30517	2.32	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4395	17538	30518	2.32	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
6216	19391	32739	3.77	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6654	19813	33201	0.61	1.0E-129	BE888934.1	EST_HUMAN	601513861F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915350 5'
7277	20360	33814	3.99	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
7340	20420	33882	4.03	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
7697	20762	34245	1.04	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
7697	20762	34246	1.04	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8513	21594		3.57	1.0E-129	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10284	23319	36920	1.03	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10284	23319	36921	1.03	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10730	23763	37370	0.52	1.0E-129	AI199117.1	EST_HUMAN	qi40d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840 MITOGEN INDUCIBLE GENE MIG-2 ;
10730	23763	37371	0.52	1.0E-129	AI199117.1	EST_HUMAN	qi40d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840 MITOGEN INDUCIBLE GENE MIG-2 ;
11497	24555	38230	3.32	1.0E-129	AA625526.1	EST_HUMAN	af72f07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5'
11578	20420	33882	5.01	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
12387	25273		4.28	1.0E-129	H83155.1	EST_HUMAN	yq49c05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199112 5' similar to SP:B48150 B48150 HP-25=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN ;
12817	25544		1.97	1.0E-129	AL120739.1	EST_HUMAN	DKFZp762K171_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K171 5'
78	13314	26341	1.01	1.0E-130	7705530	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1197	14359	27418	0.64	1.0E-130	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1700	14852	27939	22.97	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
1700	14852	27940	22.97	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
2040	15181		2.63	1.0E-130	X04092.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2830	15944		7.23	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2943	16120	29132	1.36	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
2943	16120	29133	1.36	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3658	16831	29842	1.03	1.0E-130	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3864	16120	29132	6.31	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3864	16120	29133	6.31	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4047	17203	30213	1.8	1.0E-130	AW503580.1	EST_HUMAN	UI-HF-BN0-aky-g-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4184	17334	30326	0.91	1.0E-130	M97710.1	NT	Human T-cell receptor (V alpha 22.1, J alpha RPMI4265-variant, C alpha 1) mRNA
4660	17796	30782	9.77	1.0E-130	AW843993.1	EST_HUMAN	CM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5208	18329	31300	1.49	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
5208	18329	31301	1.49	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
6960	20188	33612	1.03	1.0E-130	AW843875.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6960	20188	33613	1.03	1.0E-130	AW843875.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6975	20203	33630	0.85	1.0E-130	11425446	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7404	20482	33949	1.85	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7506	20580	34052	0.63	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7506	20580	34053	0.63	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8881	21960		0.53	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
9019	22098	35638	2.06	1.0E-130	AW956242.1	EST_HUMAN	EST368312 MAGE resequences, MAGD Homo sapiens cDNA
9415	22489	36054	1.82	1.0E-130	AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
10137	23175		0.63	1.0E-130	AW103454.1	EST_HUMAN	xd36e06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595874 3'
4	13243	26243	2.52	0.0E+00	AA228126.1	EST_HUMAN	zr58c04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
4	13243	26244	2.52	0.0E+00	AA228126.1	EST_HUMAN	zr58c04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
8	13246	26248	1.14	0.0E+00	4885136	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
16	13254	26254	3.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
16	13254	26255	3.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13261	26262	3.17	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
23	13261	26263	3.17	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
27	13265	26267	9	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
35	13273	26277	0.62	0.0E+00	5802997	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
37	13275	26280	0.89	0.0E+00	M58600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
41	13279	26285	4.6	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
58	13296	26312	1.77	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
58	13296	26313	1.77	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	13298	26317	1.45	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5'
60	13298	26318	1.45	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5'
61	13299	26319	9.83	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
63	13301	26322	16.36	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
63	13301	26323	16.36	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
67	13304	26327	2.48	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
69	13306		23.72	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
77	13313	26339	2.1	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
77	13313	26340	2.1	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26339	1.06	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26340	1.06	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
83	13318	26346	0.62	0.0E+00	AA953770.1	EST_HUMAN	cn89e04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563870 3' similar to SW:TMOD_HUMAN P28289 TROPOMODULIN. ;
84	13319	26347	16.99	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
85	13320		12.3	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
94	13329	26356	23.92	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
97	13332	26359	40.86	0.0E+00	U89277.1	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
103	13339	26366	2.4	0.0E+00	AI114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
104	13340	26367	0.9	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
110	13343	26371	0.68	0.0E+00	X91213.1	NT	H.sapiens ncx1 gene (exon 2)
118	13350	26377	0.68	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
119	13350	26377	1.58	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
120	15980	26378	1.92	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
120	15980	26379	1.92	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
123	13353	26384	1.63	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
133	13359	26392	3.65	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
133	13359	26393	3.65	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
141	13609	26647	1.9	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
143	13367	26400	0.7	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
143	13367	26401	0.7	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
157	13382		12.8	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
161	13386	26416	2.06	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
163	13388		38.39	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
166	13391	26419	12.6	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
168	13393	26420	1.03	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
169	13393	26420	0.79	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
170	13394	26421	2.4	0.0E+00	W73973.1	EST_HUMAN	zd62b05.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
171	13395	26422	0.79	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
171	13395	26423	0.79	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
172	13396	26424	4.73	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
175	13399	26427	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
175	13399	26428	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
185	13407	26435	6.75	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631 ;
185	13407	26436	6.75	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631 ;
190	13412	26439	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
190	13412	26440	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26441	1.66	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26442	1.66	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
199	13422	26453	57.89	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
204	13427	26458	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
204	13427	26459	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
206	13429	26461	7.71	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
206	13429	26462	7.71	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
216	16007	26469	12	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN);
216	16007	26470	12	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN);
218	13440	26472	1.93	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
221	13443		11.48	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
222	13444		6.53	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
228	13450	26478	1.48	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
229	13450	26478	1.34	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
230	13451	26479	2.02	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA
237	13459	26483	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
237	13459	26484	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
237	13459	26485	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
245	13467	26496	1.17	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
245	13467	26497	1.17	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
248	13469	26501	7.54	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
250	13471		3.79	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
257	13476	26507	4.65	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
259	13478	26510	1.22	0.0E+00	X89772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
267	13486		5.95	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
280	13498	26529	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
280	13498	26530	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
282	13500	26532	1.9	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
293	13510		0.96	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
294	13511	26545	1.2	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
294	13511	26546	1.2	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
295	13512		1.41	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
304	13520	26553	5.65	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
304	13520	26554	5.65	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
315	13531	26564	5.16	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
316	13532	26565	4.28	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
317	16010		8.13	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
318	13533		1.42	0.0E+00	AA480002.1	EST_HUMAN	zv18c06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753994 5'
319	13534	26566	19.55	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
320	13534	26566	24.65	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
324	13538	26570	1.59	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
337	13550	26579	1.15	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
337	13550	26580	1.15	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
338	13551	26581	4.14	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
339	13551	26581	1.82	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
354	13565	26593	4.38	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
355	13566	26594	0.74	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
358	13569	26598	4.58	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
361	13572	26603	0.96	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zf31) mRNA, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
366	13576	26607	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
366	13576	26608	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
367	16011	26609	2.53	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
369	13578	26611	1.01	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
372	13581	26615	1.59	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
373	13582	26616	2	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
374	13582	26616	1.43	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
376	13584	26618	0.66	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
387	13593	26629	3.37	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
398	13635	26673	7.56	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
399	13636	26674	1.08	0.0E+00	AI363014.1	EST_HUMAN	qy81h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
404	13601	26636	1.32	0.0E+00	AW754180.1	EST_HUMAN	RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA
407	13603	26639	2.24	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
408	13604	26640	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
408	13604	26641	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
409	13605	26642	2.18	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
410	13606	26643	1.42	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
410	13606	26644	1.42	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
411	13607	26645	1.98	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
412	13608	26646	2.55	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
413	13609	26647	2.14	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
414	13610	26648	0.96	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
414	13610	26649	0.96	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26648	1.07	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26649	1.07	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
419	13614		18.46	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
433	13233	26233	1.49	0.0E+00	R17795.1	EST_HUMAN	yg09a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31652 5'
441	13637	26675	1.39	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) mRNA
442	13638		3.85	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
443	13639	26676	2.82	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
444	13640	26677	17.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
444	13640	26678	17.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
445	13641	26679	4.23	0.0E+00	AF193607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
457	13652		1.45	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
459	13654	26692	4.44	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
464	13659		0.75	0.0E+00	BE254447.1	EST_HUMAN	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
480	13675	26706	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
480	13675	26707	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
486	13680	26715	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
486	13680	26716	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
496	13691	26722	4.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26723	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26724	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
508	13700	26729	4.25	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
508	13702	26731	1.81	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
516	13710	26737	1.66	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
517	16014	26738	1.7	0.0E+00	AW938825.1	EST_HUMAN	PM0-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
520	13713	26740	1.82	0.0E+00	AL117233.1	NT	Novel human gene mapping to chomosome 1
521	13714	26741	0.95	0.0E+00	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
525	13718		1.9	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
532	13725	26751	4.43	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
539	16015	26755	1.57	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
544	13737	26761	1.15	0.0E+00	BF028005.1	EST_HUMAN	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996998 5'
550	13743	26768	1.57	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
553	13746	26771	8.39	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
554	13747	26772	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
554	13747	26773	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
556	13749	26775	0.73	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
557	13750	26776	0.63	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
557	13750	26777	0.63	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
562	13754		4.82	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
570	13762	26786	1.39	0.0E+00	AW135324.1	EST_HUMAN	UI-H-BI1-acb-h-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
580	13772		5.31	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
599	13789	26810	1.85	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), nuclear gene encoding mitochondrial protein, mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
612	13801		7.14	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
615	13804	26824	1.87	0.0E+00	BF104898.1	EST_HUMAN	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
617	13806	26826	0.95	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
617	13806	26827	0.95	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26826	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26827	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13806	26826	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13806	26827	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
624	13809	26830	0.64	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
629	13814	26836	1.93	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
629	13814	26837	1.93	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
639	13824	26847	2.19	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
641	13826	26850	0.93	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
643	13828	26851	1.99	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
644	13829	26852	2.34	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
644	13829	26853	2.34	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
645	13830	26854	0.98	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
645	13830	26855	0.98	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
652	13838	26865	1.42	0.0E+00	AA399486.1	EST_HUMAN	zt60c07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
656	13842	26869	6.57	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
660	13846	26872	4.28	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
660	13846	26873	4.28	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
663	13849		3.58	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
670	13856	26885	2.16	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
672	13858	26888	1.25	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
675	13861	26892	1.88	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
679	13865	26895	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
679	13865	26896	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
685	13870	26901	5.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
685	13870	26902	5.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
691	16018		1.8	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
700	13883	26916	3.92	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
705	13888	26920	4.94	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
715	13897	26935	3.83	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
727	13909	26949	13.13	0.0E+00	AA614537.1	EST_HUMAN	np49d01.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
731	13913	26953	6.4	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
731	13913	26954	6.4	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
741	13923	26963	1.35	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
747	13928	26969	4.62	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
747	13928	26970	4.62	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
749	13930	26973	9.17	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
755	13936	26981	2.26	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
775	13955	27005	1.19	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
775	13955	27006	1.19	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
778	13958	27009	8.92	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
778	13958	27010	8.92	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
781	13961	27011	0.96	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
782	13962	27012	2.07	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
784	16022	27014	2.36	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
785	13964	27015	3.55	0.0E+00	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
790	13969	27021	4.04	0.0E+00	R48915.1	EST_HUMAN	yj69g08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154046 5'
791	13970	27022	2.85	0.0E+00	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
800	13979	27031	1.64	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
803	13983	27035	3.01	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
815	13994	27048	1.24	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
815	13994	27049	1.24	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
820	13999	27053	2.74	0.0E+00	X89772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
824	14003	27057	3.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
824	14003	27058	3.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
829	14007	27064	13.47	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
830	14008		11.09	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
847	14025	27085	1.65	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
848	14026	27086	2.46	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	14028	27088	1.84	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, isk-related family, member 1 (KCNE1) mRNA

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856	14033	27094	2.19	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
856	14033	27095	2.19	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
857	14034	27096	1.45	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
862	14039	27101	2.85	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
866	14042	27106	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
866	14042	27107	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
873	14049		2.07	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
877	14053	27118	5.27	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
877	14053	27119	5.27	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
878	14054	27120	11.32	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
879	14055	27121	4.03	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
880	14056	27122	3.87	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
884	14060	27125	1.54	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
884	14060	27126	1.54	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
885	14061	27127	1.82	0.0E+00	AA533272.1	EST_HUMAN	nj66d07.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997453
885	14061	27128	1.82	0.0E+00	AA533272.1	EST_HUMAN	nj66d07.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997453
886	14062		8.41	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
890	14066	27129	1.4	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
890	14066	27130	1.4	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27131	2.54	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27132	2.54	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
914	14089	27155	0.98	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
921	14096	27160	1.93	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
921	14096	27161	1.93	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
931	14106	27170	2.7	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
941	14115		9.06	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
943	14115		9.69	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
944	14117	27176	1.42	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
945	14118	27177	0.69	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
945	14118	27178	0.69	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
945	14118	27179	0.69	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
946	14119	27180	1.62	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds
949	14122	27183	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
949	14122	27184	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
973	14146	27205	0.93	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
974	14147	27206	9.11	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
975	14148	27207	0.79	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
976	14149	27208	1.24	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
976	14149	27209	1.24	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
984	16027	27216	3.95	0.0E+00	AI001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
984	16027	27217	3.95	0.0E+00	AI001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
986	14158	27219	14.34	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
997	14168	27229	1.76	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
1006	14177	27236	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1006	14177	27237	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1006	14177	27238	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1008	14179	27241	2.02	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1008	14179	27242	2.02	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1017	14188	27249	3.97	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
1029	14199	27257	1.07	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1030	14200	27258	5.81	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1031	14200	27258	9.09	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1034	14203		4	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1035	14203		29.56	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1039	14207	27264	0.96	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1040	14207	27264	4.66	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1041	14207	27264	1.3	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1042	14208	27265	1.18	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1045	14211	27268	2.11	0.0E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1049	14215	27272	1.27	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1051	14217		1.39	0.0E+00	AA458680.1	EST_HUMAN	aa86g07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8 ;
1054	14220	27277	2.43	0.0E+00	N43182.1	EST_HUMAN	EST51i24 WATM1 Homo sapiens cDNA clone 51i24 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1054	14220	27278	2.43	0.0E+00	N43182.1	EST_HUMAN	EST51i24 WATM1 Homo sapiens cDNA clone 51i24 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1065	14221	27279	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1055	14221	27280	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1058	14224		3.27	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA
1072	14238	27295	1.51	0.0E+00	4758569	NT	Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPA9B) mRNA
1090	14255	27310	1.51	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1090	14255	27311	1.51	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1094	14259	27315	2.74	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1094	14259	27316	2.74	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1095	14260	27317	13.57	0.0E+00	AJ246922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1097	14262		0.92	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1099	14264	27321	2.81	0.0E+00	5174384	NT	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA
1106	14271	27330	2.04	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1120	14285	27340	1.91	0.0E+00	BE005208.1	EST_HUMAN	MR0-BN0115-200300-003-h08 BN0115 Homo sapiens cDNA
1143	14308	27364	3.82	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1143	14308	27365	3.82	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1155	14319	27373	0.82	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1155	14319	27374	0.82	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1156	14320	27375	9.35	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1158	14322	27377	1.2	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1161	14325	27380	3.95	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1163	14327	27381	19.6	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1164	14328	27382	4.52	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1164	14328	27383	4.52	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1168	14331	27386	1.44	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1169	14332	27387	0.71	0.0E+00	X95826.1	NT	H.sapiens ART4 gene
1169	14332	27388	0.71	0.0E+00	X95826.1	NT	H.sapiens ART4 gene
1170	14333	27389	1.15	0.0E+00	AI147650.1	EST_HUMAN	qb22d10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'
1172	14335	27391	1.62	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1181	14344	27400	1.22	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1181	14344	27401	1.22	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1182	14345	27402	1.32	0.0E+00	9966844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1195	14357	27415	2.19	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1195	14357	27416	2.19	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1198	14360	27419	1.09	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1205	14367	27428	8.64	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1236	14395		1.28	0.0E+00	7657336	NT	Homo sapiens mutL (E. coli) homolog 3 (MLH3), mRNA
1250	14409	27471	0.94	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1254	14413	27475	2.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1254	14413	27476	2.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1255	14414	27477	3.33	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1256	16032	27478	2.46	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1275	14432	27503	4.86	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1276	14433	27504	1.67	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1286	14442	27510	0.69	0.0E+00	4505740	NT	Homo sapiens prefoldin 4 (PFDN4) mRNA
1295	14451		1.38	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1303	14459	27525	29.86	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1310	14466	27534	2.96	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
1316	14472	27538	1.63	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1316	14472	27539	1.63	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1328	14485	27552	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1328	14485	27553	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1328	14485	27554	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1329	14486		2.16	0.0E+00	AF096156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1339	16034	27566	1.2	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1339	16034	27567	1.2	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1345	15991	27573	1.4	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1346	14501	27574	1.86	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1347	14502	27575	0.83	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1349	14504	27576	1.7	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1350	14505	27577	1.55	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1351	14506	27578	0.71	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1353	14508	27580	4.44	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1354	14509	27581	1.34	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1355	14510	27582	4.99	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1356	14511	27583	3.83	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1356	14511	27584	3.83	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1368	14522	27597	1.36	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1429	14583	27656	1.02	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1429	14583	27657	1.02	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1440	14593	27668	1.03	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyld gene
1449	14602	27680	13.57	0.0E+00	6042206	NT	RAN, member RAS oncogene familyHomo sapiens RAN, member RAS oncogene family (RAN), mRNA
1457	14610	27690	0.97	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1457	14610	27691	0.97	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1459	14612	27694	1.99	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1459	14612	27695	1.99	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1462	14615	27697	29.09	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1471	14625	27709	4.63	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7
1490	14643	27724	4.2	0.0E+00	AL132999.1	NT	Novel human gene on chromosome 20
1491	14644	27725	1.37	0.0E+00	AL137764.1	NT	Novel human gene mapping to chomosome 1
1495	14648	27730	1.73	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1498	14651	27733	8.24	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1500	14653	27735	2.28	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1500	14653	27736	2.28	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1501	14654		3.74	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1507	14660	27742	6.62	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1507	14660	27743	6.62	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1541	14693	27772	2.61	0.0E+00	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51696), mRNA
1555	14708	27788	2.66	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5'
1562	14715	27792	27.8	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1562	14715	27793	27.8	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1564	14717	27796	1.55	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1564	14717	27797	1.55	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1565	14718	27798	1.03	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1567	14720		3.2	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1568	14721	27801	26.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1568	14721	27802	26.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1570	14723	27804	3.85	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1571	14724		9.78	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1576	14729	27810	64.77	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1578	14731	27811	0.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1578	14731	27812	0.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1579	16042		32.23	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1580	14732	27813	27.68	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1592	14745	27828	1.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1592	14745	27829	1.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1594	14747	27830	13.85	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1602	14755		3.25	0.0E+00	D00333.1	NT	human c-yes-2 gene
1611	14764	27844	11.38	0.0E+00	Z83738.1	NT	H.sapiens hH2B/e gene
1612	14765	27845	2.55	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1612	14765	27846	2.55	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1613	14766	27847	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1613	14766	27848	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1616	16043	27851	2.1	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1618	14770	27852	1.88	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1620	14772	27855	6.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1620	14772	27856	6.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1622	14774	27857	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1622	14774	27858	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1624	14776	27860	1.53	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1639	14791	27876	6.29	0.0E+00	H26973.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1648	14801	27887	1.87	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1648	14801	27888	1.87	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1668	14820	27903	1.66	0.0E+00	AW444637.1	EST_HUMAN	UI-H-BI3-ajw-c-04-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1698	14850	27936	2.12	0.0E+00	BE144364.1	EST_HUMAN	MR0-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1698	14850	27937	2.12	0.0E+00	BE144364.1	EST_HUMAN	MR0-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1702	14854	27941	1.3	0.0E+00	AI768104.1	EST_HUMAN	wg81b07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN. ;
1703	14855	27942	1.71	0.0E+00	4758513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1704	14856	27943	2.8	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1708	14859	27947	2.1	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1708	14859	27948	2.1	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1710	14861	27950	64.4	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1711	14862	27951	2.42	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1714	14865	27954	1.08	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1714	14865	27955	1.08	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1716	14856	27957	3.2	0.0E+00	4557610	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1719	14869	27960	4.3	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1719	14869	27961	4.3	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1721	14871		0.97	0.0E+00	AI149880.1	EST_HUMAN	qf43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
1722	14872	27963	10.28	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
1722	14872	27964	10.28	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
1725	14875		21.3	0.0E+00	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1734	14883	27976	6.13	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1737	14886	27979	1.63	0.0E+00	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1741	14890	27983	1.95	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1741	14890	27984	1.95	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1744	14893	27988	1.11	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1747	14896	27990	2.54	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1747	14896	27991	2.54	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1751	14900	27997	6.57	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1753	14902		2.64	0.0E+00	S94400.1	NT	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1762	14911	28006	5.29	0.0E+00	4557538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA
1784	14933	28027	3.33	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1826	16047		41.96	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1830	14978	28073	3.2	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1830	14978	28074	3.2	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1833	14980	28078	2.47	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1837	16048	28083	7.55	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1839	14985	28085	1.7	0.0E+00	AA113030.1	EST_HUMAN	zn65c09.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563056 3'
1850	14996	28099	24.06	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
1852	14998	28102	9	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1853	14999	28103	24.99	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1853	14999	28104	24.99	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1853	14999	28105	24.99	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1870	15015	28124	3.11	0.0E+00	4504626	NT	Homo sapiens immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products
1870	15015	28125	3.11	0.0E+00	4504626	NT	Homo sapiens immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products
1881	15025	28131	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1881	15025	28132	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1892	15036	28143	1.84	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1892	15036	28144	1.84	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1895	15038	28146	3.59	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1895	15038	28147	3.59	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1896	15039	28148	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1896	15039	28149	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1899	15042	28152	2.3	0.0E+00	AW207280.1	EST_HUMAN	UI-H-BI1-efn-f-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1899	15042	28153	2.3	0.0E+00	AW207280.1	EST_HUMAN	UI-H-BI1-efn-f-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1924	15067	28171	3.22	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1924	15067	28172	3.22	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1943	15086	28187	1.04	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0126-200300-012-b04 BN0126 Homo sapiens cDNA
1972	15115	28215	1.62	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1972	15115	28216	1.62	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1975	15118	28218	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1975	15118	28219	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1981	15124	28226	1.29	0.0E+00	AB037788.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1985	15128		1.64	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1986	16051	28230	57.92	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1986	16051	28231	57.92	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1991	15133	28238	3.19	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1991	15133	28239	3.19	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1994	15135	28241	2.41	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1996	15137		6.39	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2001	15142		5.28	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
2003	16052	28248	1.84	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2005	15145	28250	1.3	0.0E+00	BE018066.1	EST_HUMAN	bb73f11.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5'
2011	15151	28255	1.69	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2011	15151	28256	1.69	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2024	15165		1.04	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
2026	15167	28272	1.41	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2026	15167	28273	1.41	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2027	15168	28274	12.98	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2027	15168	28275	12.98	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2037	15178	28288	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2037	15178	28289	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2043	15184	28293	1.93	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2043	15184	28294	1.93	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2045	15186	28295	3.24	0.0E+00	AW193024.1	EST_HUMAN	xl69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'
2045	15186	28296	3.24	0.0E+00	AW193024.1	EST_HUMAN	xl69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'
2046	15187	28297	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2046	15187	28298	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2048	15189	28300	1.53	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2049	15190	28301	1.09	0.0E+00	Z47556.1	NT	H.sapiens genes for semenogelin I and semenogelin II
2049	15190	28302	1.09	0.0E+00	Z47556.1	NT	H.sapiens genes for semenogelin I and semenogelin II
2056	15197	28311	5.04	0.0E+00	AB040945.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2078	15218	28337	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2078	15218	28338	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2109	15247	28368	1.53	0.0E+00	8394546	NT	Homo sapiens chromosome 21 open reading frame 7 (YG81), mRNA
2112	15250	28370	0.98	0.0E+00	7706742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2117	15255	28374	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2117	15255	28375	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2119	15257	28376	1.02	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2121	15258	28378	57.93	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2122	14612	27694	0.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2122	14612	27695	0.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2124	15260	28380	2.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2124	15260	28381	2.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2126	15262		3.79	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA

WO 01/57272 PCT/US01/00663

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2128	15264		1.48	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2129	15265	28384	2.9	0.0E+00	Z42399.1	EST_HUMAN	HSC0IC021 normalized infant brain cDNA Homo sapiens cDNA clone c-0ic02
2131	15267		2.38	0.0E+00	AI244247.1	EST_HUMAN	qv90f08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element;
2136	15272	28393	4.37	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2138	15274	28395	2.25	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2138	15274	28396	2.25	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2144	15280	28404	3.6	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2144	15280	28405	3.6	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2152	15288	28414	3.43	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2152	15288	28415	3.43	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2153	15289	28416	1.11	0.0E+00	AJ297709.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 1
2158	15294	28420	1.16	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2162	15298	28423	1.94	0.0E+00	BE500995.1	EST_HUMAN	7a34c02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3220610 3' similar to SW:DTD_HUMAN P50443 SULFATE TRANSPORTER ;
2182	15317		3.17	0.0E+00	BE767964.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2183	15318		1.26	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLRS1) gene, exon 6 and complete cds
2185	15320	28446	4.64	0.0E+00	BF027562.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2186	15321	28447	1.5	0.0E+00	BE072624.1	EST_HUMAN	PM0-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2188	15323	28448	1.29	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2190	15325	28450	3.41	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2192	15327	28452	6.48	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2192	15327	28453	6.48	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2225	15359		1.08	0.0E+00	7657252	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA
2249	15382		1.52	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3'end
2259	15392	28518	1.26	0.0E+00	BE274696.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2261	15394	28521	0.94	0.0E+00	D87685.1	NT	Human mRNA for KIAA0244 gene, partial cds
2262	15395	28522	23.12	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2262	15395	28523	23.12	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2264	15397	28525	2.57	0.0E+00	AA931691.1	EST_HUMAN	oc32e01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2268	15401	28529	24.38	0.0E+00	BF344434.1	EST_HUMAN	602014829F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150734 5'
2269	15402	28530	40.14	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2272	15405	28533	5.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2272	15405	28534	5.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2276	16059	28539	4.06	0.0E+00	BF313617.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128622 5'
2279	15411	28542	3.13	0.0E+00	BE018750.1	EST_HUMAN	601900261F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 bb84ed02.yr1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;
2281	15413	28544	1.88	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN); zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2289	15421	28553	3.06	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2289	15421	28554	3.06	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2290	15422	28555	3.72	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2290	15422	28556	3.72	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2295	15427		2.34	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2296	15428	28561	1.02	0.0E+00	AA282281.1	EST_HUMAN	zt12b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2313	15445	28579	7.92	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2320	15452	28584	2.63	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2327	15459	28592	3.44	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2331	15463	28596	1.51	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2331	15463	28597	1.51	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2333	15464	28599	1.83	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2375	15506	28632	4.35	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2375	15506	28633	4.35	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2376	15507	28634	2.67	0.0E+00	AI076404.1	EST_HUMAN	oz09c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2378	15509	28636	2.95	0.0E+00	AA429001.1	EST_HUMAN	zv78a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2378	15509	28637	2.95	0.0E+00	AA429001.1	EST_HUMAN	zv78a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2380	15511	28639	1.82	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157339 5'
2385	15516	28645	1.33	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2385	15516	28646	1.33	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2386	15517	28647	2.34	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2393	15524	28653	2.36	0.0E+00	BE676095.1	EST_HUMAN	7f22a02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296370 3' similar to TR:O94939 O94939 KIAA0857 PROTEIN ;
2396	15527	28655	5.46	0.0E+00	AF044571.1	NT	Homo sapiens phosphorylase kinase alpha subunit (PHKA2) gene, exon 32
2397	15528	28656	2.6	0.0E+00	AI625542.1	EST_HUMAN	ty67c08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2283182 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2399	15530	28657	1.5	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2402	15533	28659	2.22	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2402	15533	28660	2.22	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2405	15536	28663	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2405	15536	28664	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2424	15553	28679	3.04	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2428	15556	28683	3.56	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2429	15557		9.82	0.0E+00	BE794026.1	EST_HUMAN	601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2430	15558	28684	3.96	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2431	15559	28685	1.39	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2431	15559	28686	1.39	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2432	15560		7.14	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2434	15562	28688	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28689	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28690	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2452	15580		1.03	0.0E+00	BE814424.1	EST_HUMAN	MR0-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA
2485	15612	28735	1.14	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2487	15614		4.63	0.0E+00	AI042035.1	EST_HUMAN	ox60b02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:O08662 O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE. ;
2489	15616	28737	0.94	0.0E+00	8923620	NT	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA
2492	15619		1.35	0.0E+00	BE895605.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2503	15630		2.22	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2505	15632	28752	6.05	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2510	15636	28756	1.99	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2510	15636	28757	1.99	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2520	15646	28769	2.42	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2524	15649	28773	0.96	0.0E+00	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
2530	15655	28780	3.64	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2538	15663	28786	1.02	0.0E+00	U13666.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2538	15663	28787	1.02	0.0E+00	U13666.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2539	15664	28788	28.11	0.0E+00	BF569144.1	EST_HUMAN	602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2547	15672	28796	4.18	0.0E+00	AW466922.1	EST_HUMAN	ha04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2550	15675	28798	3.03	0.0E+00	AW501010.1	EST_HUMAN	UI-HF-BP0p-ais-c-07-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2575	15700		2.02	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2578	15704	28824	7.28	0.0E+00	BE795542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2579	15135	28241	1.12	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2580	15705	28825	1.44	0.0E+00	BF509482.1	EST_HUMAN	UI-H-BI4-aoz-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2583	15708	28827	2.21	0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2585	15710		5.17	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
2587	15712	28830	1.07	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2588	15713	28831	2.39	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2589	15714	28832	3.09	0.0E+00	U93239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2595	15720	28838	1.66	0.0E+00	BE886490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2598	15722	28842	13.07	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2598	15722	28843	13.07	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2599	15723	28844	1.12	0.0E+00	AF245505.1	NT	Homo sapiens adlican mRNA, complete cds
2616	15740	28852	1.83	0.0E+00	BE536921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2623	15746	28860	3.66	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2623	15746	28861	3.66	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2624	15747	28862	1.25	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2624	15747	28863	1.25	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 6'
2625	15748	28864	1.04	0.0E+00	BF223041.1	EST_HUMAN	7q27h12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE: 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN ;
2628	15751	28866	8.3	0.0E+00	AF245505.1	NT	Homo sapiens adlican mRNA, complete cds
2664	15000	28901	2.18	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2664	15000	28902	2.18	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2665	15786		2.35	0.0E+00	BF513835.1	EST_HUMAN	UI-H-BW1-amp-f-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2675	15795	28912	32.6	0.0E+00	BF204131.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2675	15795	28913	32.6	0.0E+00	BF204131.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2678	15798	28915	2.15	0.0E+00	AB037742.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2679	15799	28916	2.52	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2I) mRNA
2681	15801	28918	8.53	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2682	15802	28919	1.16	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2682	15802	28920	1.16	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2690	15810		2.75	0.0E+00	BE792472.1	EST_HUMAN	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2700	15819	28935	2.52	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2710	15828		1.16	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2711	15829	28942	5.67	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2715	15833	28943	1.07	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2718	15836	28946	0.96	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2721	15839	28949	1.15	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2721	15839	28950	1.15	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2724	15842	28953	1.66	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-d07 OT0086 Homo sapiens cDNA
2727	15845	28956	4.83	0.0E+00	BE383165.1	EST_HUMAN	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2728	15846		2.8	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2763	15878	28987	1	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2785	15901		11.99	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2789	15905	29013	4.04	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2791	15907	29015	3.72	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2792	15908	29016	2.32	0.0E+00	AB051826.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2797	15912	29020	11.38	0.0E+00	BE796376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2800	16072	29024	17.3	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2801	15915		3.28	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2803	15917	29027	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2803	15917	29028	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2804	15918	29029	2.21	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2805	15919		47.74	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'
2806	15920	29030	5.84	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2806	15920	29031	5.84	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2810	15924	29034	1.15	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2810	15924	29035	1.15	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2813	15927	29039	21.96	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2814	15928	29040	1.05	0.0E+00	N44974.1	EST_HUMAN	yy35h10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773 A45773 kelch protein, long form - fruit fly ;
2816	15930	29042	1.15	0.0E+00	BE176836.1	EST_HUMAN	RC4-HT0587-170300-012-d11 HT0587 Homo sapiens cDNA
2827	15941		1.13	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2828	15942	29052	3.19	0.0E+00	BF514110.1	EST_HUMAN	UI-H-BW1-amw-e-07-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2835	15949		1.67	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2841	15955	29062	1.08	0.0E+00	7705275	NT	Homo sapiens angiopoietin-3 (ANG-3), mRNA
2841	15955	29063	1.08	0.0E+00	7705275	NT	Homo sapiens angiopoietin-3 (ANG-3), mRNA
2842	15956	29064	5.05	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2848	15962	29072	1.33	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2852	15966	29075	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2852	15966	29076	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2854	15968		14.75	0.0E+00	AI879163.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2857	15971	29081	2.14	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214679 5'
2858	15972	29082	71.97	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2860	15974	29083	2.42	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2860	15974	29084	2.42	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2861	15975	29085	64.06	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2861	15975	29086	64.06	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2867	13415	26444	5.26	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
2870	15982		1.64	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2876	13933	26978	1.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2876	13933	26979	1.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2880	14230	27287	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2880	14230	27288	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2897	16076	29094	3.73	0.0E+00	X85980.1	NT	H.sapiens serine hydroxymethyltransferase pseudogene
2898	16077		1.26	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
2900	16079		1.91	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2907	16085	29099	4.25	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2911	16089	29102	6.5	0.0E+00	M80902.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
2914	16092	29104	0.93	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2914	16092	29105	0.93	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2916	16094		2.05	0.0E+00	X73428.1	NT	H.sapiens Id3 gene for HLH type transcription factor
2918	16096		2.6	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2919	16097	29108	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2919	16097	29109	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2919	16097	29110	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2921	16099	29111	15.94	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2926	16103	29117	30.49	0.0E+00	D50657.1	NT	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene
2926	16103	29118	30.49	0.0E+00	D50657.1	NT	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene
2929	16106	29121	3.42	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2930	16107		6.12	0.0E+00	Y10658.1	NT	H.sapiens mRNA for nuclear DNA helicase II
2931	16108		1.13	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2932	16109	29122	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2932	16109	29123	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2944	16121	29134	2.54	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2947	16124	29138	1.19	0.0E+00	AL047599.1	EST_HUMAN	DKFZp586G0621_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586G0621
2948	16125	29139	0.96	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2948	16125	29140	0.96	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2949	16126		2.44	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2952	16129	29142	5.16	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2952	16129	29143	5.16	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2958	16135	29151	0.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2958	16135	29152	0.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2961	16138	29156	2.3	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2961	16138	29157	2.3	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2962	16139	29158	1.3	0.0E+00	AA215579.1	EST_HUMAN	zr96b11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element;
2969	16145		3.99	0.0E+00	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
2972	16148	29167	1.05	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2974	16150	29170	25.96	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2975	16151	29171	1.15	0.0E+00	AI561002.1	EST_HUMAN	tn18d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN. ;
2975	16151	29172	1.15	0.0E+00	AI561002.1	EST_HUMAN	tn18d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN. ;
2977	16153	29174	1.18	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
2978	16154	29175	1.04	0.0E+00	AF152338.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2994	16170	29187	3.4	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2994	16170	29188	3.4	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2995	16171	29189	6.2	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2995	16171	29190	6.2	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2998	16174	29193	3.31	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2998	16174	29194	3.31	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2999	16175	29195	4.93	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2999	16175	29196	4.93	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
3003	16178	29199	1.29	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 Q9VLN1 CG17293 PROTEIN. ;
3003	16178	29200	1.29	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 Q9VLN1 CG17293 PROTEIN. ;
3011	16187	29211	3.91	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
3011	16187	29212	3.91	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
3019	16195	29218	1.51	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3022	16198	29221	0.98	0.0E+00	AB033034.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
3024	16200	29223	9.6	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3038	16214		1.44	0.0E+00	AI149880.1	EST_HUMAN	qf43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
3045	16221	29242	0.71	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3045	16221	29243	0.71	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3046	16222	29244	0.92	0.0E+00	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3047	16223	29245	2.81	0.0E+00	AB004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3057	16233	29252	1.85	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
3058	16234	29253	1.92	0.0E+00	AW612526.1	EST_HUMAN	hh03f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954055 3' similar to TR:O60407 O60407 PAC CLONE DJ1168D11 FROM 7P21-P22, COMPLETE SEQUENCE ;
3059	16235	29254	2.4	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3059	16235	29255	2.4	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3067	16243	29263	1.17	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3067	16243	29264	1.17	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3091	16267		0.61	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3093	16269	29285	1.29	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
3102	16278	29292	0.68	0.0E+00	4506882	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3109	16285		3.53	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3112	16288	29303	4.9	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3112	16288	29304	4.9	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3114	16290		7.27	0.0E+00	AL359403.1	NT	Isoform 2 of a novel human mRNA from chromosome 22
3119	16295	29309	1.88	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3122	16298		2.21	0.0E+00	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3124	16300	29313	3.78	0.0E+00	4504664	NT	Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA
3145	16321	29333	3.23	0.0E+00	X03529.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)
3151	16326		1.92	0.0E+00	AF199355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3155	16330	29340	1.75	0.0E+00	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3175	16350	29356	4.71	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3176	16351	29357	10.17	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3181	16356	29361	3.92	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3182	16357	29362	1.29	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3187	16362	29368	1.19	0.0E+00	AW188146.1	EST_HUMAN	xj92h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664733 3' similar to SW:RNP_HYDHY P00677 RIBONUCLEASE PANCREATIC ;
3210	16384	29395	3.61	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3219	16393	29404	20.63	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3222	16396	29407	1.05	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3222	16396	29408	1.05	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3229	16403	29415	25.61	0.0E+00	T94870.1	EST_HUMAN	yc32f03.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S29539 S29539 BASIC PROTEIN, 23K - ;
3244	16418	29433	0.93	0.0E+00	BF243336.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3245	16419	29434	1.22	0.0E+00	AI968086.1	EST_HUMAN	wu12h10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516803 3'
3250	16424	29441	5.36	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3250	16424	29442	5.36	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3252	16426	29444	1.01	0.0E+00	AI685950.1	EST_HUMAN	tu38g09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICDI P03967 RAS-LIKE PROTEIN RASD ;
3262	16436	29455	1.39	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3262	16436	29456	1.39	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3270	16444	29464	9.58	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3288	16462	29482	4.54	0.0E+00	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3292	16466	29485	1.92	0.0E+00	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA

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3298	16472	29493	0.76	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3298	16472	29494	0.76	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3300	16474	29495	29.49	0.0E+00	AA774783.1	EST_HUMAN	ae87b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3308	16482	29503	8.38	0.0E+00	AF286598.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
3308	16482	29504	8.38	0.0E+00	AF286598.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
3320	16493	29510	3.04	0.0E+00	4557590	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3326	16499	29517	1.01	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3334	16507		10.18	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
3335	16508	29524	0.95	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
3338	16511	29527	4.06	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3348	16464	29535	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3348	16464	29536	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3363	16535	29549	3.56	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3364	16536	29550	0.95	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3377	16549	29563	1.42	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3388	16558	29573	0.72	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3401	16571	29586	3.14	0.0E+00	AI589294.1	EST_HUMAN	tr58f08.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT P25121 60S RIBOSOMAL PROTEIN L11. ;contains Alu repetitive element;
3404	16574	29589	9.94	0.0E+00	AW955400.1	EST_HUMAN	EST367470 MAGE resequences, MAGD Homo sapiens cDNA
3412	16581	29596	2.41	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3412	16581	29597	2.41	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3413	16582	29598	1.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3413	16582	29599	1.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3416	16585	29601	1.29	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3416	16585	29602	1.29	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3419	16588	29604	11.92	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3421	16590	29606	1.02	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3428	16596	29612	0.79	0.0E+00	BE779039.1	EST_HUMAN	601464995F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'
3441	16609	29627	0.67	0.0E+00	AI632569.1	EST_HUMAN	wb10f04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN. ;
3483	16651	29667	10	0.0E+00	AU123664.1	EST_HUMAN	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3492	16659	29671	1.16	0.0E+00	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51694), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3493	16660	29672	1.26	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
3498	16665		0.94	0.0E+00	AW867015.1	EST_HUMAN	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3511	16677	29687	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3511	16677	29688	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3512	16678	29689	0.92	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3514	16680	29690	2.35	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3523	15907	29015	3.08	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3528	16693	29703	2.46	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3532	16697	29708	5.5	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC incompatibility determinants
3535	16700	29711	1.38	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3538	16703	29714	1.83	0.0E+00	4557746	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3544	16709	29719	4.17	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE. ;
3544	16709	29720	4.17	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE. ;
3548	16713	29725	1.91	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3555	16720	29734	5.38	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3555	16720	29735	5.38	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3560	16725	29741	1.41	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3566	16731	29747	5.78	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3574	16739	29755	2.57	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3574	16739	29756	2.57	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3582	16747	29765	1.18	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3594	16758	29773	3.29	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3594	16758	29774	3.29	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3597	16761	29777	1.04	0.0E+00	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3600	16764	29780	0.8	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3603	16767	29782	0.89	0.0E+00	AI384007.1	EST_HUMAN	te35g12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498 O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3621	16785	29801	0.6	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3621	16785	29802	0.6	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds

WO 01/57272 PCT/US01/00663

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3623	16787	29803	0.68	0.0E+00	AA456282.1	EST_HUMAN	zx99h04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3623	16787	29804	0.68	0.0E+00	AA456282.1	EST_HUMAN	zx99h04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3630	16794	29811	1.45	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB Homo sapiens cDNA clone ADBDAH06 5'
3631	16795	29812	4.48	0.0E+00	4506884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3633	16797		1.17	0.0E+00	AF078868.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3642	16806	29820	1.34	0.0E+00	AL133204.1	NT	Novel human gene mapping to chomosome X
3644	16807	29821	1.16	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3665	16828	29837	0.97	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3665	16828	29838	0.97	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3667	16830	29841	1.06	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3672	16835		4.28	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3679	16842		1.28	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3680	16843	29850	7.65	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'
3704	16865	29868	0.59	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3704	16865	29869	0.59	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3705	16866		0.99	0.0E+00	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3707	16868	29871	0.76	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3707	16868	29872	0.76	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3711	16872	29876	0.89	0.0E+00	4826763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3713	16874	29879	0.93	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3720	16881	29886	0.74	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3720	16881	29887	0.74	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3737	16898	29901	2.36	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3741	16902		6.29	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3757	16918	29920	3.98	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3759	16920	29922	1.06	0.0E+00	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3761	16922	29923	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3761	16922	29924	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3767	16928	29932	32.49	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3767	16928	29933	32.49	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3770	16931	29935	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3770	16931	29936	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

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3771	16932	29937	0.99	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3771	16932	29938	0.99	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3774	16935	29941	2.4	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281099-005-e05 CT0222 Homo sapiens cDNA
3776	16937	29943	2.37	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3778	16939	29945	1.15	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3780	16941	29947	0.74	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3782	16943	29949	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3782	16943	29950	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3794	16955	29959	5.42	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3794	16955	29960	5.42	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3823	16983	29986	1.04	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 6
3824	16984	29987	1.17	0.0E+00	AA463659.1	EST_HUMAN	aa06g01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1] ;
3831	16991	29993	3.23	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3841	17000	30003	0.83	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3855	17015	30015	5.72	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3859	17019	30018	18.03	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3866	17025	30023	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3866	17025	30024	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3869	17028	30027	8.94	0.0E+00	4505594	NT	Homo sapiens plasminogen activator inhibitor, type II (arginine-serpin) (PAI2) mRNA
3922	17081	30077	1.96	0.0E+00	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3924	17083		0.73	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3925	17084	30079	2.36	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3928	17087	30083	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3928	17087	30084	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3929	17088	30085	1.74	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3935	17094	30092	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3935	17094	30093	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3936	17095	30094	1.29	0.0E+00	AI377699.1	EST_HUMAN	te62f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3937	17096		1	0.0E+00	AF152495.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3938	17097	30095	2.6	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
3940	17099	30096	15.6	0.0E+00	S78685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3942	17101	30098	2.14	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA

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3943	17102	30099	1.78	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3945	17105	30101	1.62	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3946	17105	30102	1.62	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3951	17109	30107	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2,complete and partial cds
3951	17109	30108	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2,complete and partial cds
3952	17110	30109	0.9	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3957	17115	30117	6.96	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3957	17115	30118	6.96	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3959	17117	30121	4.85	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3960	17118	30122	1.12	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3963	17121	30124	1.23	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3966	17124	30127	1.44	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3967	17125	30128	2.87	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3969	17127	30130	0.77	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3979	17136	30140	3.22	0.0E+00	AI864727.1	EST_HUMAN	wk01f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340 O43340 R28830_2. ;contains element PTR7 repetitive element ;
3980	17137	30141	1.03	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
3983	17140	30145	18.17	0.0E+00	4506742	NT	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3988	17145	30151	1.33	0.0E+00	AL040338.1	EST_HUMAN	DKFZp434N0413_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0413 5'
3994	17151	30158	1.9	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3994	17151	30159	1.9	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3996	17153	30161	3.94	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3997	17154		2.26	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
4001	17158	30164	0.97	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
4013	17170	30178	2.65	0.0E+00	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4017	17174	30182	1.9	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4026	17182	30191	5.14	0.0E+00	BF355295.1	EST_HUMAN	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA
4028	17184	30193	1.37	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5 Matrix remodeling associated gene 5
4028	17184	30194	1.37	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5 Matrix remodeling associated gene 5
4035	17191	30201	3.05	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
4038	17194	30204	1.14	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds

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4038	17194	30205	1.14	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4042	17198	30209	3.47	0.0E+00	BE378602.1	EST_HUMAN	601236966F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
4043	17199	30210	1.2	0.0E+00	BE313146.1	EST_HUMAN	601153727F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509743 5'
4051	17207	30217	1.28	0.0E+00	AW580740.1	EST_HUMAN	PM3-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA
4052	17208	30218	1.03	0.0E+00	5360215	NT	Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA
4077	17233	30238	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30239	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30240	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4084	17239	30244	9.31	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4084	17239	30245	9.31	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4093	17248		3.51	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4095	17250		7.25	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4104	17258	30258	2.93	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4112	17266	30266	2.13	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4127	17281		111.8	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4134	17287		0.99	0.0E+00	AI657076.1	EST_HUMAN	tt55g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:O60309 O60309 KIAA0563 PROTEIN. ;
4137	17289	30284	1.91	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4138	17290	30285	2.85	0.0E+00	U09366.1	NT	Human zinc finger protein ZNF133
4157	17308	30304	6	0.0E+00	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
4166	17316		3.22	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
4177	17327	30318	1.58	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4178	17328	30319	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4178	17328	30320	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4185	17335	30327	8.33	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4185	17335	30328	8.33	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4194	17344	30337	0.64	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) mRNA
4202	17351	30343	6.02	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4203	17352	30344	11.98	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4206	17355	30345	1.26	0.0E+00	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4207	17356	30346	7.08	0.0E+00	11419297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4208	17357	30347	4.33	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4209	17358		0.98	0.0E+00	AA018975.1	EST_HUMAN	ze55e09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362920 5' similar to contains Alu repetitive element;
4218	17367	30356	5.32	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4227	14319	27373	0.7	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4227	14319	27374	0.7	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4234	17381	30369	1.32	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4234	17381	30370	1.32	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4236	16795	29812	0.64	0.0E+00	4506884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
4238	17384	30372	0.91	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4238	17384	30373	0.91	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4244	17390	30377	0.85	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4252	17398	30386	5.57	0.0E+00	AI982597.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'
4252	17398	30387	5.57	0.0E+00	AI982597.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'
4255	17400	30389	1	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4255	17400	30390	1	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4259	17404		5.89	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
4265	17410	30396	2.07	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4272	17417		5.76	0.0E+00	AW675599.1	EST_HUMAN	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:THI2_BOVIN Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4277	17422	30410	1.12	0.0E+00	AW408788.1	EST_HUMAN	UI-HF-BM0-adx-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4278	17423	30411	1.55	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4278	17423	30412	1.55	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4287	17432		2.35	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4300	17443	30429	1.07	0.0E+00	AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
4309	17452	30438	11.47	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element;contains element MER35 repetitive element ;
4309	17452	30439	11.47	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element;contains element MER35 repetitive element ;
4312	17455	30443	1.2	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4338	17481	30461	8.09	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4338	17481	30462	8.09	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4345	17488		0.86	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4388	17531	30512	5.01	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds

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4402	17545	30529	0.81	0.0E+00	AW936689.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4406	16596	29612	0.65	0.0E+00	BE779039.1	EST_HUMAN	601464995F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'
4410	17552	30537	5	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fbl4 (FBL4) mRNA, partial cds
4419	17560	30544	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4419	17560	30545	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4420	17561		2.25	0.0E+00	AI189844.1	EST_HUMAN	qd23f06.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20.b2 MER20 repetitive element ;
4424	17564		4.68	0.0E+00	U14520.1	NT	Human CBFA3 (Cbfa3) gene, partial cds
4428	17568	30550	0.96	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
4445	17585	30565	0.72	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4445	17585	30566	0.72	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4451	17591	30572	1.08	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4451	17591	30573	1.08	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4460	17600	30578	10.33	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4480	17620		1.06	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4490	17630	30611	3.62	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4494	17634	30616	6.28	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
4494	17634	30617	6.28	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
4500	17640	30623	1.59	0.0E+00	X60483.1	NT	H.sapiens H4/d gene for H4 histone
4500	17640	30624	1.59	0.0E+00	X60483.1	NT	H.sapiens H4/d gene for H4 histone
4505	17644	30630	10.05	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4505	17644	30631	10.05	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4517	17656	30645	14.1	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4518	17657	30646	1.16	0.0E+00	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
4519	17658		1.24	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4522	17661	30648	1.2	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4553	17691	30671	1.9	0.0E+00	7019456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4564	17702		6.61	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4570	17708	30687	2.78	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4570	17708	30688	2.78	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4574	17711	30694	0.69	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4574	17711	30695	0.69	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

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4591	17728		2.29	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
4610	17747	30726	0.65	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cot8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft205 5'
4610	17747	30727	0.65	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cot8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft205 5'
4613	17750		0.89	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4623	17760	30742	27.37	0.0E+00	AW084964.1	EST_HUMAN	xc68e08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4625	18470		2.97	0.0E+00	8051619	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4627	17763	30745	1.48	0.0E+00	AF016050.1	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4631	17767		8.47	0.0E+00	AL163207:2	NT	Homo sapiens chromosome 21 segment HS21C007
4633	17769	30750	0.97	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-101199-002-d03 HT0305 Homo sapiens cDNA
4640	17776	30757	1.3	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4640	17776	30758	1.3	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4642	17778	30760	1.06	0.0E+00	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4643	17779	30761	2.07	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4651	17787	30770	1.02	0.0E+00	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4652	17788	30771	1.2	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4652	17788	30772	1.2	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4661	18471	30783	3.19	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4666	17801	30788	20.19	0.0E+00	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4671	17806	30795	2.17	0.0E+00	AF152337.1	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4674	17809	30799	2.17	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4685	17820	30808	59.97	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4693	17828	30814	0.73	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4697	17832	30817	1.84	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4702	17837	30823	1.03	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4707	17842		3.19	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4709	17844	30826	15.03	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4709	17844	30827	15.03	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4724	17859	30841	2.87	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4727	17862	30844	11.57	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4727	17862	30845	11.57	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4746	17881		1.68	0.0E+00	AA174072.1	EST_HUMAN	zp18g08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4749	17884		1.96	0.0E+00	7657410	NT	Homo sapiens odz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4751	17886		3.31	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4752	17887	30868	1.33	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4753	17888	30869	4.83	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4754	17889		1.95	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4756	17891	30870	0.69	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4761	17896	30876	1.06	0.0E+00	AL162331.1	NT	Novel human gene mapping to chomosome 1
4764	17899	30879	31.32	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4764	17899	30880	31.32	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4765	17900	30881	1.42	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4765	17900	30882	1.42	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4766	17901	30883	2.62	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4776	17911	30895	0.96	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4776	17911	30896	0.96	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4781	17916	30902	17.22	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4787	17922	30910	1.93	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
4788	17923	30911	1.37	0.0E+00	AA418246.1	EST_HUMAN	zv96b07.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767605 3'
4794	17929		1.9	0.0E+00	AF086641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4799	17934	30921	1.3	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4799	17934	30922	1.3	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4800	17935	30923	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4800	17935	30924	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4801	17936	30925	3.06	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4804	17939	30927	2.06	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4804	17939	30928	2.06	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4806	13367	26400	2.93	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4806	13367	26401	2.93	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4810	17943		1.18	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'

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4814	17947	30932	1.13	0.0E+00	BE390050.1	EST_HUMAN	601285248F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607067 5'
4830	17963	30951	0.95	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4830	17963	30952	0.95	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4835	17968	30956	50.79	0.0E+00	M80902.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
4838	17971	30959	3.07	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4838	17971	30960	3.07	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4842	17975	30965	2.07	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4844	17977	30967	1.05	0.0E+00	7662479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4846	17979	30968	1.73	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4851	17984	30972	1.15	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4856	17989	30977	1.29	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4872	18005	30987	0.74	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4872	18005	30988	0.74	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4882	18012	30996	1.25	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26
4886	18016	31000	0.82	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4886	18016	31001	0.82	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4907	18037	31025	1.29	0.0E+00	AW444637.1	EST_HUMAN	UI-H-BI3-ajw-c-04-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4911	18041	31031	1.18	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4913	18043		2.01	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4924	18054		1.33	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
4925	18055		0.64	0.0E+00	AW339253.1	EST_HUMAN	xz89d06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871371 3'
4966	18095		2.87	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4967	18096	31072	1.95	0.0E+00	4505394	NT	Homo sapiens nidogen (enactin) (NID) mRNA
4970	18099	31075	1.09	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4972	18101	31077	0.99	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4973	18102	31078	1.04	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4974	18103	31079	4.54	0.0E+00	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4976	18105	31081	9.88	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4977	18106	31082	1	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4982	18111	31088	3.41	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4985	18114	31091	1.35	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4985	18114	31092	1.35	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4987	18116	31094	1.3	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4987	18116	31095	1.3	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4990	18119	31098	1.46	0.0E+00	M55582.1	NT	Human collagenase type IV (CLG4) gene, exon 2
4991	18120	31099	2.55	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5000	18129	31104	1.08	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2I) mRNA
5007	18136	31110	1.19	0.0E+00	X92841.1	NT	H.sapiens MICA gene
5009	18138	31112	1.32	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
5010	18139	31113	1.39	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5011	18140	31114	2.74	0.0E+00	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
5012	18141	31115	1.02	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil prolino-rich) (MGEA6), mRNA
5013	18142	31116	0.94	0.0E+00	BE007935.1	EST_HUMAN	QV0-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
5013	18142	31117	0.94	0.0E+00	BE007935.1	EST_HUMAN	QV0-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
5014	18143	31118	4.26	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
5016	18145	31120	1.79	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
5016	18145	31121	1.79	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
5017	18146	31122	0.98	0.0E+00	7705546	NT	Homo sapiens zinc-finger DNA-binding protein (HUMHOXY1), mRNA
5020	18149	31127	11.02	0.0E+00	AF055066.1	NT	Homo sapiens MHC class 1 region
5022	18151		2.46	0.0E+00	4505508	NT	Homo sapiens opioid receptor, delta 1 (OPRD1) mRNA
5023	18152	31130	2.77	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
5036	18164	31140	1.55	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase) (FDPS) mRNA
5040	18168		1.17	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5042	18170	31145	1.14	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
5042	18170	31146	1.14	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
5043	18171	31147	7.67	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5043	18171	31148	7.67	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5049	18177	31154	1.39	0.0E+00	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
5049	18177	31155	1.39	0.0E+00	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
5067	18195	31169	1.28	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5073	18201	31173	0.71	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
5082	18210	31182	1.15	0.0E+00	8922926	NT	Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5087	18215		7.66	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
5097	18225	31197	1.25	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5099	18227		2.97	0.0E+00	BE408863.1	EST_HUMAN	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
5102	18230	31201	4.85	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
5110	18238	31205	1.43	0.0E+00	AB028966.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
5121	18247	31212	2.32	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5121	18247	31213	2.32	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5135	18259	31225	0.72	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN ;
5135	18259	31226	0.72	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN ;
5135	18259	31227	0.72	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN ;
5139	18262	31229	2.09	0.0E+00	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
5139	18262	31230	2.09	0.0E+00	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
5146	13440	26472	0.72	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5148	18270		1.09	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5160	18282	31247	0.64	0.0E+00	U53588.1	NT	Homo sapiens MHC class 1 region
5167	18289		1.69	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5170	18292		18.98	0.0E+00	D50657.1	NT	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene
5182	18304	31288	0.92	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5196	18318	31287	3.55	0.0E+00	X52988.1	NT	Bacillus amyloliquefaciens sacB gene for levansucrase (EC 2.4.1.10)
5197	18319	31288	0.61	0.0E+00	X72791.1	NT	Human endogenous retrovirus mRNA for gag protein
5213	18334	31305	1.82	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5213	18334	31306	1.82	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5214	18335	31307	1.18	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5232	18354	31322	0.82	0.0E+00	5902055	NT	Homo sapiens ring finger protein (RNF), mRNA
5234	18356	31323	4.58	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5234	18356	31324	4.58	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5236	18358	31327	0.8	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5250	18371	31338	0.65	0.0E+00	5902091	NT	Homo sapiens solute carrier family 5 (inositol transporters), member 3 (SLC5A3), mRNA
5253	18373	31339	1.91	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
5266	18385	31351	1.2	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5266	18385	31352	1.2	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5267	18386	31353	0.59	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5267	18386	31354	0.59	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5274	18393	31362	1.89	0.0E+00	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
5278	18397	31364	1.03	0.0E+00	AA425183.1	EST_HUMAN	zw44f12.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:772943 5'
5278	18397	31365	1.03	0.0E+00	AA425183.1	EST_HUMAN	zw44f12.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:772943 5'
5290	18408	31375	0.93	0.0E+00	7657442	NT	Homo sapiens protocadherin 11 (PCDH11), mRNA
5294	18412	31378	1.47	0.0E+00	AF155582.1	NT	Homo sapiens core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1) mRNA, complete cds
5297	18472	31382	1.84	0.0E+00	AF167336.1	NT	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP) gene, exon 4
5300	18417	31386	0.94	0.0E+00	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein {rearranged translocation} [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
5301	18418	31387	1.93	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
5301	18418	31388	1.93	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
5303	18420	31390	24.35	0.0E+00	5360213	NT	Homo sapiens glypican 3 (GPC3) mRNA
5306	18423	31393	1.07	0.0E+00	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
5319	18435	31405	0.79	0.0E+00	X76060.1	NT	H.sapiens mRNA for YRRM2
5321	16426	29444	0.85	0.0E+00	AI685950.1	EST_HUMAN	tu38g09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICDI P03967 RAS-LIKE PROTEIN RASD ;
5328	18441	31410	0.96	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5328	18441	31411	0.96	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5333	18446	31414	0.96	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5338	18451	31419	110.9	0.0E+00	AF006061.1	NT	Homo sapiens placental growth hormone isoform hGH-V3 (hGH-V) mRNA, complete cds
5340	18453	31421	1.06	0.0E+00	AV726632.1	EST_HUMAN	AV726632 HTC Homo sapiens cDNA clone HTCCEA03 5'
5344	18457	31423	1.29	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
5346	18459	31424	1.18	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
5356	18482		2.45	0.0E+00	AF093093.1	NT	Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5366	18569	31436	2.17	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5366	18569	31437	2.17	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5388	18590	31562	1.21	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5391	18593	31565	1.2	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDHA13), mRNA
5406	18608	31580	3.52	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0076-310800-013-b03 GN0076 Homo sapiens cDNA
5410	18612	31584	3.5	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5410	18612	31585	3.5	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5418	18619	31594	8.57	0.0E+00	X56163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5418	18619	31595	8.57	0.0E+00	X56163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5499	18698	31714	6.41	0.0E+00	BE676498.1	EST_HUMAN	7f10c06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5500	18699	31715	1.7	0.0E+00	BE220753.1	EST_HUMAN	ht99a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN P42694 HYPOTHETICAL PROTEIN KIAA0054. ;
5501	18700	31716	1.57	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5501	18700	31717	1.57	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5502	18701	31718	0.72	0.0E+00	AI189142.1	EST_HUMAN	qd04a04.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1722702 3' similar to SW:T2D3_DROME P49846 TRANSCRIPTION INITIATION FACTOR TFIID 85 KD SUBUNIT ;
5506	18705	31721	5.23	0.0E+00	M29908.1	NT	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5510	18709	31724	1.3	0.0E+00	AI791363.1	EST_HUMAN	oh68a09.y5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);
5520	25806	31732	4.52	0.0E+00	11421038	NT	Homo sapiens Sp4 transcription factor (SP4), mRNA
5530	18727		4	0.0E+00	BF665962.1	EST_HUMAN	602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276254 5'
5531	18728	31743	0.78	0.0E+00	AU134406.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5531	18728	31744	0.78	0.0E+00	AU134406.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5537	18734	31751	0.61	0.0E+00	BE538857.1	EST_HUMAN	601061489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5546	18743	31777	1.63	0.0E+00	BE292784.1	EST_HUMAN	601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310 5'
5551	18748	31783	1.65	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5551	18748	31784	1.65	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5570	20121	33535	1.71	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5573	18769	31811	1.29	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
5573	18769	31812	1.29	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
5577	18772	31816	8.95	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5577	18772	31817	8.95	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5590	18785	31831	1.34	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
5590	18785	31832	1.34	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
5606	18801	31867	2.01	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5612	18806	31873	0.79	0.0E+00	Z38133.1	NT	H.sapiens mRNA for myosin

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5630	18824	31898	0.73	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5'
5630	18824	31899	0.73	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5'
5633	18827	31903	2.92	0.0E+00	BF529931.1	EST_HUMAN	602042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'
5633	18827	31904	2.92	0.0E+00	BF529931.1	EST_HUMAN	602042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'
5638	18832	31908	2.62	0.0E+00	BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5649	18843	32124	4.23	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5664	18858	32141	0.59	0.0E+00	AI928181.1	EST_HUMAN	wo95b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:O75054 O75054 KIAA0466 PROTEIN ;
5664	18858	32142	0.59	0.0E+00	AI928181.1	EST_HUMAN	wo95b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:O75054 O75054 KIAA0466 PROTEIN ;
5682	18876	32165	1.3	0.0E+00	BE260777.1	EST_HUMAN	601150252F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502909 5'
5691	18885		3.95	0.0E+00	AW867316.1	EST_HUMAN	MR0-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5705	18898	32190	2.49	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5705	18898	32191	2.49	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5725	18918	32212	1.7	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5725	18918	32213	1.7	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5733	18926	32221	4.16	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5733	18926	32222	4.16	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5740	18933	32232	2.64	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5740	18933	32233	2.64	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5769	18961	32262	1	0.0E+00	AI198515.1	EST_HUMAN	qf94g10.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1757730 3' similar to SW:CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR ;
5773	18965	32268	7.55	0.0E+00	M85719.1	EST_HUMAN	EST02238 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCM48
5780	18972	32277	4.52	0.0E+00	AW405472.1	EST_HUMAN	UI-HF-BL0-adh-d-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'
5793	18984	32287	1.12	0.0E+00	Z26269.1	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 14 adnd 15
5804	18994	32297	1.85	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5804	18994	32298	1.85	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5804	18994	32299	1.85	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5807	18997	32302	0.59	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neurexin II, complete cds
5807	18997	32303	0.59	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neurexin II, complete cds
5809	18999	32306	1.67	0.0E+00	U36261.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5840	19030	32336	1.02	0.0E+00	AB046861.1	NT	Homo sapiens mRNA for KIAA1641 protein, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5899	19088	32400	1.49	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5899	19088	32401	1.49	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5906	19095	32410	1.23	0.0E+00	AI207616.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5928	19114	32427	4.63	0.0E+00	11416801	NT	Homo sapiens protocadherin beta 2 (PCDHB2), mRNA
5933	19119	32430	1.19	0.0E+00	BE791173.1	EST_HUMAN	601584032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938551 5'
5942	19128	32441	1.1	0.0E+00	9998943	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
5943	19129	32442	7.24	0.0E+00	BE560082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5944	19130	32443	2.46	0.0E+00	10048478	NT	Mus musculus aczonin (Acz), mRNA
5945	19131	32444	3.06	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5945	19131	32445	3.06	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5965	19151	32466	2.96	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184321 5'
5968	19154	32469	0.92	0.0E+00	AF142621.1	NT	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
5969	19155	32470	3.07	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5979	19164	32484	1.12	0.0E+00	BE503096.1	EST_HUMAN	hz83d11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214581 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
5984	19169	32491	2.09	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
5989	19174	32495	0.99	0.0E+00	AA454642.1	EST_HUMAN	zx99d06.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811883 3'
6021	19204	32524	2.15	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6023	19206	32526	4.69	0.0E+00	BE828144.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
6028	19211	32531	1.19	0.0E+00	BE958636.1	EST_HUMAN	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'
6044	19227	32550	0.58	0.0E+00	BE673986.1	EST_HUMAN	7d72e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN P51843 ORPHAN NUCLEAR RECEPTOR DAX-1. [1] ;
6044	19227	32551	0.58	0.0E+00	BE673986.1	EST_HUMAN	7d72e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN P51843 ORPHAN NUCLEAR RECEPTOR DAX-1. [1] ;
6048	19231	32555	0.8	0.0E+00	AW276760.1	EST_HUMAN	xp65f03.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335 GUANYLATE KINASE ASSOCIATED PROTEIN. ;
6058	19240	32565	0.96	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6058	19240	32566	0.96	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6070	19252	32581	0.65	0.0E+00	AW470846.1	EST_HUMAN	ha34d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR:Q9Z1N3 Q9Z1N3 MYOSIN-RHOGAP PROTEIN, MYR 7. ;
6082	19264	32592	1.09	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-290900-399-a10 HT0894 Homo sapiens cDNA
6082	19264	32593	1.09	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-290900-399-a10 HT0894 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6090	19271	32599	1.67	0.0E+00	W33069.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6090	19271	32600	1.67	0.0E+00	W33069.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6091	19272		2.3	0.0E+00	AF012618.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
6094	19275	32604	3.37	0.0E+00	BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
6100	19280	32612	2.43	0.0E+00	BE889610.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
6102	19282	32615	0.58	0.0E+00	BE388673.1	EST_HUMAN	601286320F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613085 5'
6117	19297	32633	0.65	0.0E+00	AW752848.1	EST_HUMAN	IL3-CT0220-111199-028-E04 CT0220 Homo sapiens cDNA
6120	19299	32635	1.72	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6120	19299	32636	1.72	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6121	19300	32637	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6121	19300	32638	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6121	19300	32639	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6137	25819	32656	10.17	0.0E+00	9789986	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6140	19318	32659	1.28	0.0E+00	AA193506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6140	19318	32660	1.28	0.0E+00	AA193506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6163	19339	32685	10.44	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6163	19339	32686	10.44	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6203	19378	32729	1.06	0.0E+00	BE258330.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355565 5'
6213	19388	32737	1.15	0.0E+00	BE156561.1	EST_HUMAN	QV0-HT0368-090200-099-e09 HT0368 Homo sapiens cDNA
6223	19398	32747	0.66	0.0E+00	M38107.1	NT	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6259	19433	32780	1.6	0.0E+00	BE379007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
6265	19439	32786	1.35	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
6287	19460	32812	3.33	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
6316	19488	32844	4.34	0.0E+00	AA204740.1	EST_HUMAN	zq81d03.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ; .
6317	19489	32845	3.89	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6317	19489	32846	3.89	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6353	19523	32880	2.23	0.0E+00	11426367	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6357	19527	32885	3.15	0.0E+00	BE257173.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
6371	19540		0.98	0.0E+00	AI686048.1	EST_HUMAN	tt91f10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:Q14839 Q14839 MI-2 PROTEIN. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6375	19544	32902	1.32	0.0E+00	L35930.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6383	19552	32908	0.96	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6383	19552	32909	0.96	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6393	19562	32922	0.71	0.0E+00	AI198025.1	EST_HUMAN	qi50b11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT ;
6393	19562	32923	0.71	0.0E+00	AI198025.1	EST_HUMAN	qi50b11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT ;
6395	19564	32924	1.11	0.0E+00	BF357123.1	EST_HUMAN	MR0-HT0923-220800-102-b05 HT0923 Homo sapiens cDNA
6403	19572	32934	1.3	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51296), mRNA
6413	19582	32943	0.59	0.0E+00	D55649.1	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6429	19597	32963	1.07	0.0E+00	AW178142.1	EST_HUMAN	IL3-HT0062-010999-014-A04 HT0062 Homo sapiens cDNA
6450	19617	32980	0.6	0.0E+00	BE674544.1	EST_HUMAN	7e02c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302 3' similar to SW:Y176_HUMAN Q14681 HYPOTHETICAL PROTEIN KIAA0176 ;
6454	19621	32985	0.77	0.0E+00	7662039	NT	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6468	19635		9.28	0.0E+00	AV650020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'
6477	19644	33006	3.46	0.0E+00	AW575598.1	EST_HUMAN	UI-HF-BL0-acc-g-12-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
6480	19647	33009	4.53	0.0E+00	H01255.1	EST_HUMAN	yj27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5'
6488	19655	33018	0.71	0.0E+00	11426293	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
6492	19658	33021	1.67	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
6494	19660	33023	1.17	0.0E+00	AA456375.1	EST_HUMAN	aa14e07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813252 5'
6495	19661	33024	1.04	0.0E+00	AI612841.1	EST_HUMAN	tz57d08.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292687 3' similar to SW:NTCS_HUMAN P53796 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2 ;
6501	19667	33030	4.27	0.0E+00	BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6501	19667	33031	4.27	0.0E+00	BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6505	19671	33037	0.86	0.0E+00	AW748596.1	EST_HUMAN	MR0-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA
6505	19671	33038	0.86	0.0E+00	AW748596.1	EST_HUMAN	MR0-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA
6507	19673	33040	52.21	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6507	19673	33041	52.21	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6512	19677	33047	0.8	0.0E+00	BE780453.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
6513	19678	33048	0.84	0.0E+00	X92217.1	NT	H.sapiens germline immunoglobulin heavy chain, variable region, (13-2)
6527	19691	33065	1.71	0.0E+00	AI989483.1	EST_HUMAN	ws25c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498220 3'
6541	19704	33076	4.06	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
6541	19704	33077	4.06	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
6573	19735	33114	1.07	0.0E+00	BE867657.1	EST_HUMAN	601443175F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847291 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6609	19769	33158	1.81	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BL0-aco-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
6609	19769	33159	1.81	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BL0-aco-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
6640	19799	33188	0.94	0.0E+00	AV719444.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLCEHC06 5'
6649	19808	33195	0.74	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6649	19808	33196	0.74	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6652	19811	33199	2.13	0.0E+00	AF190860.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
6655	19814	33202	0.64	0.0E+00	L48546.1	NT	Homo sapiens tuberin (TSC2) gene, exons 38, 39, 40 and 41
6657	19816	33203	0.99	0.0E+00	11420658	NT	Homo sapiens transformation/transcription domain-associated protein (TRRAP), mRNA
6664	19823	33210	3.5	0.0E+00	AW163640.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ;
6664	19823	33211	3.5	0.0E+00	AW163640.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ;
6668	19827	33214	1.06	0.0E+00	W37163.1	EST_HUMAN	zb20e06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302626 5' similar to SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45 ;
6668	19827	33215	1.06	0.0E+00	W37163.1	EST_HUMAN	zb20e06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302626 5' similar to SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45 ;
6684	19842	33232	1.21	0.0E+00	BE794853.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6691	19849	33239	5.1	0.0E+00	BE799873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
6692	19850	33240	1.38	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6692	19850	33241	1.38	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6696	19854	33244	6.83	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6696	19854	33245	6.83	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6705	19863	33253	4.51	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6710	19868	33257	2.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6710	19868	33258	2.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6716	19874	33265	3.68	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6720	19877	33268	4.12	0.0E+00	AI638412.1	EST_HUMAN	tt31f11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR. ;
6722	19879	33270	1.46	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
6735	19891	33283	0.82	0.0E+00	AW505430.1	EST_HUMAN	UI-HF-BN0-ama-c-01-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6737	19893	33284	4.11	0.0E+00	AA434584.1	EST_HUMAN	zw52c03.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773668 5'
6751	19907		1.13	0.0E+00	BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
6756	19912	33307	1.63	0.0E+00	BE925875.1	EST_HUMAN	QV3-BN0047-300800-278-c06 BN0047 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6789	19944	33342	0.76	0.0E+00	11426768	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6789	19944	33343	0.76	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6790	19945	33345	0.59	0.0E+00	AW611964.1	EST_HUMAN	hg82e04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952126 3'
6808	19962	33366	1.64	0.0E+00	AU125928.1	EST_HUMAN	AU125928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6810	19964	33368	0.58	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6810	19964	33369	0.58	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6832	19985	33393	1.27	0.0E+00	BE142363.1	EST_HUMAN	CM0-HT0143-270999-062-d08 HT0143 Homo sapiens cDNA
6854	20007	33416	2.43	0.0E+00	BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6854	20007	33417	2.43	0.0E+00	BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6876	20028	33438	7.79	0.0E+00	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6878	20030	33440	2.04	0.0E+00	BF085667.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6915	20230	33663	3.33	0.0E+00	AA190755.1	EST_HUMAN	zp88e03.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627292 5'
6926	20241	33676	0.83	0.0E+00	U39573.1	NT	Human salivary peroxidase mRNA, complete cds
6930	20245	33678	0.76	0.0E+00	BE671987.1	EST_HUMAN	7e49b07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285 TEKTIN. ;
6940	20253	33689	5.73	0.0E+00	AI940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6940	20253	33690	5.73	0.0E+00	AI940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6951	20264	33703	2.15	0.0E+00	11435626	NT	Homo sapiens CD6 antigen (CD6), mRNA
6963	20191	33617	0.73	0.0E+00	AL042443.1	EST_HUMAN	DKFZp434D2021_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2021 5'
6964	20192	33618	11.05	0.0E+00	X56163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
6967	20195	33621	0.92	0.0E+00	AI168270.1	EST_HUMAN	oo10d01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1565761 3' similar to TR:Q26623 Q26623 TEKTIN C1. ;
6972	20200	33626	0.85	0.0E+00	BE734087.1	EST_HUMAN	601567370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
6991	18510	31502	1.28	0.0E+00	BE566381.1	EST_HUMAN	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682267 5'
6998	18517	31509	13.63	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6998	18517	31510	13.63	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
7004	20140	33558	1.74	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
7004	20140	33559	1.74	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
7030	20166	33588	1.66	0.0E+00	BF088376.1	EST_HUMAN	CM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA
7036	20172	33594	1.4	0.0E+00	AA195106.1	EST_HUMAN	zr34g03.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665332 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7044	20097		11.81	0.0E+00	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
7046	20099	33515	1.11	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
7061	20114	33529	2.69	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7068	20121	33535	0.66	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
7076	20129		2.06	0.0E+00	J03069.1	NT	Human MYCL2 gene, complete cds
7083	20177	33599	2.56	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7083	20177	33600	2.56	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7084	20178	33601	1.07	0.0E+00	M38113.1	NT	Human neurofibromatosis type 1 gene, exon x6
7095	18522	31515	3.59	0.0E+00	11420775	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7099	18526	31518	0.7	0.0E+00	BE256708.1	EST_HUMAN	601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356330 5'
7111	18537	31493	0.62	0.0E+00	AI660911.1	EST_HUMAN	wf21c09.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEOBOX PROTEIN HOX-A4 (HUMAN);contains PTR5.b1 MER22 MER22 repetitive element ;
7111	18537	31494	0.62	0.0E+00	AI660911.1	EST_HUMAN	wf21c09.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEOBOX PROTEIN HOX-A4 (HUMAN);contains PTR5.b1 MER22 MER22 repetitive element ;
7120	18546	31457	1.21	0.0E+00	AU118478.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003679 5'
7123	18549	31461	7.52	0.0E+00	BE262941.1	EST_HUMAN	601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5'
7124	18550	31462	2.72	0.0E+00	Z37976.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7124	18550	31463	2.72	0.0E+00	Z37976.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7125	18551	31464	3.01	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7125	18551	31465	3.01	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7132	18558	31472	1.26	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7137	20272	33711	0.61	0.0E+00	BE762770.1	EST_HUMAN	QV3-NT0022-140600-223-f01 NT0022 Homo sapiens cDNA
7142	20277	33717	2.56	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7144	20279	33719	0.78	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7144	20279	33720	0.78	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7148	20283	33725	3.25	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
7153	20287	33729	0.72	0.0E+00	AW502362.1	EST_HUMAN	UI-HF-BR0p-aka-d-10-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7153	20287	33730	0.72	0.0E+00	AW502362.1	EST_HUMAN	UI-HF-BR0p-aka-d-10-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7162	20295	33738	0.87	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7162	20295	33739	0.87	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7171	20304	33747	5.81	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7177	20309	33752	2.13	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7219	20084	33499	1.15	0.0E+00	AL049784.1	NT	Novel human gene mapping to chomosome 13
7225	20089	33606	0.64	0.0E+00	AW513069.1	EST_HUMAN	xo40e02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2706458 3' similar to TR:O94895 O94895 KIAA0803 PROTEIN ;
7257	20340	33790	0.62	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7257	20340	33791	0.62	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7262	20345	33797	0.84	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7262	20345	33798	0.84	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7268	20351	33804	1.16	0.0E+00	AW954806.1	EST_HUMAN	EST366876 MAGE resequences, MAGC Homo sapiens cDNA
7269	20352	33805	0.72	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354566 5'
7283	20366	33819	1	0.0E+00	L01973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7291	20373	33829	1.03	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7291	20373	33830	1.03	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7297	20379	33837	1.47	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001556 5'
7313	20395	33857	1.06	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7319	20401		2.82	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'
7320	20402	33864	0.71	0.0E+00	4758839	NT	Homo sapiens netrin 1 (NTN1), mRNA
7329	20411	33872	1.25	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7329	20411	33873	1.25	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7350	18569	31436	2.43	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7350	18569	31437	2.43	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7361	20440	33901	0.67	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7361	20440	33902	0.67	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7371	20450	33913	4.07	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA
7371	20450	33914	4.07	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA
7385	20463	33927	0.63	0.0E+00	AF227744.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform ae (CACNA1G) mRNA, complete cds
7406	20484	33952	36.37	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR repetitive element ;
7406	20484	33953	36.37	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7408	20486	33955	0.74	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7408	20486	33956	0.74	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7410	20488	33958	5.41	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7410	20488	33959	5.41	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7413	20491		13.11	0.0E+00	BF337375.1	EST_HUMAN	602035089F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4182839 5'
7415	20493	33961	3.49	0.0E+00	AA128453.1	EST_HUMAN	zn60f09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562 G806562 NEBULIN. ;
7420	20497	33967	0.77	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7420	20497	33968	0.77	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7431	20508	33980	0.69	0.0E+00	AJ270996.1	NT	Homo sapiens partial mRNA for LTRPC5 protein (LTRPC5 gene)
7461	20536	34011	1.13	0.0E+00	BE295499.1	EST_HUMAN	601174576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529794 5'
7463	20538	34012	0.91	0.0E+00	11427965	NT	Homo sapiens hypothetical protein (FLJ20261), mRNA
7466	20541		1.33	0.0E+00	AU118607.1	EST_HUMAN	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
7467	20542	34015	1.71	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7467	20542	34016	1.71	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7479	20554	34026	0.83	0.0E+00	AF245505.1	NT	Homo sapiens adlican mRNA, complete cds
7487	20562	34031	6.47	0.0E+00	X70172.1	NT	H.sapiens DNA for ZNGP2 pseudogene, exon 4
7489	20564	34033	5.81	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7489	20564	34034	5.81	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7502	20577	34049	0.89	0.0E+00	AW956503.1	EST_HUMAN	EST368573 MAGE resequences, MAGD Homo sapiens cDNA
7504	20579	34051	2.31	0.0E+00	AW950516.1	EST_HUMAN	EST362586 MAGE resequences, MAGA Homo sapiens cDNA
7531	20604	34078	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7531	20604	34079	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7531	20604	34080	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7552	20624		0.58	0.0E+00	M90354.1	NT	Human BTF3 protein homologue gene, complete cds
7553	20625	34101	0.8	0.0E+00	BE408293.1	EST_HUMAN	601302679F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'
7580	20652		1.09	0.0E+00	R87430.1	EST_HUMAN	ym88h10.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:166051 5'
7581	20653	34129	1.81	0.0E+00	AW239326.1	EST_HUMAN	xb39a05.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050 HNF3/FH TRANSCRIPTION FACTOR GENESIS ;
7600	20670		1.5	0.0E+00	AU117553.1	EST_HUMAN	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5'
7602	20672	34146	3.8	0.0E+00	11427135	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7622	20692	34168	0.62	0.0E+00	AA211663.1	EST_HUMAN	zn56f02.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7629	20698	34174	0.63	0.0E+00	BF229235.1	EST_HUMAN	MR0-AN0083-270900-004-f07 AN0083 Homo sapiens cDNA

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7634	20703	34182	0.67	0.0E+00	AW405627.1	EST_HUMAN	UI-HF-BL0-abs-d-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057469 5'
7641	20710	34189	0.8	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7667	20733	34209	0.9	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7667	20733	34210	0.9	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7675	20740	34220	1.09	0.0E+00	AU118767.1	EST_HUMAN	AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
7733	20794	34281	4.41	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7733	20794	34282	4.41	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7796	20852	34344	0.6	0.0E+00	AL046347.2	EST_HUMAN	DKFZp434J087_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J087 5'
7813	20868	34363	1.79	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7813	20868	34364	1.79	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7821	20876	34375	1.34	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7835	20890	34392	1	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
7863	20917	34422	0.7	0.0E+00	AI825504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363 AIBC1. ;
7863	20917	34423	0.7	0.0E+00	AI825504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363 AIBC1. ;
7871	20925	34432	1.84	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7877	20929	34435	0.88	0.0E+00	N76126.1	EST_HUMAN	za86e05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299456 3'
7881	20933	34438	6.1	0.0E+00	BF217905.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
7886	20938	34444	0.62	0.0E+00	BF569862.1	EST_HUMAN	602185808F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310256 5'
7891	20943	34449	3.52	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
7911	25855	34469	0.95	0.0E+00	AW069274.1	EST_HUMAN	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
7911	25855	34470	0.95	0.0E+00	AW069274.1	EST_HUMAN	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
7915	20966	34472	6.67	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7922	20973	34479	0.92	0.0E+00	AV758467.1	EST_HUMAN	AV758467 BM Homo sapiens cDNA clone BMFBGG05 5'
7924	20974	34480	5.78	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7924	20974	34481	5.78	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7925	20975	34482	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7925	20975	34483	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7926	20976	34484	1.05	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7926	20976	34485	1.05	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7948	20998	34508	12.57	0.0E+00	BF590267.1	EST_HUMAN	nab22c04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3263214 3' similar to contains element TAR1 repetitive element ;
7959	21009	34519	1.86	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
7959	21009	34520	1.86	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
7998	21048	34561	0.63	0.0E+00	Y16795.1	NT	Homo sapiens pslhHaA pseudogene
7999	21049	34562	3.86	0.0E+00	AI346148.1	EST_HUMAN	qp43f05.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1925793 3' similar to SW:EVX1_HUMAN P49640 HOMEOBOX EVEN-SKIPPED HOMOLOG PROTEIN 1 ;
8001	21051	34564	0.66	0.0E+00	W52673.1	EST_HUMAN	zc90f10.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:338443 5'
8002	21052	34565	0.58	0.0E+00	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
8003	21053	34566	0.59	0.0E+00	AU117333.1	EST_HUMAN	AU117333 HEMBA1 Homo sapiens cDNA clone HEMBA1001175 5'
8004	21054		0.57	0.0E+00	BE613963.1	EST_HUMAN	601504084F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905733 5'
8018	21069	34580	0.73	0.0E+00	6995995	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8018	21069	34581	0.73	0.0E+00	6995995	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8037	21120	34640	0.49	0.0E+00	AU133187.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5'
8083	21165		0.69	0.0E+00	BF217200.1	EST_HUMAN	601865317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
8096	21178	34695	0.61	0.0E+00	BE313013.1	EST_HUMAN	601150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'
8108	21190	34710	1.36	0.0E+00	AA149791.1	EST_HUMAN	zo01c06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566410 5'
8121	21203	34724	0.72	0.0E+00	BF026628.1	EST_HUMAN	601672310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
8135	21217	34738	0.55	0.0E+00	AA017021.1	EST_HUMAN	ze33h08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360831 5'
8153	21235	34756	2.06	0.0E+00	BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
8170	21252	34772	3.19	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8170	21252	34773	3.19	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8200	21282	34804	0.56	0.0E+00	AW674581.1	EST_HUMAN	bb34d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O64652 F17K2.26 PROTEIN. ;
8200	21282	34805	0.56	0.0E+00	AW674581.1	EST_HUMAN	bb34d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O64652 F17K2.26 PROTEIN. ;
8207	21289	34811	2.07	0.0E+00	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8209	21291	34812	0.85	0.0E+00	AW387131.1	EST_HUMAN	MR0-ST0031-061099-003-a11 ST0031 Homo sapiens cDNA
8212	21294		0.64	0.0E+00	AB020691.1	NT	Homo sapiens mRNA for KIAA0884 protein, partial cds
8213	21295	34814	6.15	0.0E+00	AU142402.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
8216	21298	34818	0.86	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8216	21298	34819	0.86	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8231	21313	34833	0.59	0.0E+00	7657276	NT	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
8233	21315	34835	0.84	0.0E+00	W95278.1	EST_HUMAN	ze05d01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8233	21315	34836	0.84	0.0E+00	W95278.1	EST_HUMAN	ze05d01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8235	21317		4.11	0.0E+00	BF673096.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
8239	21321		0.93	0.0E+00	AU134114.1	EST_HUMAN	AU134114 OVARC1 Homo sapiens cDNA clone OVARC1001296 5'
8253	21335	34853	0.96	0.0E+00	BF525534.1	EST_HUMAN	602069632F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8253	21335	34854	0.95	0.0E+00	BF525534.1	EST_HUMAN	602069632F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8285	21367	34886	1.35	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8285	21367	34887	1.35	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8328	21410		1.16	0.0E+00	BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887773 5'
8351	21432	34956	1.27	0.0E+00	AW500549.1	EST_HUMAN	UI-HF-BN0-akj-f-01-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077496 5'
8359	21440	34962	14.12	0.0E+00	AW157233.1	EST_HUMAN	au93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1] ;
8376	21457	34981	0.68	0.0E+00	AW072395.1	EST_HUMAN	xs07d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567639 3' similar to contains element OFR repetitive element ;
8394	21475	35002	1.11	0.0E+00	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8397	21478	35005	0.57	0.0E+00	W01616.1	EST_HUMAN	za36d05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294633 5'
8399	21480	35007	1.3	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8399	21480	35008	1.3	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8411	21492	35022	1.13	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
8431	21512	35043	0.46	0.0E+00	D45032.1	NT	Human DNA for ceruloplasmin, exon 5
8450	21531	35060	0.53	0.0E+00	AI367350.1	EST_HUMAN	qv95c12.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN. ;
8462	21543	35073	2.23	0.0E+00	BE674157.1	EST_HUMAN	7d76a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O95793 O95793 STAUFEN PROTEIN. ;
8464	21545	35075	1.96	0.0E+00	AI885671.1	EST_HUMAN	wi60b10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR ;
8477	21558	35091	1.47	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'

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8477	21558	35092	1.47	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8485	21566	35102	1.72	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8485	21566	35103	1.72	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8487	21568	35105	0.84	0.0E+00	AA403192.1	EST_HUMAN	zv66f02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD. ;
8487	21568	35106	0.84	0.0E+00	AA403192.1	EST_HUMAN	zv66f02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD. ;
8528	21609		3.61	0.0E+00	AA398511.1	EST_HUMAN	zt73a08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);
8537	21618	35155	0.5	0.0E+00	BE837593.1	EST_HUMAN	RC2-FN0094-120600-013-h07 FN0094 Homo sapiens cDNA
8538	21619	35156	1.34	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8538	21619	35157	1.34	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8557	21638	35176	1.24	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8557	21638	35177	1.24	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8572	21653	35194	1.16	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8572	21653	35195	1.16	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8581	21662	35202	0.93	0.0E+00	AI884477.1	EST_HUMAN	wm33a11.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
8588	21669	35208	0.71	0.0E+00	AA502294.1	EST_HUMAN	ne25d10.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1136434 G1136434 KIAA0187 PROTEIN. ;
8593	21674		0.66	0.0E+00	11416799	NT	Homo sapiens protocadherin beta 3 (PCDHB3), mRNA
8601	21682	35220	0.52	0.0E+00	AI580780.1	EST_HUMAN	ta04f11.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2043117 3'
8604	21685		2.08	0.0E+00	BE890797.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
8630	21710	35246	0.61	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8630	21710	35247	0.61	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8631	21711	35248	2.13	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
8631	21711	35249	2.13	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
8635	21715	35252	0.61	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8635	21715	35253	0.61	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8697	21777	35309	0.48	0.0E+00	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8704	21784	35317	0.7	0.0E+00	AJ251760.1	NT	Homo sapiens NESP55, GNAS1 antisense (partial) and XLalphas (partial) genes
8709	21789	35323	2.81	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
8709	21789	35324	2.81	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
8709	21789	35325	2.81	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase

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8723	21803	35339	0.76	0.0E+00	U82979.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
8765	21844	35385	0.81	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8765	21844	35386	0.81	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8768	21847	35388	0.67	0.0E+00	AU131671.1	EST_HUMAN	AU131671 NT2RP3 Homo sapiens cDNA clone NT2RP3003016 5'
8784	21863	35406	0.64	0.0E+00	11426572	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8788	21867		1.35	0.0E+00	AW513513.1	EST_HUMAN	xo46e01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
8790	21869		0.54	0.0E+00	BE783232.1	EST_HUMAN	601472166F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874912 5'
8791	21870	35409	1.62	0.0E+00	D52650.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02 5'
8823	21902	35442	4.15	0.0E+00	BE378495.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8829	21908	35446	2.15	0.0E+00	AA410545.1	EST_HUMAN	zt32e04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724062 5'
8831	21910		1.35	0.0E+00	BF313948.1	EST_HUMAN	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
8838	21917	35455	0.54	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
8843	21922	35460	1.41	0.0E+00	AW139673.1	EST_HUMAN	UI-H-BI1-adr-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8843	21922	35461	1.41	0.0E+00	AW139673.1	EST_HUMAN	UI-H-BI1-adr-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8879	21958	35493	2.16	0.0E+00	BE260272.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'
8884	21963	35497	2.91	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8884	21963	35498	2.91	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8884	21963	35499	2.91	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8923	22002	35541	0.84	0.0E+00	AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA
8930	22009	35547	3.69	0.0E+00	AA962527.1	EST_HUMAN	or80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
8936	22015	35555	3.41	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8936	22015	35556	3.41	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8961	22040	35583	1.65	0.0E+00	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
8963	22042	35585	1.09	0.0E+00	BE278917.1	EST_HUMAN	601156330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
8973	22052		2.86	0.0E+00	AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5'
8980	22059	35600	3.12	0.0E+00	AW337277.1	EST_HUMAN	xw73c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587 INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
8986	22065	35605	1.59	0.0E+00	AU124051.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
9063	22142	35687	0.98	0.0E+00	AU140704.1	EST_HUMAN	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000089 5'
9073	22152	35696	0.64	0.0E+00	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9078	22157	35700	0.68	0.0E+00	R17132.1	EST_HUMAN	yg09e09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 5'
9078	22157	35701	0.68	0.0E+00	R17132.1	EST_HUMAN	yg09e09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 5'
9082	22161	35703	4.78	0.0E+00	AW592233.1	EST_HUMAN	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
9082	22161	35704	4.78	0.0E+00	AW592233.1	EST_HUMAN	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
9129	22208	35751	0.93	0.0E+00	AV714764.1	EST_HUMAN	AV714764 DCB Homo sapiens cDNA clone DCBAUA06 5'
9145	22224	35766	3.17	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9145	22224	35767	3.17	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9151	22229	35773	1.32	0.0E+00	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
9153	22231	35776	2.12	0.0E+00	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9161	22239		0.61	0.0E+00	BF058289.1	EST_HUMAN	7k29b03.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476692 3' similar to TR:O36448 O36448 S GAG. ;
9191	22269	35808	2.79	0.0E+00	11422857	NT	Homo sapiens tumor protein p73 (TP73), mRNA
9201	22279	35818	1.59	0.0E+00	K01241.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
9209	22287	35828	5.28	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9209	22287	35829	5.28	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9214	22292	35835	1.84	0.0E+00	AV660739.1	EST_HUMAN	AV660739 GLC Homo sapiens cDNA clone GLCGKG12 3'
9220	22298	35841	3.41	0.0E+00	7706638	NT	Homo sapiens polycystin-L (PKDL), mRNA
9225	22303	35846	0.6	0.0E+00	BE793326.1	EST_HUMAN	601588304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'
9246	22323	35867	4.22	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9246	22323	35868	4.22	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9256	22333	35883	0.6	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
9256	22333	35884	0.6	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
9259	22336		0.54	0.0E+00	M89986.1	NT	Human polymorphic loci in Xq28
9261	22338	35888	1.65	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
9279	22355	35905	0.53	0.0E+00	AU127096.1	EST_HUMAN	AU127096 NT2RP2 Homo sapiens cDNA clone NT2RP2000579 5'
9283	22359	35909	0.83	0.0E+00	AI061395.1	EST_HUMAN	an29e04.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700094 3'
9288	22364	35913	1.96	0.0E+00	AI954607.1	EST_HUMAN	wq34a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MGB3_HUMAN O15480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
9293	22369	35919	5.69	0.0E+00	9256595	NT	Homo sapiens protocadherin alpha 8 (PCDHA8), mRNA
9303	22379	35930	2.73	0.0E+00	AW958311.1	EST_HUMAN	EST370361 MAGE resequences, MAGE Homo sapiens cDNA
9313	22389	35940	1.32	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
9328	22404	35956	0.84	0.0E+00	AU142662.1	EST_HUMAN	AU142662 Y79AA1 Homo sapiens cDNA clone Y79AA1000678 5'
9344	22420	35974	1.04	0.0E+00	11436996	NT	Homo sapiens MAP-kinase activating death domain (MADD), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9345	22421		0.76	0.0E+00	BE410768.1	EST_HUMAN	601301676F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'
9359	22434	35993	1.32	0.0E+00	BF002024.1	EST_HUMAN	7g97h12.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q9UH62 Q9UH62 HYPOTHETICAL 42.5 KD PROTEIN. ;
9373	22448	36009	1.62	0.0E+00	AB011150.1	NT	Homo sapiens mRNA for KIAA0578 protein, partial cds
9374	22449	36010	3.42	0.0E+00	BE794823.1	EST_HUMAN	601589294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'
9378	22453	36015	0.47	0.0E+00	BE810292.1	EST_HUMAN	RC3-PT0151-290600-011-c05 PT0151 Homo sapiens cDNA
9378	22453	36016	0.47	0.0E+00	BE810292.1	EST_HUMAN	RC3-PT0151-290600-011-c05 PT0151 Homo sapiens cDNA
9381	22456	36019	0.97	0.0E+00	AU136229.1	EST_HUMAN	AU136229 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'
9386	22461	36024	1.19	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9386	22461	36025	1.19	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9403	22477	36040	0.57	0.0E+00	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9407	22481	36044	1.43	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
9407	22481	36045	1.43	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
9464	22521	36083	0.96	0.0E+00	AW673469.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
9464	22521	36084	0.96	0.0E+00	AW673469.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
9498	22554	36116	0.99	0.0E+00	BE207063.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9498	22554	36117	0.99	0.0E+00	BE207063.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9509	22775	36346	1.95	0.0E+00	BF348013.1	EST_HUMAN	602023150F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158300 5'
9545	22810	36178	3.1	0.0E+00	BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-b08 HT0698 Homo sapiens cDNA
9577	22719	36287	0.49	0.0E+00	BF034377.1	EST_HUMAN	6014551116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9577	22719	36288	0.49	0.0E+00	BF034377.1	EST_HUMAN	6014551116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9583	22725	36295	0.58	0.0E+00	AI906351.1	EST_HUMAN	RC-BT108-040399-032 BT108 Homo sapiens cDNA
9586	22728	36297	0.77	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9586	22728	36298	0.77	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9596	22651	36223	0.85	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: hteo3) Homo sapiens cDNA clone DKFZp434L0120 5'
9631	22686	36257	1.3	0.0E+00	AI088043.1	EST_HUMAN	ow60h01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 Q14677 KIAA0171 PROTEIN. ;
9638	21081	34592	0.67	0.0E+00	BF309962.1	EST_HUMAN	601892245F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138066 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9640	21083	34595	2.32	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9640	21083	34596	2.32	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9642	21085	34599	6.52	0.0E+00	AI290909.1	EST_HUMAN	qm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ;
9642	21085	34600	6.52	0.0E+00	AI290909.1	EST_HUMAN	qm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ;
9643	21086	34601	2.15	0.0E+00	AW953836.1	EST_HUMAN	EST366026 MAGE resequences, MAGC Homo sapiens cDNA
9670	22632	36201	3.95	0.0E+00	AF153466.1	NT	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
9673	22635	36205	0.69	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9673	22635	36206	0.69	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9683	22732		5.87	0.0E+00	BE255829.1	EST_HUMAN	601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
9686	22735	36305	1.44	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9686	22735	36306	1.44	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9688	22737	36307	5.46	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
9697	22746	36315	0.58	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9709	22758	36329	3.41	0.0E+00	BE263191.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
9727	22792	36364	4.49	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9727	22792	36365	4.49	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9729	22794	36368	3.38	0.0E+00	BE746215.1	EST_HUMAN	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9739	22804	36378	2.03	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9739	22804	36379	2.03	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9739	22804	36380	2.03	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9759	22697	36265	1.91	0.0E+00	BE900549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
9776	22816	36394	1.5	0.0E+00	AV701829.1	EST_HUMAN	AV701829 ADB Homo sapiens cDNA clone ADBBYH01 5'
9788	22828	36405	2.55	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
9788	22828	36406	2.55	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
9821	22861	36442	1.13	0.0E+00	BE082977.1	EST_HUMAN	RC2-BT0642-130300-017-g01 BT0642 Homo sapiens cDNA
9841	22881	36464	1.72	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9841	22881	36465	1.72	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9850	22890	36470	1.87	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9850	22890	36471	1.87	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9852	22892	36472	0.52	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9852	22892	36473	0.52	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9861	22901	36485	0.63	0.0E+00	W56629.1	EST_HUMAN	zd16e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9861	22901	36486	0.63	0.0E+00	W56629.1	EST_HUMAN	zd16e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9874	22914	36499	0.46	0.0E+00	AF208054.1	NT	Homo sapiens non-inhibitory killer-cell Ig-like receptor KIR (KIR2DS5) mRNA, complete cds
9875	22915	36500	1.04	0.0E+00	AB035356.1	NT	Homo sapiens mRNA for neurexin I-alpha protein, complete cds
9879	22919		0.64	0.0E+00	AI124780.1	EST_HUMAN	am56a11.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539548 3'
9881	22921	36505	3	0.0E+00	AW500526.1	EST_HUMAN	UI-HF-BN0-akj-c-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
9925	22965	36554	2.65	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
9953	22992	36585	2.69	0.0E+00	S78466.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 6 of 5]
9953	22992	36586	2.69	0.0E+00	S78466.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9956	22995	36591	2.72	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688680 5'
9976	23015	36608	1.26	0.0E+00	AW363135.1	EST_HUMAN	CM2-CT0311-301199-043-h11 CT0311 Homo sapiens cDNA
9997	23035	36627	0.66	0.0E+00	11436432	NT	Homo sapiens multimerin (MMRN), mRNA
9998	23036	36628	0.52	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
10007	23045	36638	0.91	0.0E+00	BE206710.1	EST_HUMAN	bb26c01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2964000 3'
10024	23062	36658	4.49	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10024	23062	36659	4.49	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10033	23071	36671	0.95	0.0E+00	AW500936.1	EST_HUMAN	UI-HF-BP0p-air-f-05-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'
10039	23077	36677	13.26	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10039	23077	36678	13.26	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10052	23090	36692	1.56	0.0E+00	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
10069	23107	36710	1.54	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'
10074	23112	36716	0.57	0.0E+00	AL041084.2	EST_HUMAN	DKFZp434B2416_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2416 5'
10084	23122	36723	2.32	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10085	23123	36724	2.16	0.0E+00	AF152308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
10112	23150	36751	2.84	0.0E+00	AF009220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
10112	23150	36752	2.84	0.0E+00	AF009220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
10128	23166	36765	1.13	0.0E+00	BF092898.1	EST_HUMAN	MR4-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA
10160	23197	36793	2.75	0.0E+00	BE280793.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'
10169	23206	36799	6.57	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10169	23206	36800	6.57	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
10178	23215	36806	0.87	0.0E+00	AW236269.1	EST_HUMAN	xn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10179	23216	36807	0.84	0.0E+00	AA341305.1	EST_HUMAN	EST46740 Fetal kidney II Homo sapiens cDNA 5' end
10188	23225	36819	0.59	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
10208	23244	36834	0.94	0.0E+00	AW964113.1	EST_HUMAN	EST376186 MAGE resequences, MAGH Homo sapiens cDNA
10222	23258	36845	5.99	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10222	23258	36846	5.99	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10225	23261	36849	3.31	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10228	23263	36851	2.75	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10228	23263	36852	2.75	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10261	23296	36894	3.07	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10261	23296	36895	3.07	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10277	23312	36909	.2	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
10277	23312	36910	.2	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
10282	23317	36917	0.73	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKC Homo sapiens cDNA clone GKCDXA07 5'
10282	23317	36918	0.73	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKC Homo sapiens cDNA clone GKCDXA07 5'
10288	23323	36925	0.72	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10290	23325	36928	2.42	0.0E+00	AA196387.1	EST_HUMAN	zp97h11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
10317	23352	36959	0.76	0.0E+00	AA131248.1	EST_HUMAN	zi31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10317	23352	36960	0.76	0.0E+00	AA131248.1	EST_HUMAN	zi31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10359	23394	37005	1.61	0.0E+00	AF179309.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10404	23439	37046	0.99	0.0E+00	BE880658.1	EST_HUMAN	601491565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893657 5'
10417	23452	37057	5.34	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10417	23452	37058	5.34	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10422	23457	37062	0.8	0.0E+00	AU127403.1	EST_HUMAN	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 5'
10432	23467	37073	0.89	0.0E+00	BE958511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10432	23467	37074	0.89	0.0E+00	BE958511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10450	23485	37094	0.48	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10460	23495	37107	0.91	0.0E+00	AA311624.1	EST_HUMAN	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10461	23496	37108	0.65	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
10473	23508	37121	0.64	0.0E+00	BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'
10475	23510	37123	0.77	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10486	23521	37130	1.56	0.0E+00	AB029290.1	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10487	23522	37131	0.5	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10487	23522	37132	0.5	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10494	23529	37137	5.8	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10494	23529	37138	5.8	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10502	23537	37147	0.77	0.0E+00	AA704457.1	EST_HUMAN	zj19b06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gb:M14123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10504	23539	37148	1.08	0.0E+00	M22921.1	NT	Human beta 1,4-galactosyl-transferase mRNA, complete cds
10506	23541	37151	4.81	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184939 5'
10506	23541	37152	4.81	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184939 5'
10530	23565	37172	0.59	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10530	23565	37173	0.59	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10595	23630	37237	1.07	0.0E+00	AI631818.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE ;
10595	23630	37238	1.07	0.0E+00	AI631818.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE ;
10610	23644	37252	1.64	0.0E+00	T03078.1	EST_HUMAN	FB23A4 Fetal brain, Stratagene Homo sapiens cDNA clone FB23A4 3'end
10638	23672	37282	0.67	0.0E+00	AU122429.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002368 5'
10644	23678	37288	0.48	0.0E+00	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10668	23702	37312	2.22	0.0E+00	BF436218.1	EST_HUMAN	nab45e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
10669	23703		1.71	0.0E+00	AV654765.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLCDZC07 3'
10689	23722	37328	3.08	0.0E+00	AW517960.1	EST_HUMAN	xu74b01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M69066 MOESIN (HUMAN);
10693	23726	37332	2.88	0.0E+00	BE549213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10709	23742	37348	0.82	0.0E+00	11436005	NT	Homo sapiens hypothetical protein DKFZp761P1010 (DKFZp761P1010), mRNA
10735	23768	37378	0.52	0.0E+00	X89893.1	NT	H.sapiens mRNA for NK receptor (183 Act1)
10736	23769	37379	3.35	0.0E+00	BE781742.1	EST_HUMAN	601467419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
10758	23791	37409	2.32	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA
10758	23791	37410	2.32	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA
10764	23797	37417	0.57	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10772	23805	37426	0.77	0.0E+00	AI656890.1	EST_HUMAN	tt54e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2244612 3'
10779	23812	37435	9.15	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10779	23812	37436	9.15	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10784	23817	37439	0.63	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10784	23817	37440	0.63	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10786	23819	37442	0.46	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10786	23819	37443	0.46	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10809	23842	37465	0.51	0.0E+00	H39805.1	EST_HUMAN	yp01a10.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:186138 5'
10835	23868	37491	0.54	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10846	23879	37499	0.59	0.0E+00	BE392276.1	EST_HUMAN	601308167F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626126 5'
10863	25866	37518	0.52	0.0E+00	AU125996.1	EST_HUMAN	AU125996 NT2RM4 Homo sapiens cDNA clone NT2RM4002536 5'
10872	23957	37586	1.84	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
10872	23957	37587	1.84	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
10874	23959		2.55	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
10882	23966	37595	5.5	0.0E+00	AW963563.1	EST_HUMAN	EST375636 MAGE resequences, MAGH Homo sapiens cDNA
10895	23979	37610	2.52	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10895	23979	37611	2.52	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10898	23982	37614	1.7	0.0E+00	AW057621.1	EST_HUMAN	wy61f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR:Q60566 Q60566 VDX ;
10906	23989	37621	8.59	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
10907	23990	37622	2.72	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element ;
10907	23990	37623	2.72	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element ;
10912	23995	37628	1.48	0.0E+00	BF306642.1	EST_HUMAN	601888704F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122649 5'
10913	23996	37629	1.74	0.0E+00	BE872908.1	EST_HUMAN	601451502F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3855289 5'
10913	23996	37630	1.74	0.0E+00	BE872908.1	EST_HUMAN	601451502F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3855289 5'
10920	24003	37637	3.59	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10920	24003	37638	3.59	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10936	24018	37651	1.52	0.0E+00	AW404795.1	EST_HUMAN	UI-HF-BL0-acm-d-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
10940	24022	37656	2.85	0.0E+00	11424829	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
10941	24023	37657	8.39	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10941	24023	37658	8.39	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10942	24024	37659	2.68	0.0E+00	AI991827.1	EST_HUMAN	wu32b06.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
10946	24028	37665	3.22	0.0E+00	BE882109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'
10950	24032	37667	6.12	0.0E+00	BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'
10952	24034	37668	1.55	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10952	24034	37669	1.55	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10965	24046	37680	22.14	0.0E+00	BE903304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
10968	19087	32399	1.85	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10990	24069	37703	4.49	0.0E+00	BE793498.1	EST_HUMAN	601568829F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
10998	24077	37710	2.4	0.0E+00	BE729706.1	EST_HUMAN	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'
10998	24077	37711	2.4	0.0E+00	BE729706.1	EST_HUMAN	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'
10999	24078	37712	11.66	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
10999	24078	37713	11.66	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
11003	24082	37718	1.6	0.0E+00	R17132.1	EST_HUMAN	yg09e09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 5'
11003	24082	37719	1.6	0.0E+00	R17132.1	EST_HUMAN	yg09e09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 5'
11009	24088		2.62	0.0E+00	AW139414.1	EST_HUMAN	UI-H-BI1-adq-e-06-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717674 3'
11014	24093	37732	11.81	0.0E+00	AW516055.1	EST_HUMAN	xy04g10.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);
11020	24099	37737	4.44	0.0E+00	AU135741.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'
11026	24105	37741	2.56	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element ;
11026	24105	37742	2.56	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element ;
11026	24105	37743	2.56	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element ;
11028	24107	37744	1.67	0.0E+00	Z34897.1	NT	H.sapiens mRNA for H1 histamine receptor
11029	24108	37745	2.76	0.0E+00	F13069.1	EST_HUMAN	HSC3IC031 normalized infant brain cDNA Homo sapiens cDNA clone c-3ic03
11037	24116	37750	2.35	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
11054	24131	37767	1.71	0.0E+00	AW338094.1	EST_HUMAN	xw66f01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);
11055	24132	37768	3.75	0.0E+00	AW451230.1	EST_HUMAN	UI-H-BI3-alh-a-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11055	24132	37769	3.75	0.0E+00	AW451230.1	EST_HUMAN	UI-H-BI3-alh-a-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11058	13443		9.52	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
11060	24136	37771	1.79	0.0E+00	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
11073	24148	37787	1.92	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
11087	24161	37797	1.47	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
11092	24166	37803	1.39	0.0E+00	AA377505.1	EST_HUMAN	EST90347 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to LERK-2, placenta
11106	24178	37813	3.3	0.0E+00	BE792155.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'
11107	24179		76.9	0.0E+00	BF684061.1	EST_HUMAN	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11108	24180	37814	1.45	0.0E+00	BE269288.1	EST_HUMAN	601186342F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544259 5'
11110	24182	37816	7.93	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
11111	24183		1.81	0.0E+00	AW236269.1	EST_HUMAN	xn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
11116	24188	37820	5.71	0.0E+00	AI149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
11116	24188	37821	5.71	0.0E+00	AI149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
11117	24189	37822	2.53	0.0E+00	AW391937.1	EST_HUMAN	QV4-ST0234-121199-032-b06 ST0234 Homo sapiens cDNA
11127	24199		11.83	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
11130	24202	37827	9.67	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR), mRNA
11132	24204	37828	2.14	0.0E+00	AI367350.1	EST_HUMAN	qv95c12.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN. ;
11132	24204	37829	2.14	0.0E+00	AI367350.1	EST_HUMAN	qv95c12.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN. ;
11137	24209	37835	1.63	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184979 5'
11139	24211	37837	13.91	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
11144	24216	37843	2.19	0.0E+00	AB029040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds
11147	24219	37846	1.51	0.0E+00	AB007932.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
11151	24222	37850	3.89	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
11155	24226	37855	2.43	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
11155	24226	37856	2.43	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
11177	24246	37879	51.22	0.0E+00	AA740782.1	EST_HUMAN	ob32e07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSR1 repetitive element ;
11186	24255	37890	2.81	0.0E+00	AF252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
11199	24268	37903	1.71	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536867 5'
11199	24268	37904	1.71	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536867 5'
11201	24270	37906	4.9	0.0E+00	C05089.1	EST_HUMAN	C05089 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4817
11208	24277	37914	2.1	0.0E+00	AA746375.1	EST_HUMAN	oa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11208	24277	37915	2.1	0.0E+00	AA746375.1	EST_HUMAN	oa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11218	24287	37926	2.69	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
11218	24287	37927	2.69	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
11221	24290	37930	1.76	0.0E+00	BF353525.1	EST_HUMAN	QV2-HT0698-020800-295-d07 HT0698 Homo sapiens cDNA
11222	24291	37931	6.5	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761J2116_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'
11234	24303	37940	1.86	0.0E+00	BE562822.1	EST_HUMAN	601336530F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690390 5'
11236	24305	37942	6.05	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11250	24319	37959	1.75	0.0E+00	AV693656.1	EST_HUMAN	AV693656 GKC Homo sapiens cDNA clone GKCCNC03 5'
11260	24329	37969	2.97	0.0E+00	BF366553.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
11288	24354	37994	2.4	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
11288	24354	37995	2.4	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
11290	24356		1.51	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAAD06 5'
11305	24370	38011	3.02	0.0E+00	BE896423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
11311	24375	38019	1.83	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-akg-d-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
11311	24375	38020	1.83	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-akg-d-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
11314	24378	38023	2.49	0.0E+00	BE018293.1	EST_HUMAN	bb78c04.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048486 5' similar to gb:Y00345_cds1 POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for poly(A) binding protein (MOUSE);
11345	25869	38058	1.45	0.0E+00	AW387766.1	EST_HUMAN	MR4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA
11345	25869	38059	1.45	0.0E+00	AW387766.1	EST_HUMAN	MR4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA
11353	24415	38070	3.23	0.0E+00	BE897953.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
11355	24417	38073	2.24	0.0E+00	AI459545.1	EST_HUMAN	ao86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11355	24417	38074	2.24	0.0E+00	AI459545.1	EST_HUMAN	ao86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11369	24430	38087	1.89	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'
11390	24451	38112	1.37	0.0E+00	AI073917.1	EST_HUMAN	ou61d04.x1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR ;
11390	24451	38113	1.37	0.0E+00	AI073917.1	EST_HUMAN	ou61d04.x1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR ;
11390	24451	38114	1.37	0.0E+00	AI073917.1	EST_HUMAN	ou61d04.x1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR ;
11404	24465	38130	3.8	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
11405	24466	38131	24.41	0.0E+00	BF206561.1	EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
11411	24472	38137	11.85	0.0E+00	AW207734.1	EST_HUMAN	UI-H-BI2-age-h-01-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11416	24477	38141	3.93	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11416	24477	38142	3.93	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11418	24479	38144	2.63	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;

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11418	24479	38145	2.63	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
11429	24490	38155	2.37	0.0E+00	11526409	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
11438	24499	38166	1.68	0.0E+00	AI075915.1	EST_HUMAN	ov46g07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640412 3' similar to TR:Q14507 Q14507 EPIDIDYMIS-SPECIFIC GENE PRODUCT, ALPHA. ;
11445	24506	38172	1.73	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11448	24509	38176	1.98	0.0E+00	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
11449	20710	34189	1.94	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11452	24512	38178	4.61	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11452	24512	38179	4.61	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11475	24534	38204	1.66	0.0E+00	AW673469.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
11475	24534	38205	1.66	0.0E+00	AW673469.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
11490	24549	38223	4.84	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-aok-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11490	24549	38224	4.84	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-aok-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11498	24554	38229	4.65	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5'
11501	24559	38234	2.07	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11501	24559	38235	2.07	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11503	24561	38238	4.06	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11503	24561	38239	4.06	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11511	24569	38246	1.61	0.0E+00	D87682.1	NT	Human mRNA for KIAA0241 gene, partial cds
11516	24573		3.87	0.0E+00	BF240536.1	EST_HUMAN	601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5'
11531	24587	38262	1.81	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11531	24587	38263	1.81	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11535	24591	38266	3.09	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11535	24591	38267	3.09	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11553	24608	38287	6.13	0.0E+00	4503544	NT	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
11560	24615	38294	2.06	0.0E+00	BF576267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11562	24617	38297	3.53	0.0E+00	AW328173.1	EST_HUMAN	dr04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11567	24622		42.5	0.0E+00	M55083.1	NT	Human gamma actin-like pseudogene, complete cds
11571	24626	38305	1.75	0.0E+00	AI660968.1	EST_HUMAN	wf20e11.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
11574	24629	38307	3.37	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'

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11574	24629	38308	3.37	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11581	24635	38315	47.2	0.0E+00	BF362462.1	EST_HUMAN	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA
11601	24654	38338	2.32	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11601	24654	38339	2.32	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11606	24659		4.33	0.0E+00	BE897051.1	EST_HUMAN	601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11607	24660		2.37	0.0E+00	4503786	NT	Homo sapiens fyn-related kinase (FRK) mRNA
11621	24672	38361	2.34	0.0E+00	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11623	24674		2.07	0.0E+00	BF207662.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11636	24716	38407	4.53	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
11636	24716	38408	4.53	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
11638	24718	38410	3.69	0.0E+00	AW763028.1	EST_HUMAN	QV0-CT0225-101299-071-f06 CT0225 Homo sapiens cDNA
11643	24723		3.01	0.0E+00	AA558707.1	EST_HUMAN	nl42c08.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11644	18590	31562	2.56	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
11645	24724	38416	7.51	0.0E+00	AW327895.1	EST_HUMAN	dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
11664	25870	38435	1.78	0.0E+00	AW292776.1	EST_HUMAN	UI-H-BW0-aij-d-07-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729509 3'
11671	23899	37522	1.93	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
11677	24676	38367	1.35	0.0E+00	BE254058.1	EST_HUMAN	601113903F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354600 5'
11680	24679	38369	1.79	0.0E+00	BE965909.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11680	24679	38370	1.79	0.0E+00	BE965909.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11681	24680	38371	3.81	0.0E+00	BE185656.1	EST_HUMAN	IL5-HT0731-020500-077-f05 HT0731 Homo sapiens cDNA
11682	24681		1.39	0.0E+00	BF513960.1	EST_HUMAN	UI-H-BW1-amv-a-05-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071121 3'
11696	24693	38384	7.19	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11696	24693	38385	7.19	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11706	24703	38395	10.19	0.0E+00	AI923116.1	EST_HUMAN	wn83g03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11708	24748	38440	4.47	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 Q13686 ALKB HOMOLOG PROTEIN. ;
11708	24748	38441	4.47	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 Q13686 ALKB HOMOLOG PROTEIN. ;
11713	24753	38447	2.21	0.0E+00	BE910546.1	EST_HUMAN	601501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902926 5'

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11723	23909	37533	11.64	0.0E+00	BE676347.1	EST_HUMAN	7f27f12.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295919 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR 1. ;
11725	23911	37535	1.47	0.0E+00	AI683358.1	EST_HUMAN	tx66b09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2274521 3' similar to gb:M55542 INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (HUMAN);
11727	23913	37537	3.13	0.0E+00	BE615666.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11727	23913	37538	3.13	0.0E+00	BE615666.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11734	23920	37545	1.59	0.0E+00	AV757420.1	EST_HUMAN	AV757420 BM Homo sapiens cDNA clone BMFAGH03 5'
11739	23925	37550	7.33	0.0E+00	AL037746.1	EST_HUMAN	DKFZp564C187_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564C187 5'
11740	23926	37551	4.2	0.0E+00	U62769.1	NT	Human oxytocinase variant 2 mRNA, complete cds
11745	23931	37557	1.33	0.0E+00	BE883386.1	EST_HUMAN	601509139F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910833 5'
11766	24759	38454	1.75	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
11769	24761	38455	3.69	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11769	24761	38456	3.59	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11784	24774	38470	2.03	0.0E+00	AU138211.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
11797	24787	38485	6.43	0.0E+00	BE622317.1	EST_HUMAN	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
11833	24822	38512	17.72	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11833	24822	38513	17.72	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11845	24834	38527	4.58	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11845	24834	38528	4.58	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11848	24837	38531	2.7	0.0E+00	AW006022.1	EST_HUMAN	wz91h01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2 CE11040 ZINC FINGER, C2H2 TYPE ;
11853	25871	38537	2.73	0.0E+00	BF002333.1	EST_HUMAN	7h22b10.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458 TRIO. ;
11864	24852	38548	1.32	0.0E+00	C06264.1	EST_HUMAN	C06264 Human pancreatic islet Homo sapiens cDNA similar to insulin receptor
11868	24856		1.56	0.0E+00	BE727811.1	EST_HUMAN	601564180F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833730 5'
11872	24860	38555	2.36	0.0E+00	AI472010.1	EST_HUMAN	tj80a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2147802 3' similar to gb:M31661 PROLACTIN RECEPTOR TYPE 2 PRECURSOR (HUMAN);
11878	24866	38563	2.84	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
11878	24866	38564	2.84	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
11889	24877		1.8	0.0E+00	AW863777.1	EST_HUMAN	MR3-SN0010-310300-107-h03 SN0010 Homo sapiens cDNA
11901	24889	38589	3.67	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11901	24889	38590	3.67	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11907	24894	38596	4.38	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
11911	24898	38600	26.74	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11911	24898	38601	26.74	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11917	24903	38606	4.87	0.0E+00	AW500056.1	EST_HUMAN	UI-HF-BN0-akl-b-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077332 5'
11932	24918	38621	2.05	0.0E+00	BE794758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11934	24920	38622	65.18	0.0E+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11935	24921	38623	1.6	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11941	24927	38629	1.38	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
11941	24927	38630	1.38	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
11946	24932	38635	1.68	0.0E+00	AF053543.1	NT	Homo sapiens glutathione transferase zeta 1 (GSTZ1) gene, exons 6 and 7
11953	24939	38642	7.29	0.0E+00	BE409993.1	EST_HUMAN	601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
11954	24940	38643	2.22	0.0E+00	BE148650.1	EST_HUMAN	MR0-HT0241-150500-011-f02 HT0241 Homo sapiens cDNA
11955	24941	38644	2.89	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11955	24941	38645	2.89	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11956	18785	31831	1.48	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
11956	18785	31832	1.48	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
11958	24943	38647	11.38	0.0E+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'
11958	24943	38648	11.38	0.0E+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'
11964	24949	38655	1.79	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP4000929 5'
11967	24952	38657	4.99	0.0E+00	BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
11983	24968	38671	1.56	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11983	24968	38672	1.56	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11986	24971	38675	3.4	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11986	24971	38676	3.4	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11998	24983		1.96	0.0E+00	BE906402.1	EST_HUMAN	601498553F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900396 5'
12013	24997	38700	1.46	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12028	25872		8.57	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
12029	25012	38713	2.37	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
12029	25012	38714	2.37	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
12032	25015	38717	60.96	0.0E+00	BE297175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532968 5'
12046	25027	38733	1.42	0.0E+00	BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12046	25027	38734	1.42	0.0E+00	BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12054	25035	38741	2.02	0.0E+00	BE257612.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'
12054	25035	38742	2.02	0.0E+00	BE257612.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12084	25064	38770	2.85	0.0E+00	BE545535.1	EST_HUMAN	601070391F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456407 5'
12087	25067	38773	1.34	0.0E+00	AA399001.1	EST_HUMAN	zt93e01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729912 5' similar to SW:PMT1_SCHPO P40999 DNA METHYLTRANSFERASE PMT1 ;
12088	25068	38774	1.55	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
12088	25068	38775	1.55	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
12091	25071	38778	1.72	0.0E+00	BE780453.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12108	25088	38792	2.15	0.0E+00	AW269990.1	EST_HUMAN	xv46h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816213 3' similar to gb:L11706_cds1 HORMONE SENSITIVE LIPASE (HUMAN);
12118	25098	38803	1.99	0.0E+00	AU132394.1	EST_HUMAN	AU132394 NT2RP3 Homo sapiens cDNA clone NT2RP3004339 5'
12131	25111	38815	1.35	0.0E+00	BE292840.1	EST_HUMAN	601105652F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988325 5'
12147	26185	31540	9.34	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
12160	26005		3.02	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12162	26013		5.49	0.0E+00	AI190993.1	EST_HUMAN	qe17b12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
12172	25134		3.73	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12192	25149		6.87	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12194	25151		1.35	0.0E+00	AB016195.1	NT	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)
12201	25156		3.2	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12220	26170		4.95	0.0E+00	5802973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
12254	25973	31767	1.47	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12267	25983		3.47	0.0E+00	AL041931.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434K0819 5'
12295	26146		3.39	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
12304	25222		4.77	0.0E+00	AL046544.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218 5'
12317	26017		2.92	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
12356	26172		1.88	0.0E+00	N54484.1	EST_HUMAN	yv40e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;
12371	25265		4.08	0.0E+00	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
12374	14042	27106	5.36	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12374	14042	27107	5.36	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12383	26021		3.07	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
12415	13754		4.88	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12450	25781	31937	3.95	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12510	25950	31765	1.64	0.0E+00	AW590082.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
12542	25982		1.34	0.0E+00	L20493.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
12573	26015		2.73	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12618	25416		4.61	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12638	25429		1.19	0.0E+00	AV720678.1	EST_HUMAN	AV720678 GLC Homo sapiens cDNA clone GLCEPG09 5'
12660	26009		3.51	0.0E+00	AI204914.1	EST_HUMAN	an05h04.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12694	25462		1.33	0.0E+00	AI904646.1	EST_HUMAN	QV-BT065-020399-103 BT065 Homo sapiens cDNA
12702	26006		2.29	0.0E+00	BE439792.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
12714	15187	28297	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12714	15187	28298	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12739	25490	32027	1.21	0.0E+00	AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12751	14869	27960	3.26	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12751	14869	27961	3.26	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12755	13979	27031	1.6	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12766	25509		33.13	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
12771	25514	31997	5.44	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12771	25514	31998	5.44	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12776	25518		7.88	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12798	15294	28420	1.7	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12837	25557		2.11	0.0E+00	AW664999.1	EST_HUMAN	hl86e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979154 3'
12847	25563	31988	1.43	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12892	14409	27471	1.74	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
12927	16558	29573	3.11	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12935	18494	31532	2.3	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12938	25617		1.88	0.0E+00	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
12981	25639	31983	1.82	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
13010	26197		2.93	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
13017	13828	26851	2.46	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13113	25726	31943	1.17	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
13116	25728		1.4	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13119	25731		3.11	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
13140	25740		5.96	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
13151	26207		1.16	0.0E+00	AW505176.1	EST_HUMAN	UI-HF-BN0-aly-g-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081399 5'
13190	25774		1.51	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
13209	16135	29151	1.37	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13209	16135	29152	1.37	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13215	14345	27402	1.29	0.0E+00	9966844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

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CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.

3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.

4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,233 - 26,232.

5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.

6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.

7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,232 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human placenta.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,233 - 26,232 or a complementary sequence or a fragment thereof.

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human placenta.

16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample derived from human placenta, comprising:

contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

24. A method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence according to the method of claim 23; and then

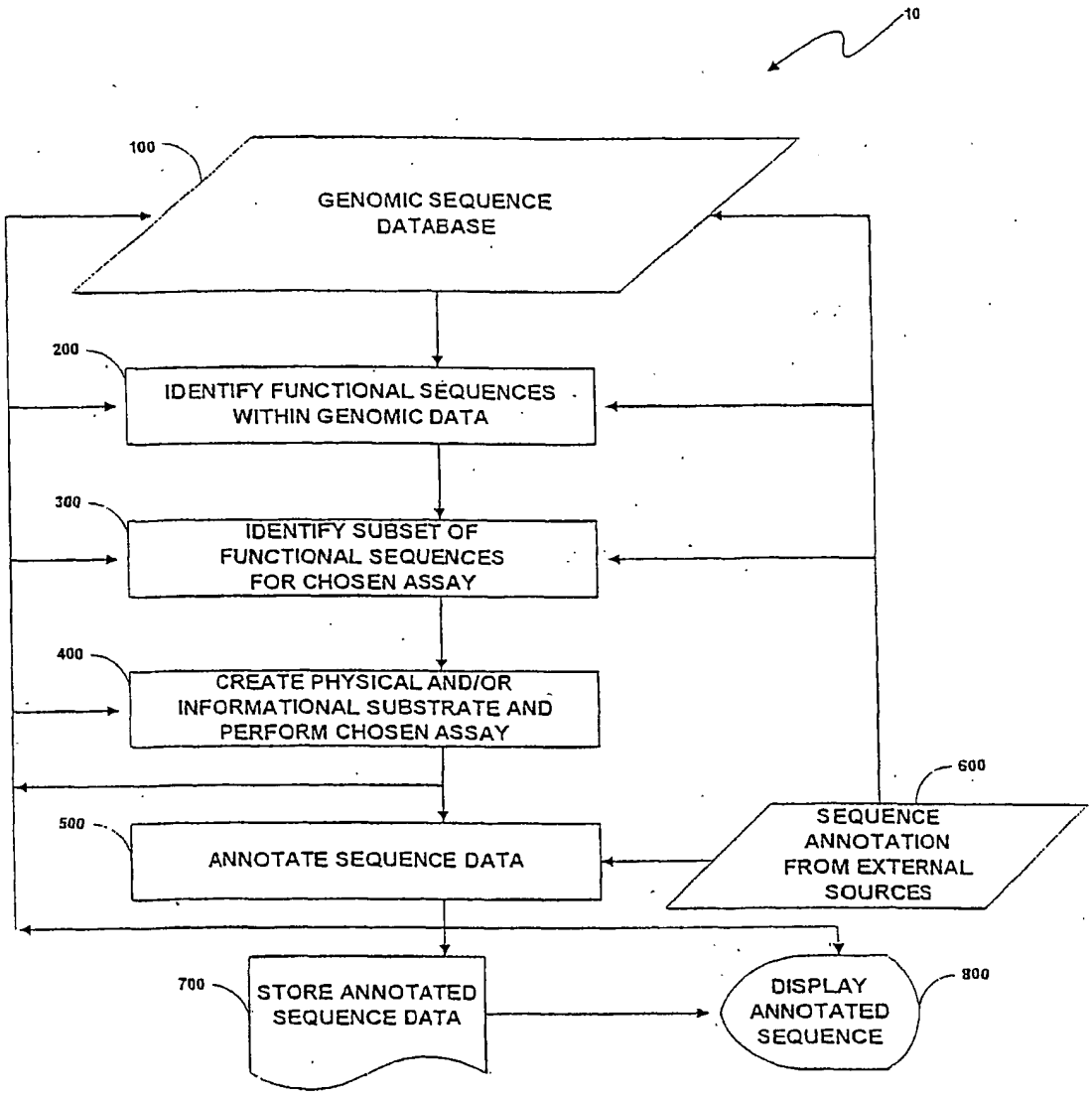
measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 26,232 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 26,232.

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 26,233 - 38,837.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400
CREATE PHYSICAL AND/OR INFORMATIONAL SUBSTRATE AND PERFORM CHOSEN ASSAY
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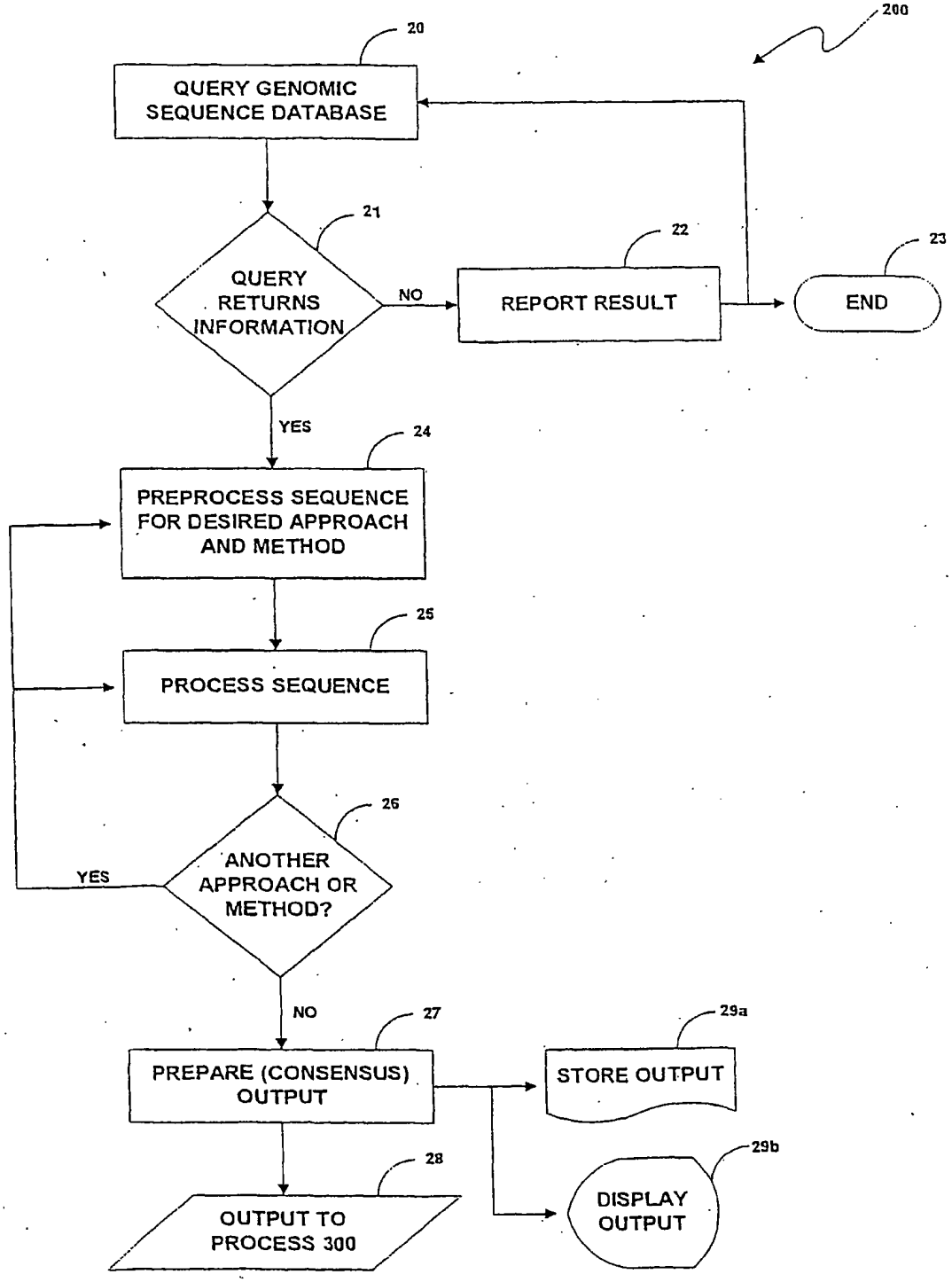
600
SEQUENCE ANNOTATION FROM EXTERNAL SOURCES
700
STORE ANNOTATED SEQUENCE DATA
800
DISPLAY ANNOTATED SEQUENCE

Fig. 1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22
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23
END
YES
24
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25
PROCESS SEQUENCE
26
ANOTHER APPROACH OR METHOD?
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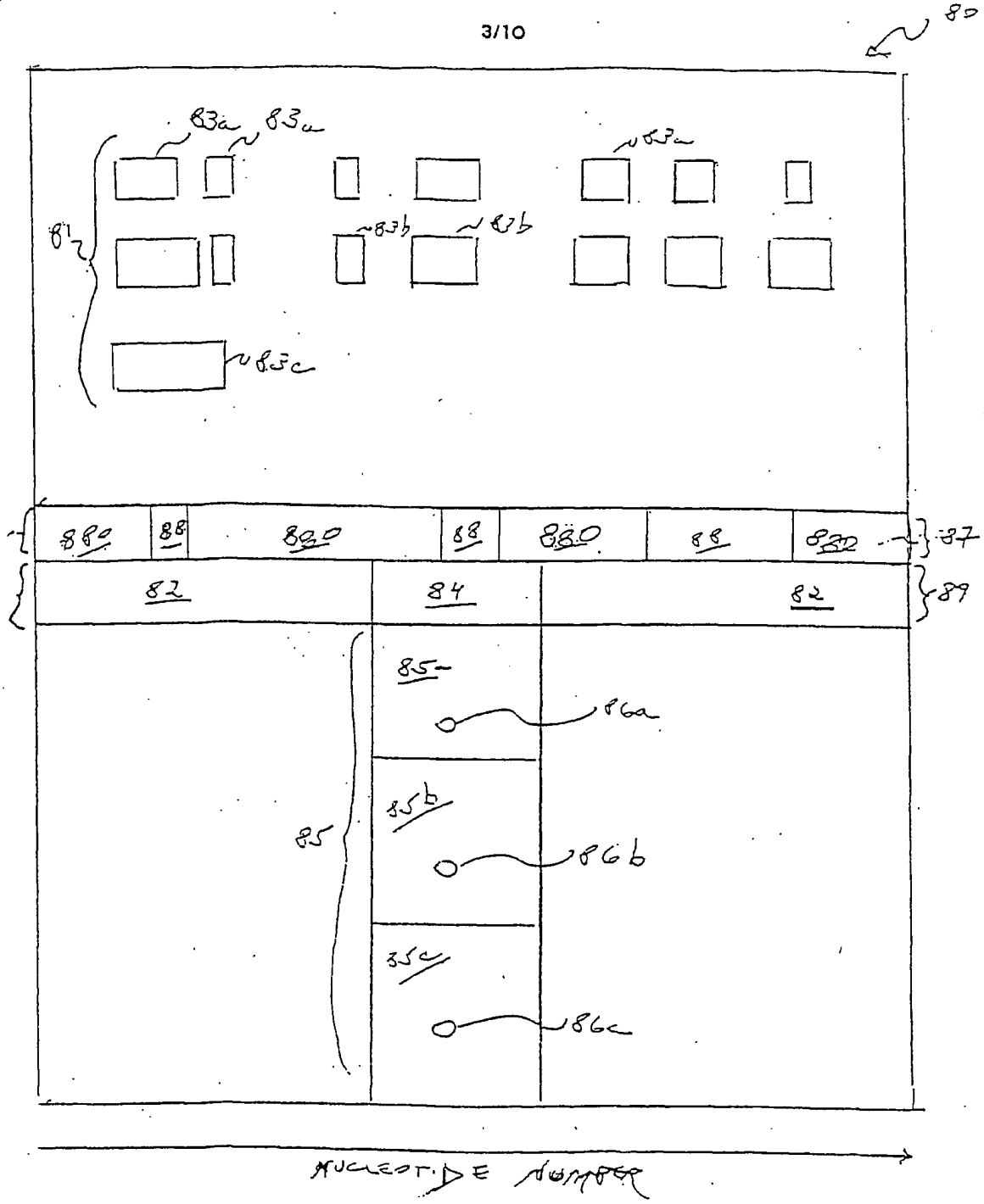
STORE OUTPUT
28
OUTPUT TO PROCESS 300
29b
DISPLAY OUTPUT

Fig. 2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83b
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82
84
82
89
85
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86a
85b
86b
85
85c
86c
NUCLEOTIDE NUMBER

Fig. 3

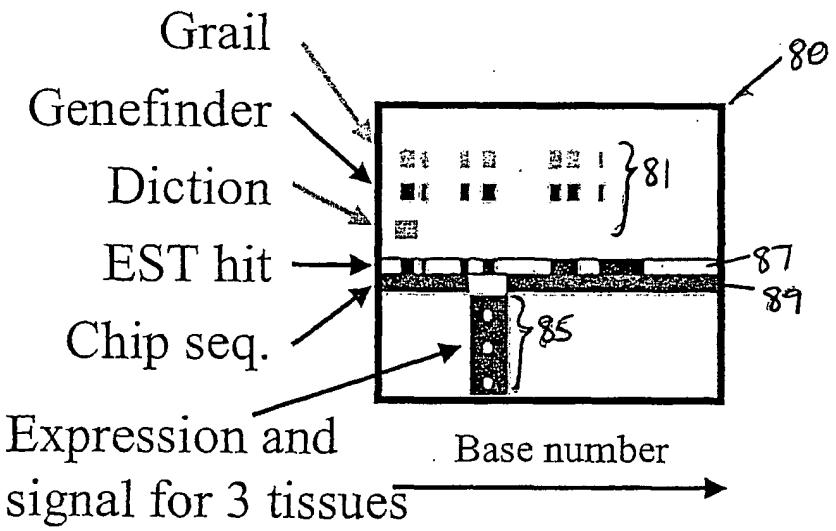
Grail
Genefinder
Diction
EST hit
Chip seq.
Expression and signal for 3 tissues
Base number
80
81
87
89
85

Fig. 4

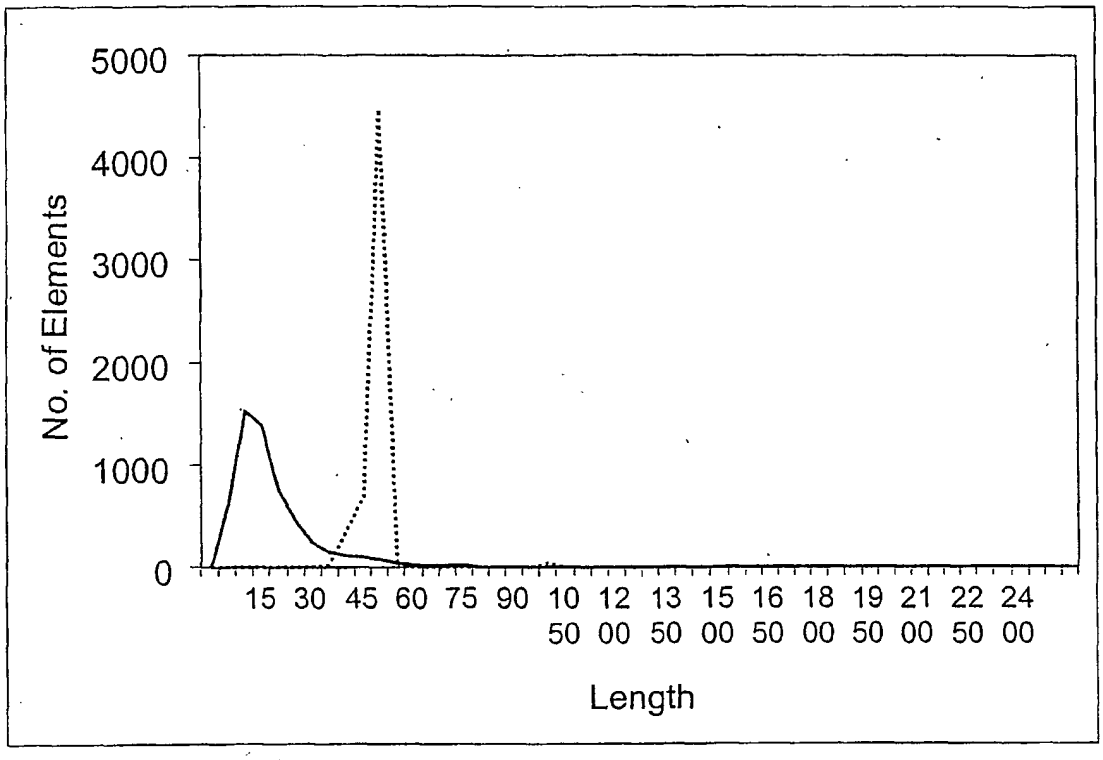
5000
4000
3000
2000
1000
0
No. of Elements
15 30 45 60 75 90 10 50 12 00 13 50 15 00 16 50 18 00 19 50 21 00 22 50 24 00
Length

Fig. 5

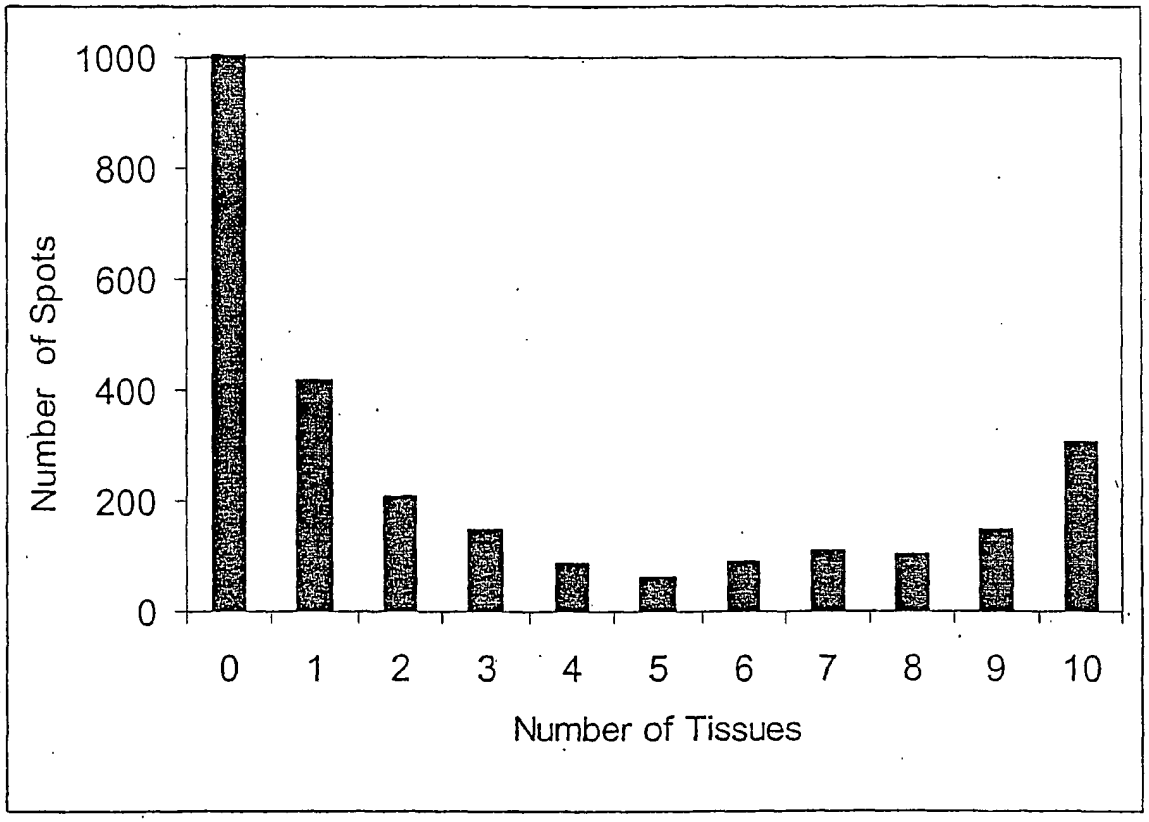
1000
800
600
400
200
0
Number of Spots
0
1
2
3
4
5
6
7
8
9
10
Number of Tissues

Fig. 6

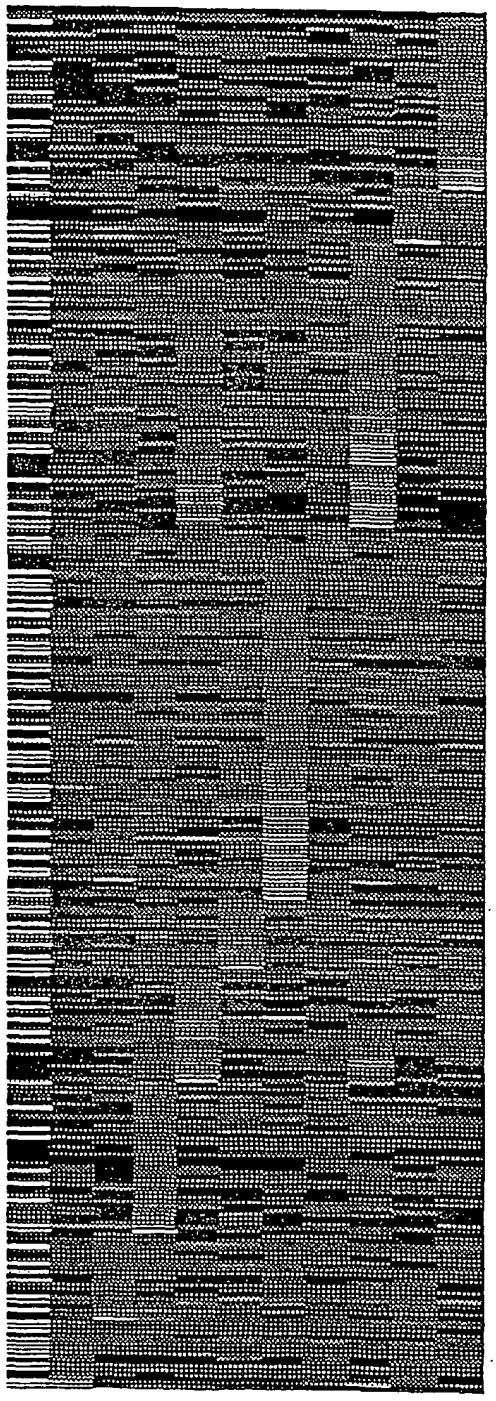

Fig. 7a

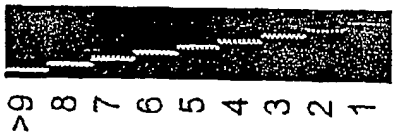

Fig. 7b

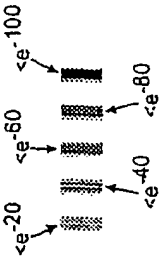

Fig. 7c

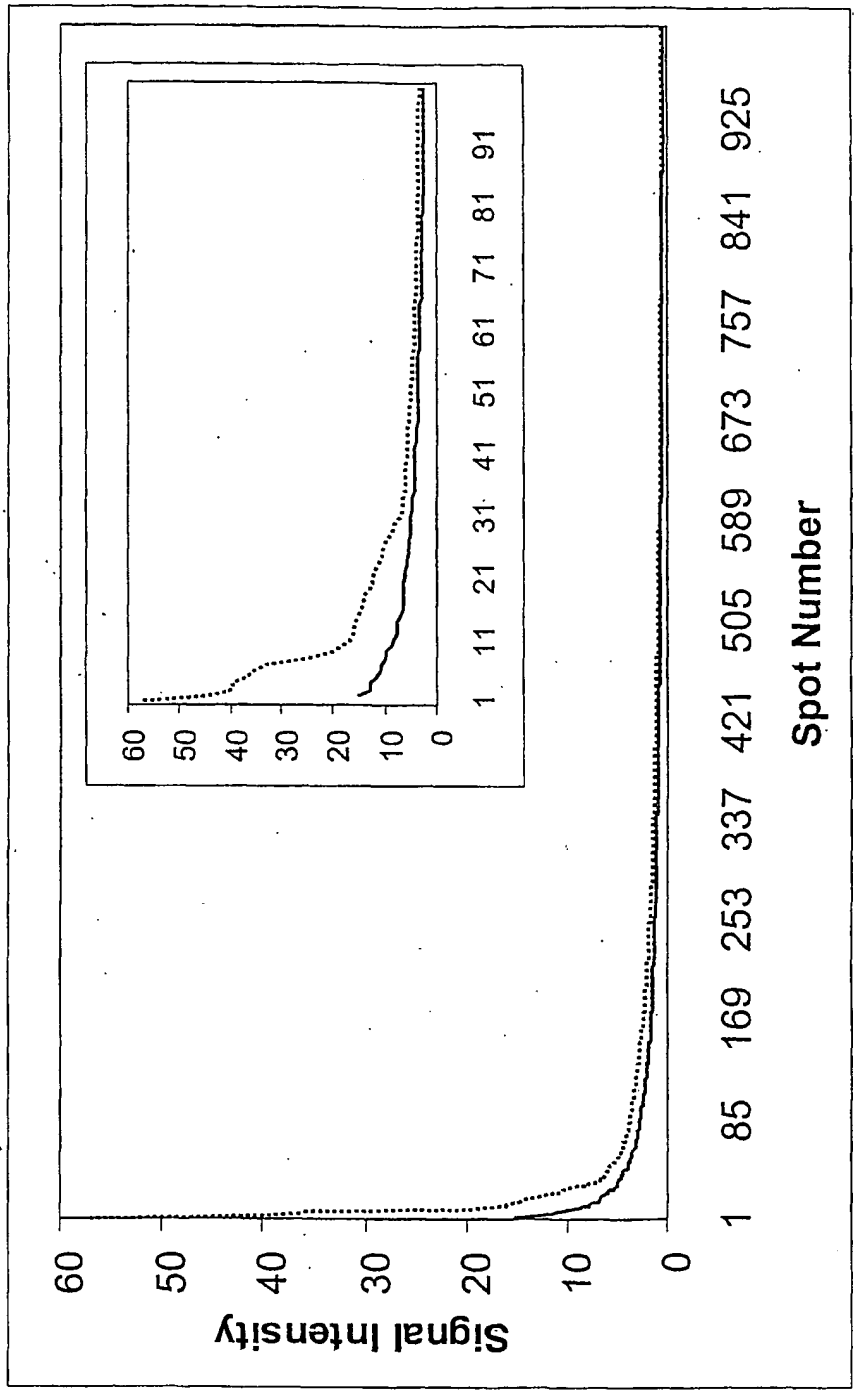
Signal Intensity
0
10
20
30
40
50
60
1
85
169
253
337
421
505
589
673
757
841
925
Spot Number
0
10
20
30
40
50
60
1
11
21
31
41
51
61
71
81
91

Fig. 8

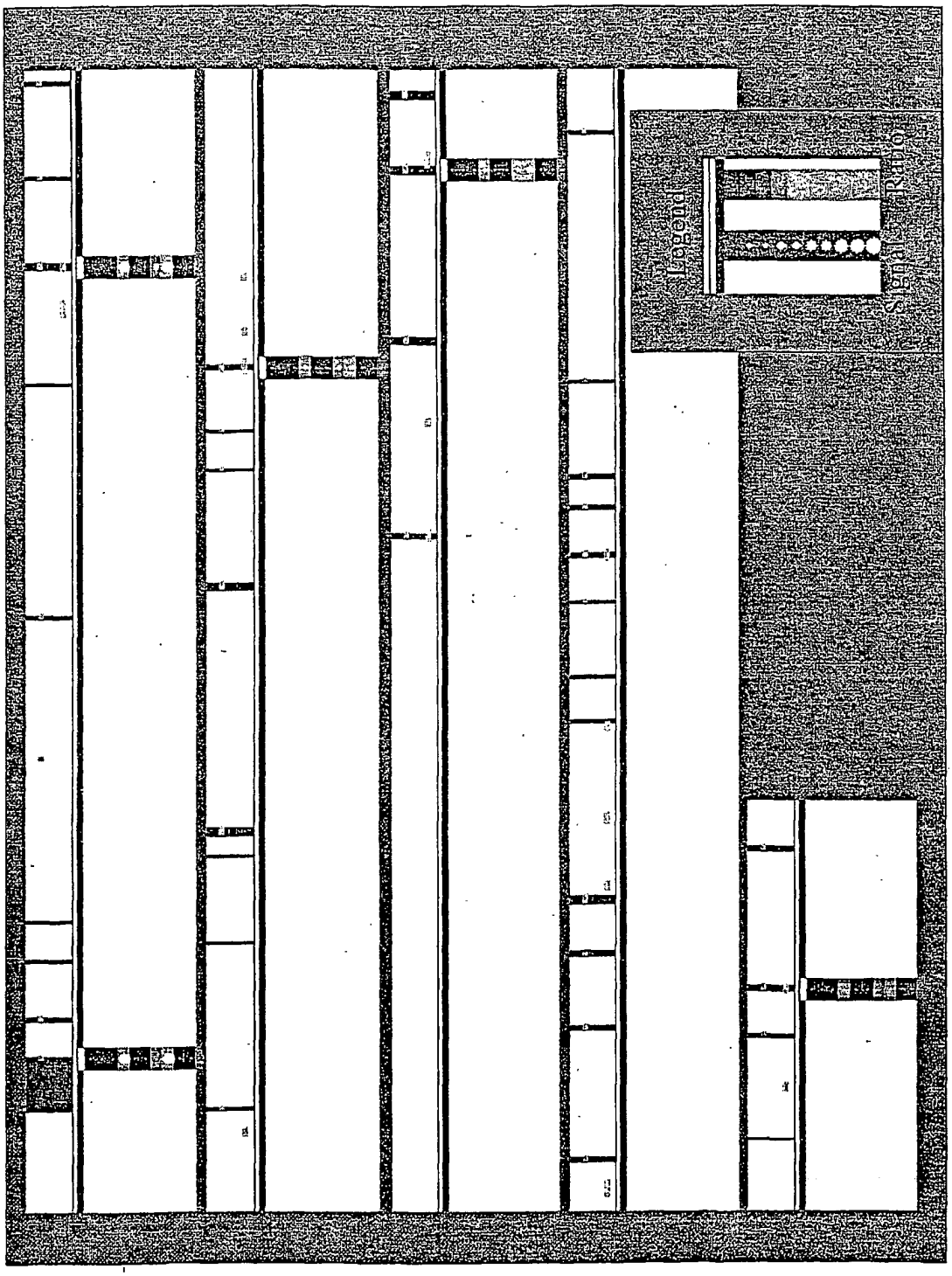

Fig. 9
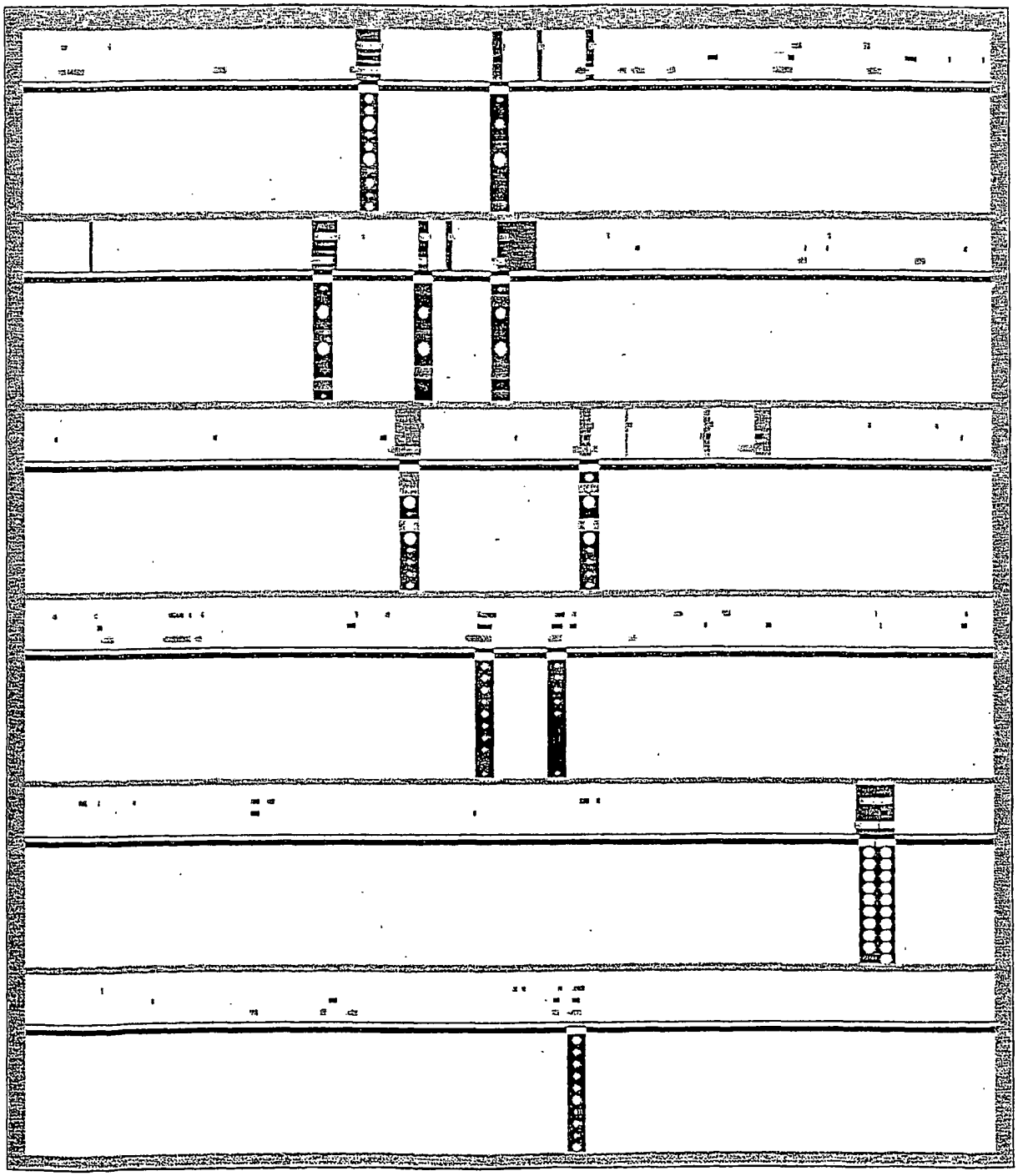
Fig. 10